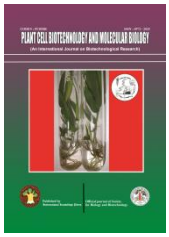

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Unraveling Genetic Variability, Correlation and Path Analysis for Yield and Its Components in Barley (*Hordeum vulgare* L.)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The current study aimed to assess the genetic variability of yield and yield-related traits while examining the direct and indirect effects of trait interactions. Conducted at a research farm in Chaudhary Charan Singh University, Meerut, Uttar Pradesh, India, the experiment involved fourteen parents and their BC_1F_1 crosses, analyzed using a randomized block design (RBD). Significant differences were observed among the varieties for most traits, indicating a broad range of mean values and diversity. Both phenotypic and genotypic coefficients of variance (PCV and GCV) were generally low, with biological yield showing the highest values (26.57 for GCV and 40.48 for PCV).

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PCV values were slightly higher than GCV values. Traits such as seed per spike, biological yield, flag leaf breadth, days of heading, and days of maturity exhibited relatively high heritability. Notably, grain yield showed high heritability and genetic progress, making it a favourable selection indicator. Several traits, including days of anthesis, days of maturity, and spike length, demonstrated significant positive correlations with yield while also showing significant negative correlations with grain filling period and biological yield. Conversely, these traits showed highly non-significant positive correlations with harvest index, plant height, thousand seeds weight, and chlorophyll content and highly non-significant negative correlations with tiller number and seeds per spike.

Keywords: Genotypic and phenotypic variance; heritability; coefficient; variability.

ABBREVIATIONS

DTH : Days to Heading,
DTA : Date of 50% Anthesis,
DTM : Date of Maturity,
GFD : Grain Filling Period,
APH : Average Plant Height,
FL : Flag Leaf Length,
FW : Flag Leaf Width,
SL : spike Length,
ATN : Average Tiller Number,
NG : No. of Grains per Spike,
BY : Biological Yield,
GER : Germination Percentage,
CC : Chlorophyll Content,
GY : Grain Yield,
TGW : Thousand-grain Yield,
HI : Harvest Index,
& : And,
% : Percent,
SEm : Standard Error of Mean,
CV : Critical Variance (5%),
CD : Critical Difference (1%),
GCV : Genotypic Coefficient of Variance,
PCV : Phenotypic Coefficient of Variance,
Heri. (BS) : Heritability (Broad Sense),
GA : Genetic Advance

1. INTRODUCTION

Barley belongs to the genus *Hordeum* and Poaceae family [1,2]. 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 significant cereal crop [3,4]. It is a commercially significant cereal crop, ranking fourth in the world after wheat, rice, and maize in quantity produced and cultivated area *(FAO, 2014).* Barley is native to the Eastern Mediterranean, where plants are subjected to various abiotic stresses in the field. It is grown in many places where the climate could be more favourable. Though it has a lower commercial value than wheat, it replaces 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 [5]. 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. Cultivated and wild barley have fourteen chromosomes (2n=14) and are diploid species. *Hordeum vulgare* L [6]. It is the only cultivated species with two phenotypic variants, six-rowed *(Hordeum vulgare, H. hexasstichum)* and two-rowed *(Hordeum vulgare, H. hexasstichum) (H. distichum).* They have the same chromosomal number (2n=14) and may intercross freely to create fertile hybrids despite their spike morphological variances [7,8]. Barley contains a great deal of genetic variety used to classify the species. There are many different methods to categorize barley. Identifying whether the spike has two, four, or six rows of spikelet's is one technique to classify barley. Most cultivated barley has six rows, while wild barley has two.

2. MATERIALS AND METHODS

2.1 Experimental Site, Data Collection, Material and Procedures

The experimental material for the present study was obtained from *Eternal University, Baru Sahib, 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*

Table 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	Hull less 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 andanthocyanin 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

Campus, Meerut (UP) during the year 2020-2021, 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 randomly selected from each plot in the middle three rows. 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.

2.2 Statistical Analysis

Analysis of variance was performed using the plant breeding statistical program SPSS software. The genotypic and phenotypic variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense (h2b), genetic advance in percentage of mean (GA), genotypic correlation coefficients (rg) and phenotypic correlation coefficients (rp), genotyping and phenotyping path analysis were estimated following [9]. The estimates of the Genetic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) were categorized into low, medium, and high according to the classification proposed by Sivasubramanian and Madhavamenon in 1973 [10]. Heritability in a broad sense and genetic advance were calculated according to methods given by [11,9]. Path coefficient analysis was done using R software.

