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


## 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 $BC_1F_1$ 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.



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


## 1. Introduction

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

*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 *(Hordeumvulgare 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 ofHordeum 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. 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 *(Poehlman, 1987)*. Barley contains a lot of genetic variety, which is used to classify the species. There are many different methods to categories 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 categories barley is to look at how the beards (awns) connect to the kernels.

## 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 laboratoryofDept.ofGeneticsandPlantBreedingC.C.S. UniversityCampus, Meerut(UP)during theyear2019-2020, 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), thousandgrain yield (TGW), Harvest index (HI), wereused for assessing the genetic diversity and characters association among these genotypes ofbarley.

**Table no. 1: Alist ofbarleycultivarusedforevaluation andcrossinginthepresentstudy**

| S.No. | Nameofcultivar/ varieties | 2rows/ 6rows | Remarks |
|---|---|---|---|
| 1. | IITR-39 | 6rows | Hulllessbarley |
| 2. | PL-830 | 6rows | Hulledbarley |
| 3. | PL-172 | 6rows | Hulledbarley |
| 4. | PL-707 | 6rows | Hulledbarley |
| 5. | PL-419 | 6rows | Hulledbarley |
| 6. | PL-751 | 6rows | Hulledbarley |
| 7. | PL-426 | 6rows | Hulledbarley |
| 8. | PL-758 | 6rows | Hulledbarley |
| 9. | IITR-104 | 6rows | Hulledbarley |
| 10. | IITR-38 | 2rows | Hulledbarleyanda nthocyaninrich |
| 11. | IITR-35 | 2rows | Hulledbarley |
| 12. | VIJY-102 | 2rows | Hulledbarley |
| 13. | DWRUB-52 | 2rows | Hulledbarley |
| 14. | PL-838 | 2rows | Hulledbarley |



### 2.2.Statistical analysis

Analysis of variance was performed using the plant breeding statistical programmeSPSS 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 *(Singh and*

*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.

## 3. Results and discussion

Creation of genetic variability and selection for important traits is crucial 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)*.

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), thousandgrain 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), thousandgrain 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 lengthalso 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 maturityharvest 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).*

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.

