SAARC J. Agric., 21(2): 15-25 (2023) *DOI: https://doi.org/10.3329/sja.v21i2.69889*

GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS FOR YIELD AND ITS CONTRIBUTING TRAITS IN BARLEY (*HORDEUM VULGARE* L.)

M.S. Kobir[1*], M.H.O. Rashid[2], D. Halder[1], M. Rahman[1], M.S. Akter[1], M.S. Hossain[3], F.A. Nasim[1], S. Paul[1] and K.U. Ahammad[1]

[1]Bangladesh Agricultural Research Institute (BARI), Bangladesh
[2]International Maize and Wheat Improvement Centre (CIMMYT), Bangladesh Office
[3]Bangladesh Rice Research Institute (BRRI), Bangladesh

ABSTRACT

In breeding programs, direct selection based on crop yields is paradoxical due to its complex polygenically inherited nature, that is impacted by its component traits. To determine the degree of relationship between yield and yield components and other traits in nine barley varieties, a field experiment was carried out at the Regional Agricultural Research Station, Jashore during Rabi 2021–2022. For plant height, disease and insect reaction, and grain yield, substantial heritability together with strong genetic progress as a percentage of mean were detected, indicating a prevalence of additive gene action in the expression of these traits. At both the genotypic and phenotypic levels, the correlation coefficient between grain yield was shown to be positively correlated with plant height and thousand grain weight, indicating that an increase in these traits will boost grain production. Both genotypic and phenotypic analysis of the path coefficient demonstrated that plant height and thousand grain weight had a direct positive impact on grain production, highlighting the significance of these parameters as the primary contributors to yield. For the purpose of genetically improving barley yield, a genotype with a higher extent of these qualities could be chosen as a parent from among genotypes that already exist.

Keywords: Genetic variability, Barley, *Hordeum vulgare L.*, Grain yield

INTRODUCTION

Barley (*Hordeum vulgare L.*), a self-pollinating, diploid species with 14 chromosomes ($2n = 2x = 14$) is an early domesticated grain (Zohary and Hopf, 2000). It is considered as an important cereal with a low Glycemic Index (GI 30) rich in beta-glucan, a soluble fibre that aids in lowering blood cholesterol and making it

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[*] Corresponding author: Shahriar1302027@gmail.com

Received: 14.10.2023 *Accepted: 23.12.202*

beneficial for individuals in managing blood glucose levels. Despite its significance, barley exhibits a low national average yield of 244 metric tons per 297 hectares of land, ranking fourth among all grains behind maize, rice, and wheat (Khayer, 2021). This emphasizes the need for genetic improvement to enhance barley crop yield.

Genetic improvement of barley, aimed at achieving better yields under diverse agro-climatic conditions, relies on the presence of genetic variability for various traits (Ahmad et al., 2018). Yield, a multifaceted quantitative trait, is shaped by various contributing factors (Xie, 2015). The complexity of barley yield is well-established as a quantitative variable controlled by pleiotropic genes, strongly influenced by environmental factors, and regulated by a diverse array of traits (Wiegmann et al., 2019). In such intricate scenarios, a selection strategy solely centered on direct yield may be misleading. Instead, valuable insights into character associations and the direct and indirect contributions of each trait to yield, along with the segmentation of correlations into components of direct and indirect effects (Giriraji and Vijayakumar, 1974), prove more beneficial in guiding the selection process.

In genetic studies, it is essential to distinguish between genetic and environmental correlations among characters (Hailu, 2016). Correlation coefficients quantify the magnitude and direction of influences on economic productivity, but relying solely on simple correlation coefficients without considering interactions may misguide breeders (Del Moral et al., 2003; Majumder et al., 2008). Moreover, path analysis the useful statistical tool is used, to calculate the quantitative impact on grain yield through direct and indirect effects, and cause-and-effect relationships within traits (Ahmed et al., 2003; Rajput, 2019; Majumder et al., 2008). This analytical approach aids in formulating effective selection strategies by examining specific factors contributing to correlations (Da Silva et al., 2009).

In establishing a systematic breeding program, understanding genotypes and the range of responses linked to selection for yield and quality is crucial. A population with high variability offers the potential for selection to generate desired characteristics. The current study was undertaken in the Jashore region to elucidate variability, heritability, genetic advancement, character associations, and the path leading to yield for subsequent breeding programs.

MATERIALS AND METHODS

The experiment was established at Regional Agricultural Research Station, BARI, Jashore (23°18' latitude and 89°18' longitude with the altitude of 19 m) (Fig.1) during Rabi season of 2021-22.