3. RESULTS AND DISCUSSION

Creating genetic variability and selecting key traits are crucial activities every plant breeder should undertake to enhance yield and other desirable agronomic characteristics. However, to effectively select, it is essential to have information on the available genetic variation among barley genotypes. Thus, effective selection depends not only on estimating genetic variation among genotypes but also on the proportion of heritable variation and the expected genetic gain that would be obtained [12,9]. Heritable variation is helpful for permanent genetic improvement [9]. Heritability broadly estimates the ratio of total genetic variance, including additive, dominant and epistatic variances to the phenotypic variance [12,13].

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 and 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 the 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 per cent, 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 2).

The highest GCV (26.57) and PCV (40.48) estimates for grain yield should have a 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 the role of environmental variation for GCV and PCV estimates, thus having sufficient genetic variability for the improvement of these traits [2]. Some traits like the number of plants germinated, seeds per spike, thousand seeds weight, and average flag leaf length also had moderate values for GCV and PCV estimates, thus having sufficient genetic variability to improve these traits [14]. A meagre 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.2) showed the tiny scope of improvement in the genotypes for these traits and similar results also reported by Yadav et al., [15].

Heritable variation is helpful for permanent genetic improvement [15]. Heritability broadly estimates the ratio of total genetic variance, including additive, dominant and epistatic variances, to the phenotypic variance [12,16,13]. The Highest heritability, along with the highest genetic advance, was recorded for biological yield, seeds per spike, thousand seeds weight and average plant height, similar results reported by [17] (Table 2 & Fig. 1). Hence these traits are under control for additive genes. These can be improved by selection based on phenotypic performance.

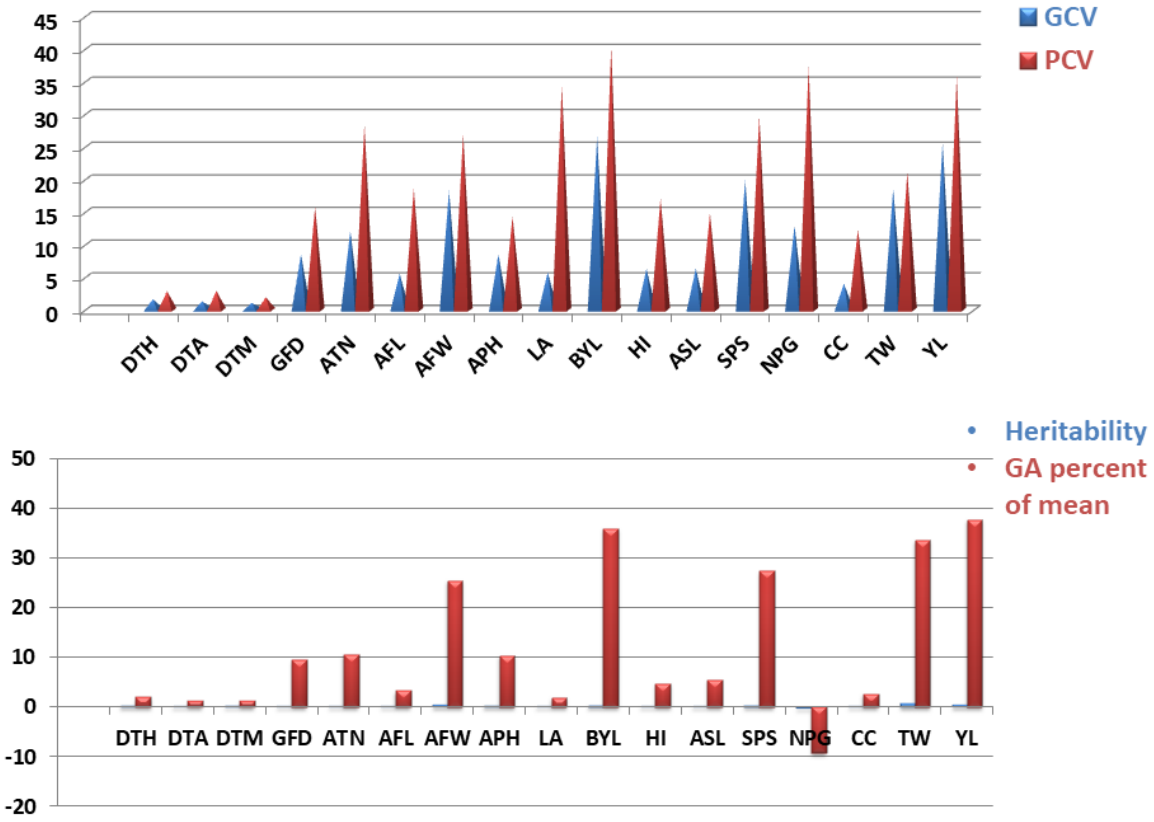

Fig. 1. Estimation of genetic variability (GCV, PCV and Heritability)

