Forage Res., **51**(2) : pp. 158-165 (2025) **http://forageresearch.in**

APPLICATION OF REGRESSION ANALYSIS TO IDENTIFY THE VARIABLES AFFECTING BARLEY YIELD

YOGENDER KUMAR*, SATYAWAN ARYA, SACHIN AND DEEPAK KAUSHIK

Department of Genetics and Plant Breeding
CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India
**(e-mail : yogenderkgulia@gmail.com)*

(Received: 2 August 2025; Accepted: 12 September 2025)

SUMMARY

Barley being a nutri-rich and hardy crop fitted well in the North-Western Indian cropping system. Screening of the diverse germplasm and developing a definite set of traits for their evaluation became crucial to get the elite barley varieties. This study aimed to develop a regression model that fitted the dependent variable sufficiently well to account for the total variability. The study evaluated 10 quantitative traits of 71 barley genotypes under timely sown irrigated conditions during crop season 2023-24 at the Research Area, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. The experiment was planted in Randomized Block Design (RBD) with four replications. Each genotype occupied a plot size of 6.9 m^2. The yield was found to be explained by harvest index and biological yield per plot. Multiple regression analysis revealed 95.80% of the variability, explained by the studied quantitative traits. The stepwise regression analysis retained a total of two traits viz., harvest index and biological yield per plot, resulted in the development of two yield prediction models. Model 2 was found to be the most reliable predictor of yield in barley as it explained 95.60% of the total variability.

Key words: Barley, regression, yield traits

One of the most significant cereal crops in India, barley (*Hordeum vulgare* L.) dates back to the beginning of agriculture. Compared to other cereals, it is thought to be one of the most suitable crops because it can grow and thrive well on a variety of soil types and climatic conditions (Shahmoradi *et al.*, 2015). In terms of global cereal production, it comes at fourth place, behind rice, wheat and maize. Globally, barley occupied approximately 47.50 million hectares and produced around 142.29 million tonnes. Nationally, this crop is being cultivated on 0.55 million hectares with production and productivity of 1.65 million metric tonnes and 2998 kg/ha, respectively (ICAR-IIWBR, 2024). The majority of crop improvement programs are intended to increase crop yield, which necessitates the knowledge of the relationship between grain yield and its constituents (Kumar *et al.,* 2024). As a result, regression investigations were conducted in different crops to identify the yield determinants. In recent years, agricultural scientists worldwide have viewed breeding new barley varieties with high yield and good quality as a critical research approach, and several new varieties of barley have been developed (Leilah and Al-Khateeb, 2005). Yield in barley is a highly complicated feature that is determined by the interaction of several yield components (Ashok et al., 2024).

Regression analysis is a multivariate procedure used to investigate the interrelationships and interdependence of variables. In many crops, particularly cereal crops, yield is determined by various plant attributes. These plant traits are known as independent variables, covariates, predictors or regressors, and yield is the corresponding dependent variable. Each of these regressors influences the variation in yield; however, the amount varies from variety to variety. Breeders can use information on the nature and extent of regression to determine selection criteria for improving certain traits while increasing production. Regression technique facilitates to determine whether there is a linear relationship between the dependent and independent variables or not (Budka *et al.,* 2015). Simple linear regression is used when there is only one independent or predictor variable is in consideration, but in multiple regression or multivariate regression analysis, several independent or predictor variables are considered together (Ahuja and Sharma, 1988).

The goal of multiple regression analysis is to identify the optimal set of independent variables that can explain the dependent variable under the assumptions which are presented. The term regression refers to determining the real relationship between two or more variables. In this research, we frequently need to provide actual relationships between two or more variables. For this goal, we use the method of all possible regressions. This method needs the investigator to fit all subset regression models including one predictor variable, two predictor variables and so on (Agarwal, 1991). The best subset regression model was chosen after evaluating each model using appropriate criteria such as R^2, R^2-adjusted, p predictors and AIC (Akaike Information Criterion) (Mansouri *et al.*, 2018). The study aimed to analyze barley genotypes for yield components and to identify the key variables determinant to grain yield by comparing different prediction models using best subset regression.