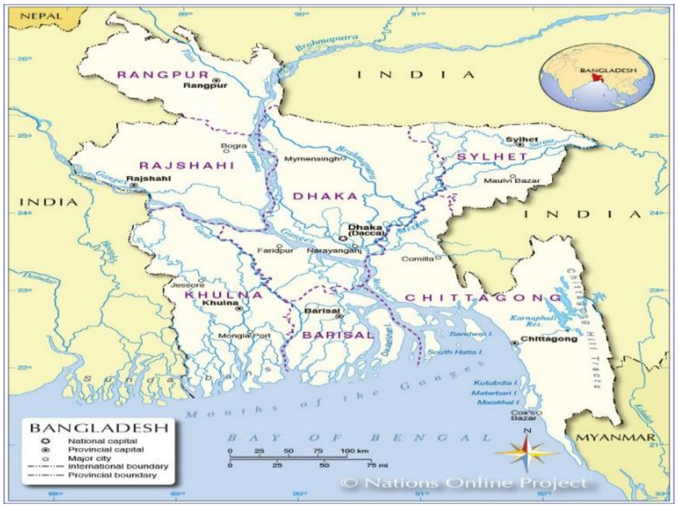

Figure 1. Location map of the experimental site

The experimental site during the cropping period have undergone average temperature of (18^0C -35^0C) and a minimal rainfall along with a sudden precipitation in the early season of crop establishment (Fig. 2). Nine BARI released barley varieties (BARI Barley-1, BARI Barley-2, BARI Barley-3, BARI Barley-4, BARI Barley-5, BARI Barley-6, BARI Barley-8, BARI Barley-9) were grown in RCBD with 3 replications.

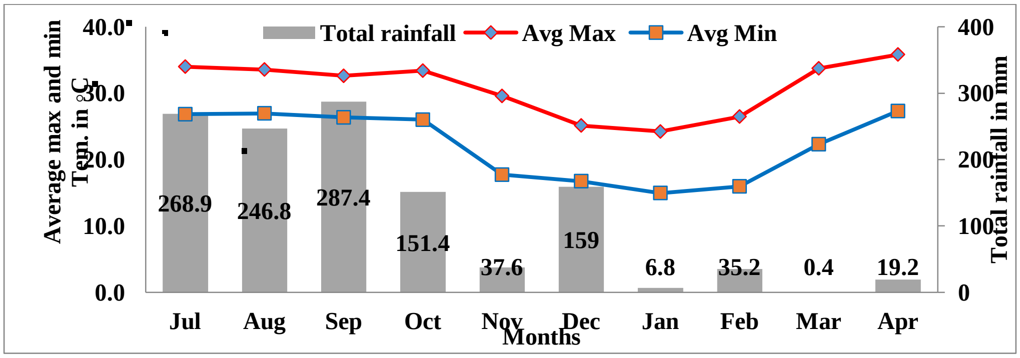

Figure 2. Weather data of RARS, Jashore from July-2021 to April-2022

Seeds were sown in unit plot of 5 rows x 5 m maintaining row to row spacing of 25 cm on 25 November 2021. Proper soil fertility was maintained by applying N, P, and K @ 100:60:40 kg/ha respectively. From each plot, five sample plants were randomly chosen, omitting the border plants, to record traits. viz days of heading, days to maturity, plant height, effective tiller per plant, length of spike, no. of grains per spike, thousand grain weight, disease and insect reaction score (0-10 scale) (Mujeeb-

Kaji et al 1996) and yield per ha was calculated by harvesting total unit plot. Statistical analysis was done by using statistical software package “R Studio” at 5% level of probability (R Core Team, 2021).

RESULTS AND DISCUSSION

Mean performances, Genetic variability (GCV and PCV), heritability and genetic advance

The mean performances of yield and yield contributing characters of nine barley varieties are presented in fig. 3. The heading days were ranged from 64 to 75 days and the mean value of heading days of studied barley varieties were 68 days. The highest and lowest maturity days were 112 days and 94 days and the average maturity days of nine varieties were 101 days. The highest, lowest and average plant height was 101.60 cm, 70.60 cm and 88.24 cm, respectively. Number of effective tillers were ranged from (11-14) with mean of 13. The minimum thousand grain weight was 32 g whereas the maximum was 37 g and average of nine varieties were 35 g. The disease and insect reactions were ranged within (0.90-4.80) and grand mean value was 1.45. The highest grain yield was observed as 2720 kg ha^{-1} whereas the lowest was 800 kg ha^{-1} and the mean yield of the nine varieties were 1723 kg ha^{-1}.