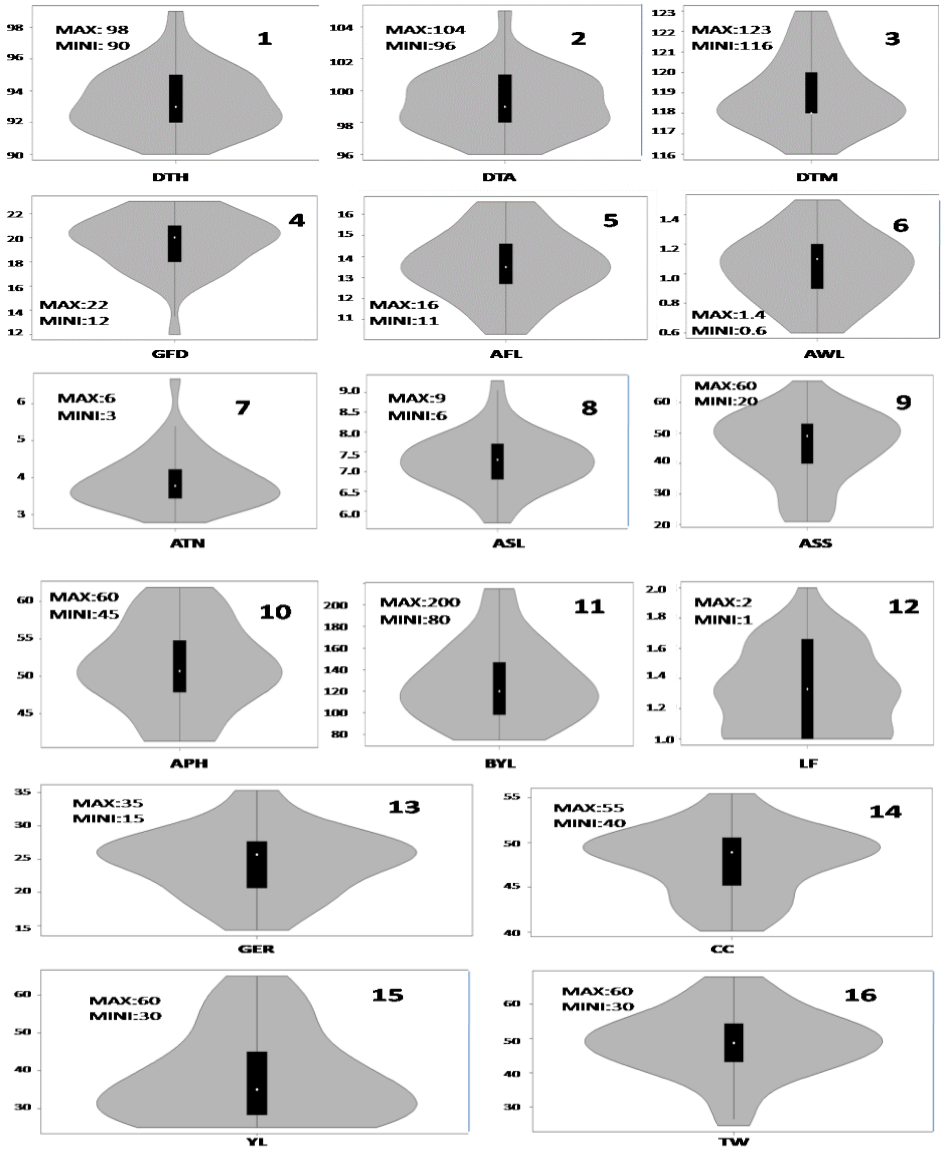

Fig. 2. Violin plot (A box or marker indicating the inter quartile range; and possibly all sample points for 16 different traits)

3.1 Estimations of Genotypic and Phenotypic Correlation

The study identified significant correlations among various growth and yield-related traits in the crop. Days to 50% heading were positively correlated with days of anthesis and spike length but showed a non-significant positive correlation with days of maturity. Conversely, they were negatively correlated with grain filling period, flag leaf length, seeds per spike, chlorophyll content, and biological yield. Day 50 anthesis was positively correlated with spike length and non-significantly correlated with maturity, tiller number, plant height, harvest index, and thousand seed weight but negatively correlated with grain filling period, flag leaf length, seeds per spike, and chlorophyll content. Additionally, traits such as days of maturity, spike length, and days to 75% maturity were positively correlated with days of anthesis and spike length and non-significantly correlated with days to maturity. Plant height, tiller number, and biological yield also displayed significant positive correlations with certain traits but showed negative correlations with others. These findings highlight complex trait interactions, which can inform breeding strategies for improving crop yield and quality.