MATERIALS AND METHODS

The experimental material included seventy one barley genotypes, evaluated at the Research Area of Wheat and Barley Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar, during crop season 2023-24 under timely sown irrigated conditions. The experiment was laid in Randomized Block Design (RBD) with four replications. Each genotype was planted in 6 rows of 5.0 m length spaced at 23 cm, occupied a plot size of 6.9 m^2. To ensure the optimal crop growth, recommended agronomic package of practices were followed. Observations were recorded for ten quantitative traits *viz*., days to heading, days to maturity, plant height (cm), number of effective tillers per meter, spike length (cm), number of grains per spike, 1000-grain weight (g), biological yield per plot (kg), harvest index (%) and grain yield per plot (kg). The recorded data was subjected to regression analysis (Simple, Multiple and Step-wise regression) using R Studio software (2025.05.01+513).

RESULTS AND DISCUSSION

The mean performance of genotypes and the estimates of various genetic parameters pertaining to 10 quantitative traits are presented in Table 1. The results indicated a wide range of difference among the traits that offered score for selection of desirable types. The coefficient of variation (CV) was also varied widely, ranging from 2.09 to 47.31%. It was recorded maximum for number of grains per spike followed by number of effective tillers per meter and harvest index. Likewise, days to heading and maturity, and plant height illustrated lower magnitude of variability. Hence, the experimental material could be considered appropriate for further analysis to identify yield determinants through regression studies.

The analysis of variance for regression is depicted in Table 2, indicated significance of p value for the regression. The regression sum of squares is the entire variation in the dependent variable that the regression model can explain. It is the total of the squared differences between the predicted value and the mean of all data points. However, the residual sum of squares is the entire variation in the dependent variable that the regression model cannot explain. It is also known as the error sum of squares and is calculated by squaring the difference between the actual and predicted values of all data points. The regression SS recorded was 14.116 compared to total SS of 14.735, indicating that the regression model accounts for about 95.80% of the dataset's variability. The lower estimate of residual SS (0.619) indicated efficacy of the regression model to explain the variation in the data set. Further, p-value (0.00***) indicates that a significant relationship exists between dependent and independent variables.

Simple (Linear) Regression Analysis:

Simple regression is the simplest statistical technique for examining the relationship between two variables. The line of best fit is represented as $y = a + bx$, where, 'a' represents the intercept and 'b' represents the slope. The coefficient of determination, R^2, indicated the contribution of individual variables to total variability, explained by the regression line. Each dot represents a genotype having two axis; x-axis contains the mean value of independent traits, whereas, the y-axis corresponds to the mean value of the dependent trait (grain yield). Linear regression line along with all the observations and slop of the trend line had been given in the scatter plots of independent and dependent variables (Fig. 1) for all the studied traits. Line of the best fit for residuals vs. predicted values (Fig. 2) represented that data set lies around the regression line and similar pattern for scatter plots was also observed by Marzougui and Chargui (2018). The regression techniques were also explored by Shastry *et al.* (2017) and Shar *et al.* (2024) for yield prediction.