**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 differenttraits.**

| Traits | 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 |

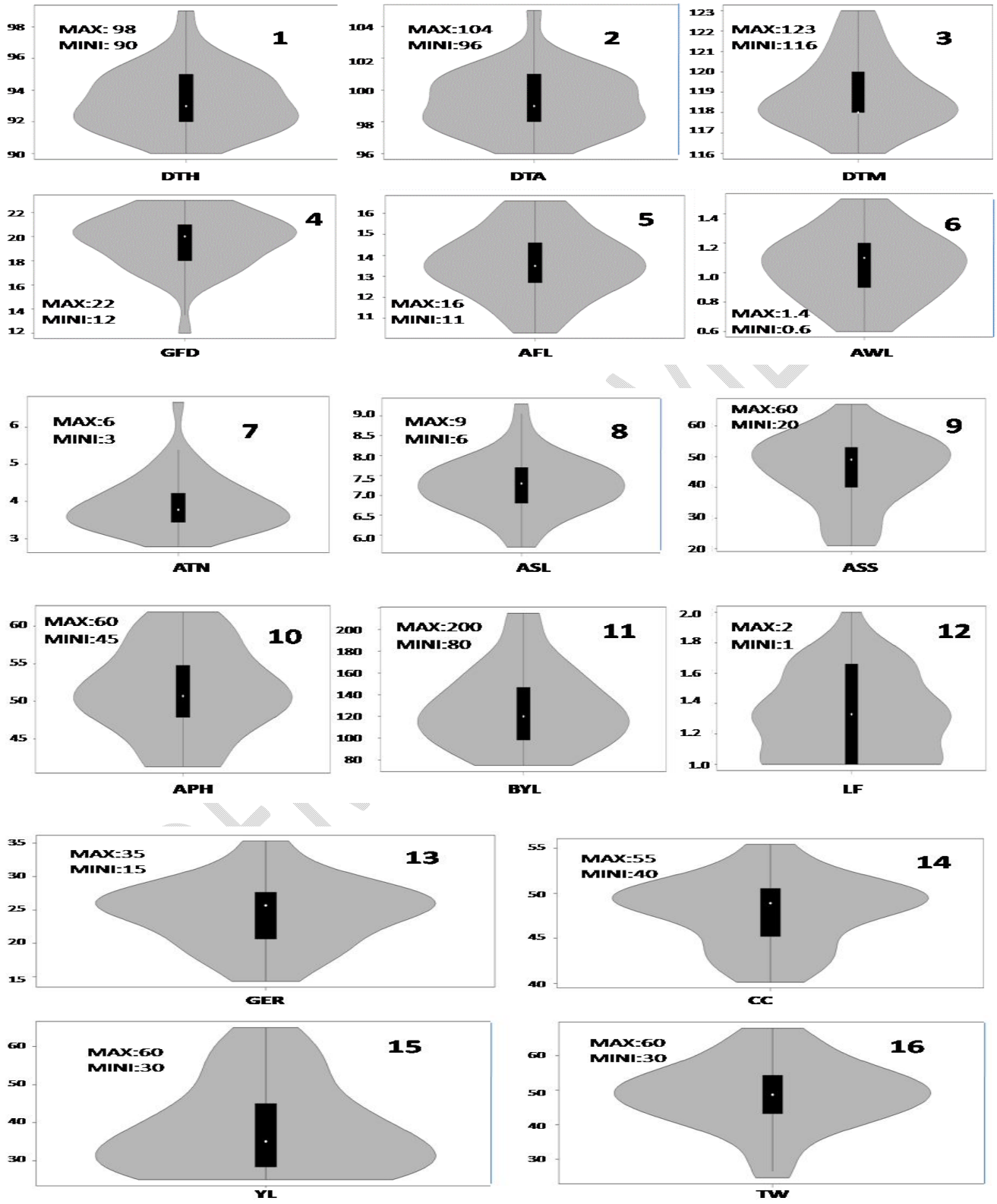
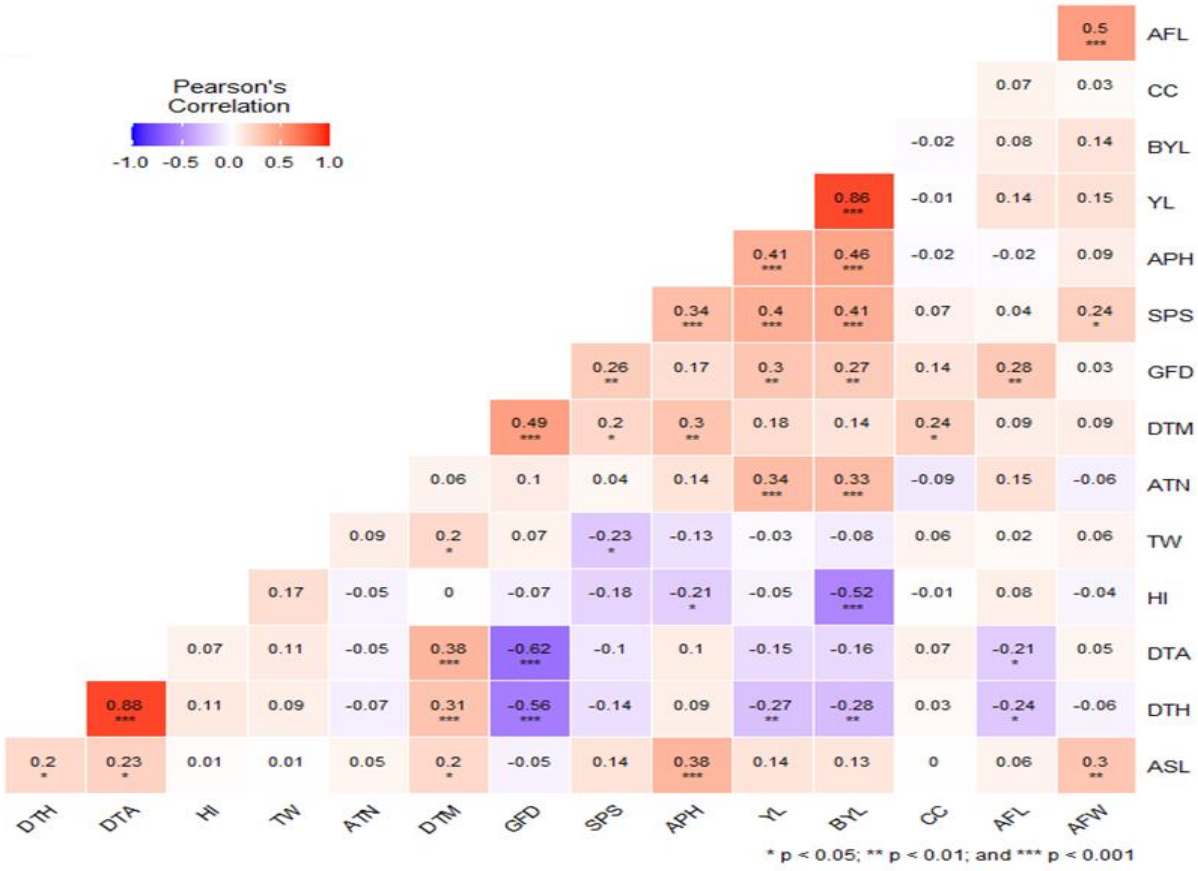



**Figure 1: Violin plot (A box or marker indicating the inter quartile range; and possibly all sample points for 16 different traits).**

**Table no. 2: Genotypic correlation and phenotypic correlation**

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

**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 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.

**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 cultivarsand crosses (*Hordeum vulgare L)*,was undertaken in barley for phenotypic characterization and to evaluate divergence among barley genotypes. Ineachvarietyfiveplantswereselectedforvariousmorphologicalobservations. Phenotypic data for various morphological traits were analyzing, with the help of some statistical tools like ofMean, 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. Highergenotypic 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). Thereforein correlation study revealed that days to anthesis, average spike length showedstrongly positiveassociation with biological yield,grainyieldpergenotype and grain filling period, average flag leaf length, seeds per spike and chlorophyll content showed negative association withmanytraits.Therefore obtained results indicates presence of sufficient genetic variability for the studied traits showing genotypes are suitable for breeding purpose.

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