Table 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

Traits	Range		SEm	GV	PV	GCV	PCV	Heri. (BS)	G. advance	GA as % of mean
	Maxi.	Mini.								
DTH	101	89	1.25	2.46	7.13	1.63	2.86	0.34	1.9	2.03
DTA	105	93	1.47	1.7	8.2	1.32	2.89	0.21	1.22	1.23
DTM	126	114	1.1	1.67	5.29	1.09	1.93	0.32	1.5	1.26
GFD	26	9	1.51	2.79	9.63	8.48	15.76	0.29	1.85	9.41
ATN	9	2	0.58	0.23	1.24	12.09	28.33	0.18	0.42	10.62
AFL	23.63	8	1.39	0.56	6.35	5.52	18.58	0.09	0.05	3.37
AFW	1.73	0.4	0.12	0.04	0.08	18.24	26.93	0.46	0.27	25.45
APH	75.7	35.33	3.42	19.1	54.21	8.47	14.27	0.35	5.34	10.36
LA	2	1	0.27	0.01	0.22	5.77	34.4	0.03	0.03	1.97
BYL	240	45	19.27	843.26	1956.7	26.57	40.48	0.43	39.27	35.93
HI	41.18	16.12	2.48	2.91	21.31	6.29	17.03	0.14	1.3	4.79
ASL	11	4.67	0.56	0.21	1.14	6.3	14.75	0.18	0.4	5.54
SPS	74.66	14	5.92	84.42	189.58	19.88	29.79	0.45	12.63	27.33
NPG	40	3	5.69	-10.44	86.69	12.92	37.23	-0.12	-2.31	-9.24
CC	65.1	32.9	3.23	3.62	34.9	3.96	12.31	0.1	1.26	2.63
TW	72	22.1	2.83	81.74	105.72	18.58	21.14	0.77	16.38	33.66
YL	75	25	5.63	99.61	194.85	25.59	35.79	0.51	14.7	37.69

Table 3. Genotypic correlation and phenotypic correlation

Traits	DTH	DTA	DTM	GFD	ATN	AFL	AFW	APH	BYL	HI	ASL	SPS	CC	TW	YL
DTH	1**	0.96**	0.10N	-0.67**	0.18NS	-0.69**	-0.19NS	0.23NS	-0.02NS	0.08NS	0.46**	-0.36**	-0.49 **	0.13 NS	-0.06NS
DTA	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 *	0.20 NS	0.04 NS
DTM	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	0.12 NS	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 NS	0.61 **	0.39 *	0.10 NS	0.34 *
ATN	-0.03 NS	-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 **	0.09 NS	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	-0.02 NS	0.32 NS	0.53 **
AFW	-0.07 NS	0.01NS	0.04 NS	0.01 NS	-0.04 NS	0.50 **	1 **	-0.23 NS	0.27 NS	-0.01NS	0.47 **	0.43 **	0.13 NS	0.11 NS	0.32 NS
APH	0.10 NS	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 **	-0.05 NS	-0.37 *	0.65 **
BYL	-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 *	-0.21 NS	0.95 **
HI	0.06 NS	0.06 NS	-0.0 NS	-0.11 NS	-0.05 NS	9e-04 NS	-0.06 NS	-0.17 NS	-0.47 **	1 **	0.46 **	-0.63 **	-0.06 NS	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	-0.31 NS	-0.06 NS	0.31 NS
SPS	-0.11 NS	-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 **	-0.08 NS	-0.43 **	0.72 **
CC	0.01 NS	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**	0.01 NS	0.35 *
TW	0.08 NS	-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 *	0.03 NS	1**	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 **	-0.03 NS	-0.03 NS	1**

Table 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 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