TABLE 1

Mean performance of barley genotypes for different quantitative traits

Genotypes	DH	DM	PH	T/M	SL	G/S	TGW	GY	BY	HI
BH 22-14	89	137	109	120	9.3	70	44.1	3.91	12.5	31.7
BH 22-05	88	131	98	142	8.2	26	45.9	3.39	11.7	29.0
BH 22-13	83	127	91	126	8.2	70	37.7	3.78	10.5	36.5
BH 22-02	81	125	93	112	7.2	25	38.3	3.12	10.2	30.8
BH 22-08	87	128	101	176	8.2	30	44.6	3.45	11.7	29.7
BH 22-18	91	127	119	180	7.0	58	42.8	3.11	12.6	25.0
BH 22-04	90	135	115	146	8.9	27	46.8	3.44	12.8	27.0
BH 22-07	87	128	105	106	8.0	25	49.2	4.24	12.4	34.8
BH 946	88	129	110	127	7.8	60	38.5	3.66	11.4	32.8
BH 22-06	82	125	105	170	6.4	21	41.3	2.84	9.9	28.8
DWRB 101	85	125	105	190	7.8	25	42.7	3.31	11.0	30.0
BH 22-16	81	124	119	164	7.2	23	47.4	3.46	11.5	30.1
BH 22-15	85	129	106	146	8.1	27	51.6	3.88	11.9	33.0
BH 22-09	84	126	113	204	8.0	24	50.8	3.59	13.5	26.7
BH 22-10	84	127	102	158	8.3	25	49.4	3.27	13.3	24.9
BH 22-19	85	126	115	112	7.1	58	38.7	3.71	13.8	27.0
DWRB 137	82	126	96	107	6.6	60	43.1	3.67	10.9	34.3
BH 393	80	125	93	100	8.2	70	37.1	3.41	10.7	32.2
BH 22-25	89	129	104	132	7.2	25	40.2	2.78	13.0	21.5
BH 22-01	86	126	109	162	7.8	25	46.8	3.27	11.3	29.2
BH 22-17	90	127	103	180	8.1	25	51.9	3.90	12.1	33.0
DWRB 92	89	128	112	214	7.8	27	52.6	3.58	12.4	29.3
BH 22-20	90	127	113	140	8.4	26	55.4	3.33	11.1	30.4
BH 20-15	86	126	102	166	7.8	23	36.6	3.27	10.6	31.1
BH 22-26	84	128	112	104	7.7	62	49.5	3.58	12.0	30.1
BH 21-06	89	131	105	126	8.3	68	31.9	3.11	11.4	27.6
BH 20-16	90	132	101	158	7.8	25	49.2	3.52	12.2	29.0
BH 22-27	92	129	113	190	8.4	66	38.3	3.90	15.0	26.1
BH 22-31	92	131	116	148	8.9	64	36.1	3.10	13.1	24.1
BH 20-13	89	129	107	142	8.2	29	49.8	3.23	12.7	25.4
BH 22-33	91	130	112	174	10.0	76	37.8	3.53	13.1	27.1
BH 22-30	89	129	102	112	6.3	62	35.6	3.95	12.3	32.3
BH 22-32	90	131	106	150	6.8	58	33.0	3.51	10.4	34.0
BH 22-11	86	126	108	190	8.3	29	45.2	3.07	12.0	25.9
BH 21-03	85	130	109	168	10.0	76	33.3	4.13	12.4	33.8
RD 2849	89	129	116	92	9.9	71	33.1	3.08	11.6	26.7
BH 21-05	90	131	113	206	7.2	23	47.4	3.25	12.0	27.5
BH 20-11	90	133	102	148	6.8	23	48.9	3.65	12.3	29.8
BH 22-36	84	128	98	100	8.2	62	41.1	3.18	10.9	29.4
BH 21-09	91	131	114	192	9.3	25	56.8	4.20	15.1	28.0
BH 22-22	88	130	120	96	6.7	60	40.4	3.75	13.0	29.5
BH 22-03	85	128	118	170	8.3	26	43.7	4.41	9.9	44.8
BH 23-04	83	127	118	118	10.2	32	43.4	3.43	11.3	30.3
BH 23-09	80	124	96	130	6.2	58	41.5	3.91	11.4	34.2
BH 23-05	89	126	102	136	8.2	24	43.7	2.88	12.3	23.5
BH 23-07	88	131	106	140	9.8	29	40.2	2.95	12.7	23.6
BH 23-10	83	126	104	146	9.2	27	54.6	2.66	11.6	22.9
DWRB 123	87	128	106	192	7.3	26	46.1	3.41	11.3	30.5
BH 23-08	82	124	105	166	6.8	27	41.7	2.38	12.2	19.8
BH 23-03	88	125	118	166	9.3	29	46.5	3.45	12.6	27.7
BH 23-01	83	127	96	106	6.8	52	36.1	3.30	12.4	26.8

Contd..,

Table 1 contd.