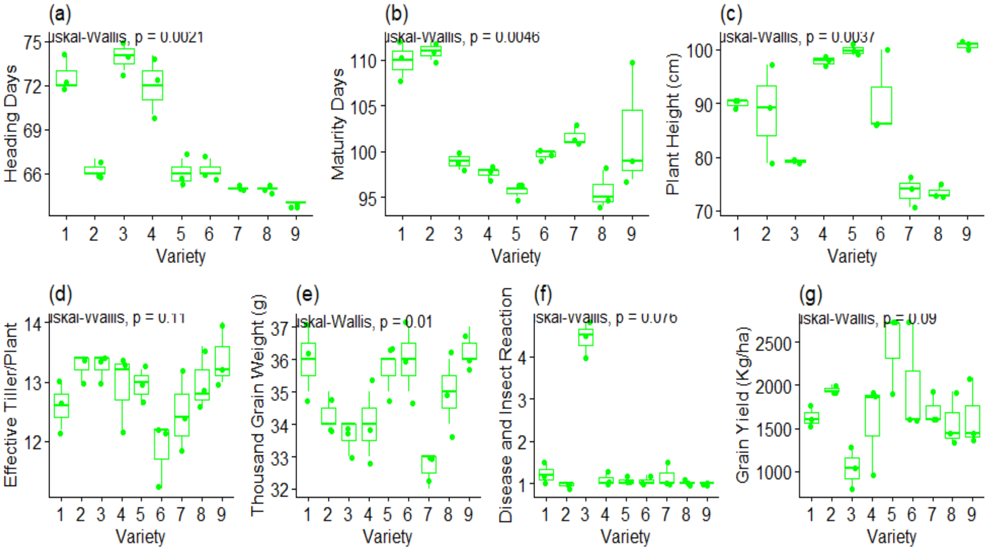

Figure 3. Mean performances of yield and yield contributing characters

For yield and yield component traits, Table 1 provides data on PCV, GCV, heritability, and genetic advance in percent of mean. Examining these findings revealed that grain yield had the greatest range of variability, followed by disease and insect reactivity. All of the characters evaluated in the current investigation showed higher phenotypic coefficients of variation than genotypic coefficients of variation, showing the importance of environment. Both Jewel et al. (2011) and Hossain et al. (2023) reported the same conclusions.

Nevertheless, high (>20%) phenotypic co-efficients of variation for disease and insect response and grain yield in the current study were found to be closely and significantly related with high genotypic co-efficients of variation for the trait, indicating the absence of significant environmental influence and the presence of high genetic variability for the trait in the experimental material. Therefore, selection of these genotypes based on phenotype may be useful for increasing grain yield. Maniruzzaman et al. (2023) previously described outcomes like these. However, the present study found that the genotypic and phenotypic coefficients of variation for plant height were moderate (10–20%). These outcomes concur with those of Debsharma et al. (2023). In contrast, heading days, maturity days, the number of tiller plants^{-1}, and thousand grain weight showed low estimates of genotypic and phenotypic coefficients of variation (10%) in the current study, indicating low variability for these characters in the present experimental material and little room for improvement of these traits. Hossain et al. (2020) previously published similar findings.

Table 1. Genetic variability, heritability (broad sense) and genetic advance as percent of mean for yield and its component traits

	HD	MD	PH	NT	TGW	DIR	GY
Environmental Variance	0.97	6.80	20.19	0.27	0.68	0.04	117021
Genotypic Variance	14.34	29.61	107.93	0.14	1.36	1.24	107023
Phenotypic Variance	15.31	36.41	128.13	0.41	2.04	1.28	224044
Environmental Coefficient of Variance	1.45	2.57	5.09	0.41	2.36	14.05	19.85
Genotypic Coefficient of Variance	5.57	5.37	11.77	4.04	3.35	76.79	18.99
Phenotypic Coefficient of Variance	5.76	5.95	12.83	4.99	4.10	78.06	27.47
Heritability (Broad Sense)	0.94	0.81	0.84	0.35	0.67	0.97	0.88
Genetic Advance	7.55	10.11	19.64	0.46	1.96	2.26	465.78
Genetic Advance as percentage of mean	11.11	9.97	22.26	3.57	5.64	155.5	27.03

HD=Heading days, MD=Maturity days, PH=Plant height (cm), NT=No. of tiller plant^{-1}, TGW=Thousand grain weight (g), DIR=Disease and Insect reaction (0-10), GY=Grain yield (kg ha$^{-1)}$