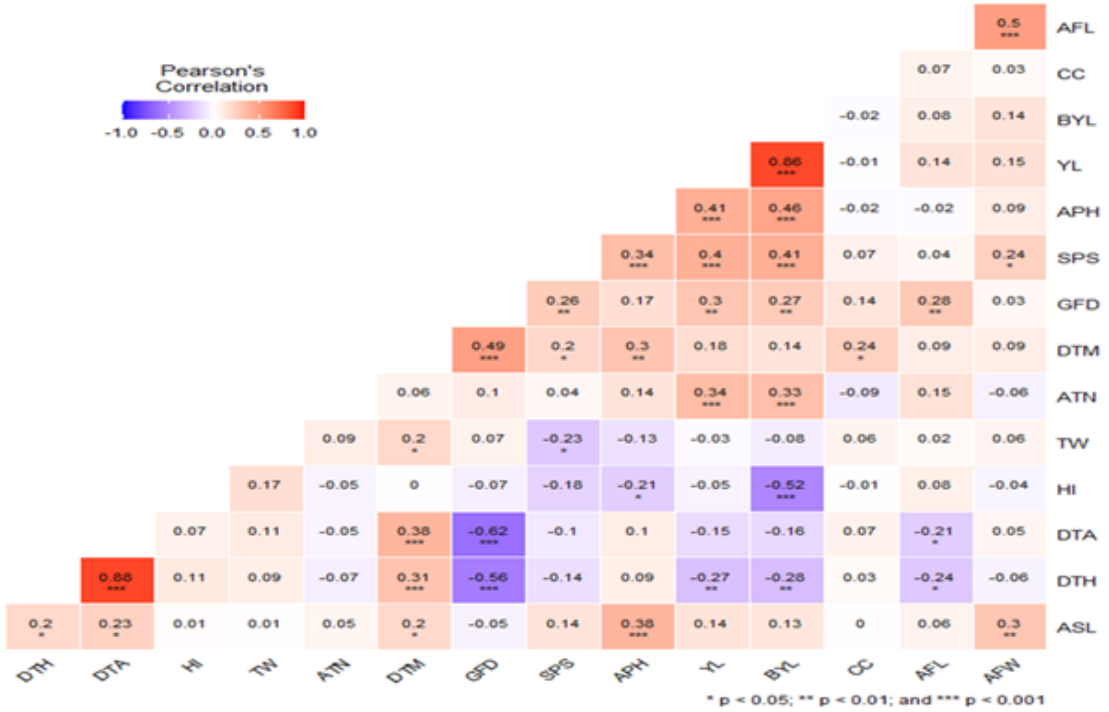

Fig. 3. Pearsons correlation

3.2 Path Coefficient Analysis

Phenotypic and Genotypic path coefficient analysis is presented in Tables 4 & 5. The direct impact of characters on grain yield revealed that their relationships significantly contributed to the final grain yield, making them pivotal factors in enhancing grain production. Genotypic correlation coefficients were partitioned using the path analysis method to determine the direct and indirect effects of yield contributing traits towards grain yield. Path analysis (Tables 4 & 5) revealed that the highest positive direct effect and genotypic correlation with grain yield were 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 [18,10]. Plant height, thousands of seeds weight, spike length, flag leaf width, adequate tiller number and chlorophyll content had a negative direct effect with significant genetic correlation with grain yield.

On the other hand, days to heading had a positive indirect effect with anthesis, maturity, flag leaf width, harvest index, chlorophyll content and adverse indirect effects with grain filling period, tiller number, flag leaf length, plant height, biological yield, spike length, thousands seeds weight. The residual effect of the present study was -0.0055, indicating that about 98 per cent of the variability in grain yield might be contributed by these 16 yield-contributing traits studied in the path analysis. This gives the impression that some other minor characters than those involved in the present study also contributed to the variability of grain yield [19-21].

4. CONCLUSION

The current investigation, titled "Genetic Variability, Heritability, Correlation, and Path Coefficient Studies for Yield and Yield-Related Components of Selected Barley Cultivars and Crosses (*Hordeum vulgare* L.)," aimed to conduct phenotypic characterization and assess divergence among various 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 Mean, Range (Minimum and 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. A Higher genotypic coefficient of

variation was found in no. Biological yield, grains yield, followed by seed per spike, average flag leaf width, thousand grains yield and higher phenotypic coefficient variation were found in biological yield and followed by grains yield, average flag leaf width, leaf area, and germination percentage, respectively. Genetic advance is highest in biological yield followed by seeds per spike, thousand-grain yield and grains yield (Table 2). Therefore, a correlation study revealed that days to anthesis, average spike length showed a strong positive association with biological yield, grain yield per genotype and grain filling period, average flag leaf length, seeds per spike and chlorophyll content showed a negative association with many traits. Therefore, the obtained results indicate the presence of sufficient genetic variability for the studied traits, showing that genotypes are suitable for breeding purposes.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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