BH 22-21	89	127	95	214	7.2	27	39.5	2.60	9.8	26.6
BH 22-24	90	125	105	104	7.2	70	31.8	3.53	11.8	30.1
BH 23-06	91	126	101	192	8.3	27	37.2	3.00	13.2	22.9
BH 23-02	84	125	115	176	9.8	27	49.9	2.18	12.6	17.6
BH 22-23	90	127	115	126	8.3	64	37.0	3.73	12.6	29.7
BH 22-34	91	126	126	142	8.0	29	42.4	3.27	9.2	35.9
BH 23-14	88	126	109	184	7.8	25	42.1	4.04	9.0	44.8
BH 23-11	91	125	125	190	9.8	29	36.1	3.10	11.4	27.4
DWRB 160	90	128	103	94	10.0	31	58.2	3.45	9.9	35.3
BH 22-35	88	125	103	126	6.2	68	36.0	3.66	9.2	40.0
BH 23-15	81	124	98	170	7.1	23	42.3	2.55	9.2	28.0
BH 23-19	89	126	98	192	8.4	25	33.8	3.84	9.9	38.6
BH 23-16	80	124	94	114	7.3	64	47.1	3.63	7.4	49.4
BH 23-17	84	124	105	118	8.3	25	51.9	2.63	9.8	26.9
BH 23-20	80	125	101	192	8.2	25	40.2	2.81	10.0	28.6
BH 23-18	88	126	123	152	10.3	32	37.7	2.88	8.9	32.7
BH 22-13	90	126	111	218	9.8	27	43.1	3.12	10.6	29.6
BH 885	85	125	110	176	8.4	25	35.6	2.87	11.4	25.5
BH 21-22	89	126	96	116	7.9	64	38.5	3.19	9.8	32.7
BH 22-12	86	127	104	156	9.9	29	41.5	2.62	12.0	22.0
Mean	86.80	127.46	107.01	150.68	8.12	39.72	42.82	3.36	11.55	29.77
Min.	80.00	124.00	91.00	92.00	6.20	21.00	31.80	2.18	7.40	17.60
Max.	92.00	137.00	126.00	218.00	10.30	76.00	58.20	4.41	15.10	49.40
Range	12.00	13.00	35.00	126.00	4.10	55.00	26.40	2.23	7.70	31.80
S.E. (m)	0.41	0.32	0.97	4.03	0.13	2.23	0.75	0.05	0.17	0.65
S.D.	3.42	2.67	8.14	33.96	1.07	18.79	6.35	0.46	1.43	5.47
Var.	11.70	7.11	66.33	1153.11	1.14	353.09	40.31	0.21	2.04	29.88
CV (%)	3.94	2.09	7.61	22.54	13.17	47.31	14.83	13.65	12.37	18.36

DH: Days to heading; DM: Days to maturity; PH: Plant height (cm); T/M: Number of effective tillers per meter; SL: Spike length (cm); G/S: Number of grains per spike; TGW: 1000-grain weight (g), BY: Biological yield per plot (kg); HI: Harvest index (%); GY: Grain yield per plot (kg).

TABLE 2

Analysis of variance for regression analysis in barley

Source	d.f.	Sum of Squares	Mean squares	F-stat	p-value
Regression	9	14.116	1.568	154.505	0.000***
Residual	61	0.619	0.010		
Total	70	14.735			

***Significance at p= 0.001.

The line of best fit for yield contributing traits *viz.***,** days to heading (y =0.022x + 1.371, $R^2 = 0.012$), days to 50% maturity (y = 0.056x + 2.880^{**}, $R^2 = 0.094$), plant height (y = 0.003x + 0.513, $R^2 = -0.011$), number of effective tillers per meter (y = -0.002x - 1.201, $R^2 = 0.006$), Spike length (y = -0.053x-1.029, $R^2 = 0.001$), number of grains per spike (y = 0.008x+2.794**, $R^2 = 0.089$), 1000-grain weight (y = 0.003x + 0.391, $R^2 = -0.012$), biological yield (y = 0.051x + 1.327, $R^2 = 0.011$) and harvest index (y = 0.055x + 7.314***, $R^2 = 0.429$), are presented in Fig. 1. The genotypes (dots) appearing closer to the trend line had a strong relationship between the variables. The detailed results of the model are presented in Table 3. The adjusted R^2 of the model was 95.80% ($p < 0.01$). Similar findings were also observed by the Guan et al. (2019) and three significant coefficients were also reported in the successful regression equation by Khanghah *et al.* (2014).