Nearly all of the examined traits had heritability estimates in the broadest sense (h2b) that were considerably higher (>60%). Evaluations of high heritability have been found to be useful in choosing superior genotypes based on phenotypic performance. Plant height, disease and insect reaction, and grain yield all showed high heritability together with high genetic progress as a percentage of mean, indicating that the high heritability is attributable to additive gene effects and selection may be successful for these traits. Hossain et al. (2022) noted comparable results for yield per plant. On the other hand, heading days showed strong heritability together with a moderate genetic advance in percent of mean, showing the importance of both additive and non-additive gene influences in regulating the character. In addition, Maniruzzaman et al. (2022) used information on genetic variation, heritability, and genetic progress assessments to provide a clearer understanding of the effectiveness of selection. For disease and insect reaction as well as grain yield, high GCV and PCV along with high heritability and high genetic advance in percent of mean were observed in the current study, indicating the preponderance of additive gene action and the potential for trait improvement through selection. Maniruzzaman et al. (2023) earlier reported similar findings.

Correlation coefficients analysis

Correlation coefficients between yield and other characters and inter relations among them were estimated and presented in Table 2. In case of genotypic correlation, grain yield was observed to be positively associated with maturity days, plant height and thousand grain weight indicating with an increase in these features, increase in grain production. Therefore, while making selections to improve yield, priority should be given to these features. The findings are in agreement with the reports of Liakat et al. (2011). On the contrary negative association was noticed for heading days, number of tiller and disease and insect reaction. However, negative and highly significant genetic correlation was observed in plant height and 1000 grain weight by Tiwari et al., (2019).

In case of phenotypic correlation grain yield was observed to be positively associated with plant height and thousand grain weight. indicating with an increase in these features, increase in grain production. Therefore, while making selections to improve yield, priority should be given to these features. The findings are in agreement with the reports of Akter et al. (2019). On the other hand negative association was noticed for heading days, maturity days, number of tiller and disease and insect reaction. Singh et al. (2015) found correlation coefficient with grain yield per plant exhibit positive and significant correlation with plant height and 1000 grain weight. Madakemohekar et al. (2015) found days to heading possessed positive association with grain yield while plant height showed negative association.

Effective selection strategies for complex (polygenic) traits depend on the information of the association/relationship between these traits. Grain yield was observed to be positively associated with plant height and thousand grain weight at both genotypic and phenotypic level which indicating that with an increase in these features, increase in grain production. Therefore, while making selections to improve yield, priority should be given to these features.

Table 2. Genotypic and Phenotypic Correlation analysis between different traits

Genotypic Correlation							
	HD	MD	PH	NT	TGW	DIR	GY
HD	1**	0.13 NS	0.01 NS	0.11 NS	-0.24 NS	0.64 NS	-0.61 NS
MD	0.13 NS	1 **	0.04 NS	-0.02 NS	0.04 NS	-0.15 NS	0.02 NS
PH	0.01 NS	0.04 NS	1 **	0.18 NS	0.69 *	-0.34 NS	0.60 NS
NT	0.11 NS	-0.02 NS	0.18 NS	1 **	-0.08 NS	0.32 NS	-0.43 **
TGW	-0.24 NS	0.04 NS	0.69 *	-0.08 NS	1 **	-0.38 NS	0.42**
DIR	0.64 NS	-0.15 NS	-0.34 NS	0.32 NS	-0.39 NS	1 **	-0.80 **
GY	-0.62 NS	0.02 NS	0.60 NS	-0.43 NS	0.42 NS	-0.80 **	1 **
Phenotypic Correlation							
	HD	MD	PH	NT	TGW	DIR	GY
HD	1 **	0.13 NS	0.01 NS	0.01NS	-0.13 NS	0.61 **	-0.47 *
MD	0.13 NS	1 **	0.04 NS	0.12 NS	0.09 NS	-0.13 NS	-0.05 NS
PH	0.01 NS	0.04 NS	1**	0.09 NS	0.49 **	-0.30 NS	0.30 NS
NT	0.01 NS	0.12 NS	0.09 NS	1 **	-0.10 NS	0.24 NS	-0.18 **
TGW	-0.13 NS	0.09 NS	0.49 **	-0.10 NS	1 **	-0.32 NS	0.32 **
DIR	0.61 **	-0.13 NS	-0.30 NS	0.24 NS	-0.32 NS	1 **	-0.54 **
GY	-0.47 *	-0.05 NS	0.30 NS	-0.18 NS	0.32 NS	-0.54 **	1 **