Multiple Regression Analysis

The coefficients of regression for different traits viz., days to heading (-9.448), days to maturity (6.794), plant height (4.554), number of effective tillers per meter (-3.035), spike length (-5.040), number of grains per spike (-1.080), 1000-grain weight (-2.703), biological yield per plot (2.947) and harvest index (1.032) are presented in Table 4. Similar findings were also observed by El-Mohsen (2013), Kumar et al. (2016), Mokarram and Bijanzadeh (2016) and Guan et al. (2019). Based on these results, the predicting

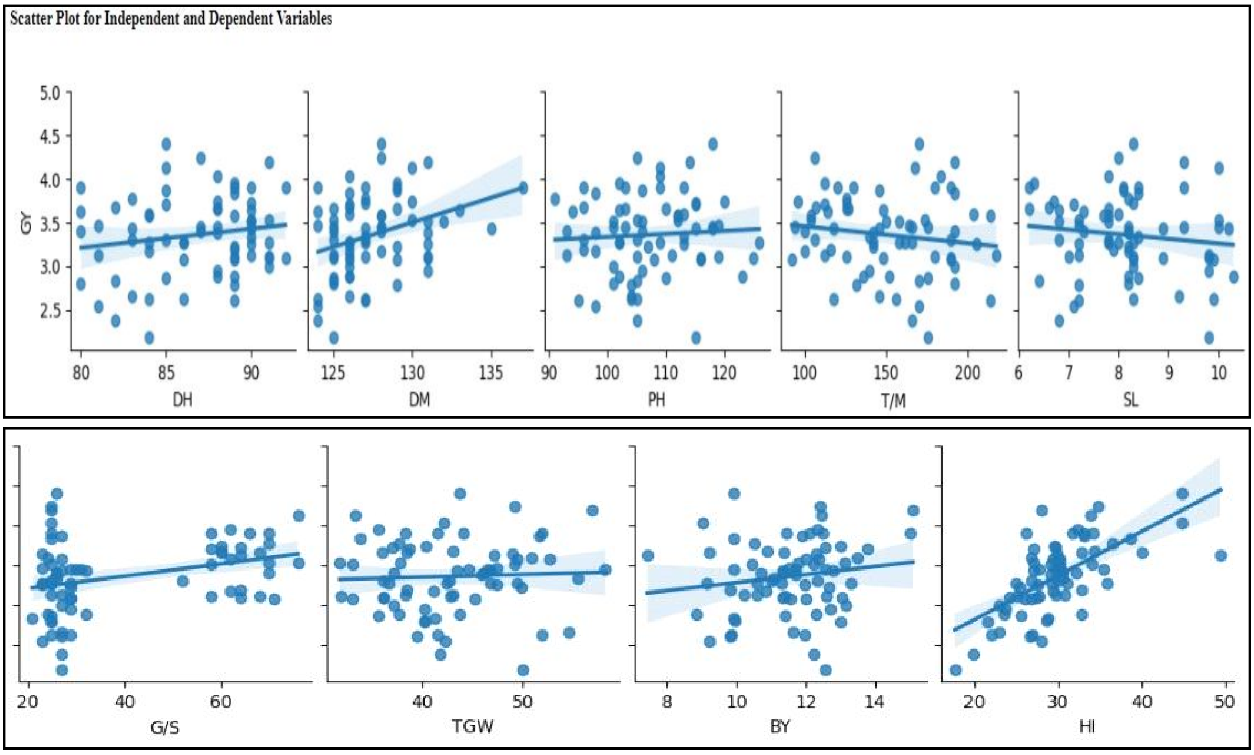

Fig. 1. Scatter Plots between independent and dependent variables.

model equation for the grain yield per plot (y) was formulated as follows:

$$y = -3.657 - 9.448\ DH + 6.794\ DM + 4.554\ PH - 3.035\ T/M - 5.040\ SL - 1.080\ G/S - 2.703\ TGW + 2.947\ BY + 1.032\ HI$$

Fig. 2 presented the scatter plot of the standardized residuals against the predicted values of grain yield per plot from the model to assess the goodness of fit of the model. In the scatter plot of residuals (standardized residuals against predicted values), the points were around the zero line at the vertical axis without displaying a particular pattern. Model summary for multiple regression is given in the Table 5. The multiple regression model explained 95.80 per cent (R^2= 0.958) of the total variability in grain yield per plot via. yield attributing traits. The findings

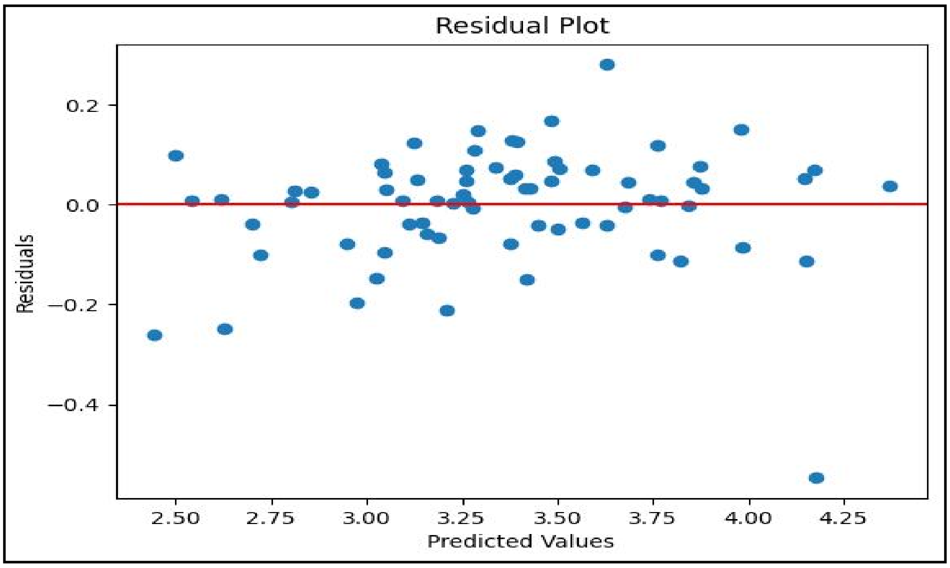

Fig. 2. Scatter Plot of standardized residuals against predicted values of grain yield per plot.

TABLE 3
Simple (Linear) regression analysis for different traits in barley

S. No.	Traits	Coefficient estimate	Std. error	t value	p value	Adj. R^2
1.	Days to heading	0.022	0.016	1.371	0.175	0.012
2.	Days to maturity	0.056	0.020	2.880	0.005 **	0.094
3.	Plant height	0.003	0.007	0.513	0.610	-0.011
4.	Number of effective tillers per meter	-0.002	0.002	-1.201	0.234	0.006
5.	Spike length	-0.053	0.051	-1.029	0.307	0.001
6.	Number of grains per spike	0.008	0.003	2.794	0.007 **	0.089
7.	1000-grain weight	0.003	0.009	0.391	0.697	-0.012
8.	Biological yield per plot	0.051	0.038	1.327	0.189	0.011
9.	Harvest index	0.055	0.008	7.314	0.000 ***	0.429

**, ***Significance at p= 0.01 & 0.001, respectively.

TABLE 4
Multiple regression analysis of different traits in barley

S. No.	Traits	Coefficient ± S.E
	Constant	-3.657 ±0.6301***
1.	Days to heading	-9.448 ±0.00469
2.	Days to maturity	6.794 ±0.00612
3.	Plant height	4.554 ±0.00176
4.	Number of effective tillers/meter	-3.035 ±0.00045
5.	Spike length	-5.040 ±0.01266
6.	Number of grains/spike	-1.080±0.00101
7.	1000 grain weight	-2.703±0.00250
8.	Biological yield/plot	2.947±0.01389***
9.	Harvest index	1.032 ±0.00325***

of linear and multiple regressions are in congruence with Abdullah (2007) and Marzougui and Chargui (2018).