HD=Heading days, MD=Maturity days, PH=Plant height, NT=No. of tiller, TGW=Thousand grain weight, DIR=Disease and Insect reaction, GY=Grain yield

Path analysis

Through path analysis at the genotypic levels, the direct and indirect effects of yield were determined. The results are shown in the Table 3. Path coefficient analysis (genotypic) revealed that number of tiller and thousand grain weight exhibited positive direct effects on grain yield. The negative direct relationship between plant height and heading days and yield suggested that short-lived barley may be created without compromising grain output. Singh *et al*. (1987) found that grain yield in barley was significantly correlated with plant height. Except for maturity days and plant height most of the examined parameters revealed a positive indirect relationship between thousand grain weight and grain yield. The residual impact was 0.26, which means that they were responsible for 84% of the variation in grain yield. This result suggests that few traits other than those present in the current experiment may also influence yield.

Table 3. Direct and indirect effects (genotypic) of different characters on yield of barley

	HD	MD	PH (cm)	NT	TGW	DIR	Y/P
HD	-0.44	0.02	0.008	-0.12	0.17	-0.23	-0.37
MD	-0.05	0.17	0.05	0.02	-0.03	0.05	0.16
PH	-0.002	0.006	1.45	-0.19	-0.48	0.12	0.90
NT	-0.04	-0.003	0.25	-1.11	0.06	-0.12	-0.92
TGW	0.10	0.008	0.99	0.09	-0.71	0.14	0.76
DIR	-0.28	-0.02	-0.49	-0.36	0.27	-0.36	0.59
Y/P	-0.27	-0.11	-0.37	1.03	0.44	-0.21	0.61

Residual= 0.26

HD=Heading days, MD=Maturity days, PH=Plant height, NT=No. of tiller, TGW=Thousand grain weight, DIR=Disease and Insect reaction, Y/P= Yield plant^{-1}

Principal Component Analysis with Biplot and Cos2 value

Biplot based on principal component analysis is presented in Fig. 4. The biplot based on principal component analysis showed that component 1 and component 2 denotes the maximum composition for variability. The highest cos2 value was found in yield and in disease and insect score and the lowest was found in maturity days and in number of effective tiller plant^{-1}. The principal component analysis also revealed that yield was positively related with thousand grain weight and plant height but negatively related with disease and insect reaction. These results are in accordance with Madakemohekar et al. (2015)

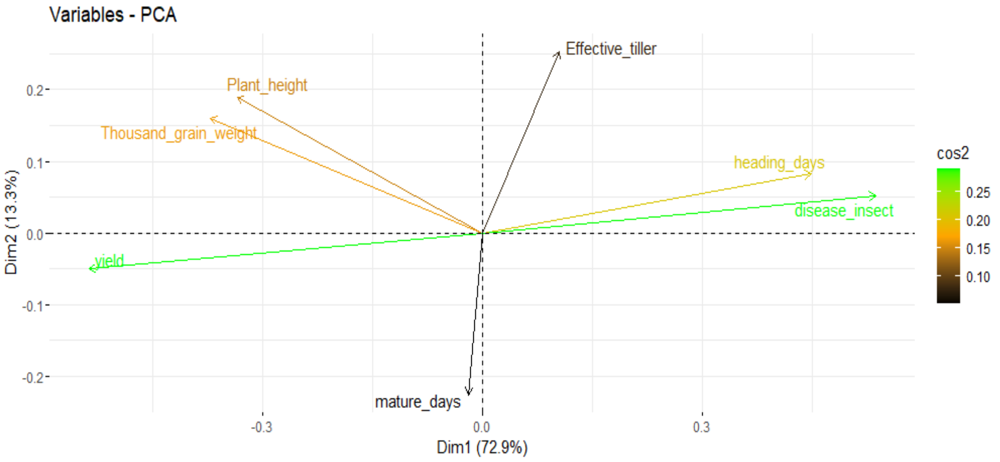

Figure 4. Biplot analysis based on principal component analysis and cos2 value

CONCLUSION

The possibility for increasing grain production by selection was highlighted by the results of the current study's analyses of variability, heritability, genetic advance, correlation, and path analysis. The majority of the examined characters displayed notable genetic variation. High heritability coupled with high genetic advance as percent of mean was observed for plant height, disease and insect reaction and grain yield suggesting preponderance of additive gene action in the expression of these characters. Studies on path coefficients and character association demonstrated the value of plant height, number of tiller and thousand grain weight as selection criteria for effective yield improvement as they contain highest positive direct effect on yield. Breeders can identify potential genotypes that could be employed as higher gain yield with effective characters.

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