Step-wise Regression Analysis

TABLE 6
Stepwise regression analysis in barley

Steps	Variable included	Deviance	d.f.	Residual deviance	AIC
1	Intercept	-	70	14.74	-109.64
2	Harvest index	6.44	69	8.30	-148.40
3	Biological yield/plot	7.65	68	0.65	-327.27

The stepwise regression analysis retained a total of two traits viz., biological yield per plot and harvest index. While the backward stepwise selection and both direction stepwise selection yielded the same results and confirmed that it was the best explanation of the grain yield per plot. The analysis revealed (Table 6) that harvest index was the most important predictor of grain yield in barley, accounting for a significant reduction in residual deviance (8.30). The subsequent inclusion of biological yield per plot further enhanced the model fit, leading to a near-complete explanation of yield variability as reflected by the very low residual deviance (0.65) and highly reduced AIC value (-327.27). The results are confirmed by the findings of Ali *et al.* (2022), Zare-Kohan *et al.* (2022) and Karuna *et al.* (2024).

Stepwise regression analysis led to the development of two predictive models for grain yield in barley (Table 7). In Model 1, harvest index was identified as the sole significant predictor. The regression equation was:

$$Y = 1.709+0.55\ HI$$

The coefficient of harvest index (0.55 ± 0.008***) was highly significant, indicating that each unit increase in harvest index contributed to an increase of 0.55 units in grain yield. The model recorded a correlation coefficient (R) of 0.661, with $R^2 = 0.437$ and adjusted $R^2=0.429$, thereby explaining about 43.7% of the total variability in grain yield per plot. This suggested that harvest index alone played a key role in determining grain yield performance.

TABLE 5
Model summary for multiple regression

Dependent Variable	Number of observations	d.f. (Residuals)	d.f. (Model)	R^2	Adj. R^2	F-Stat	Prob.
Grain Yield	71	61	9	0.958	0.952	154.505	0.00

TABLE 7

Regression models in barley

Models	Steps	Variables included	Coefficient±SE	R	R^2	Adj. R^2
Model 1	1	Constant	1.709±0.229	0.661	0.437	0.429
	2	HI	0.55±0.008***			
Model 2	1	Constant	-3.112±0.182	0.978	0.956	0.955
	2	HI	0.103±0.003***			
	3	BY	0.295±0.010***			

In Model 2, both harvest index and biological yield were retained as significant variables and the regression equation was:

$$Y = -3.112+0.103\ HI + 0.295\ BY$$

The coefficient of harvest index (0.103 ± 0.003***) remained highly significant, although its effect was reduced compared to Model 1 due to the inclusion of biological yield. Biological yield also exhibited a highly significant and positive coefficient (0.295 ± 0.010***), indicating its strong influence on yield. The model showed a very high correlation coefficient (R = 0.978), with R^2=0.956, thereby explaining 95.6% of the variability in grain yield per plot. Overall, Model 2 demonstrated a superior predictive ability compared to Model 1, emphasizing that grain yield in barley was jointly determined by harvest index and biological yield. These two traits together contributed most effectively to yield prediction under the studied conditions. Similar results were also found by the Ali *et al.* (2022).

CONCLUSION

The findings concluded that the results of simple linear regression can be supplemented by the multiple and stepwise regression analysis for the enhancement of the barley grain yield. The coefficient of multiple regression (r=0.958) showed a positive correlation between the dependent and independent variables, explaining 95.80% of the variability. Similarly, the modified R^2 = 0.952 indicated that, even with the modification, the regression model closely reflects the variance in the data set without changing the parameter. Stepwise regression revealed that harvest index alone explained 43.7% of the variation in grain yield, while the inclusion of biological yield increased the explained variation to 95.60%, making Model 2 the most reliable predictor of yield in barley.

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