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Study on genetic variability, correlation and path analysis in barley (*Hordeum vulgare* L.)

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ABSTRACT

The present investigation entitled “Study on Genetic Variability, Correlation and Path Analysis in Barley (*Hordeum vulgare* L.)” was conducted during the Rabi season of 2025-26 at the Agricultural Research Farm, School of Agriculture, Suresh Gyan Vihar University, Jaipur (Rajasthan) to assess the extent of genetic variability, heritability, genetic advance, correlation coefficients and path coefficients for yield and yield-attributing traits. Twenty-two diverse barley genotypes were evaluated in a Randomized Block Design (RBD) with three replications. Observations were recorded on eleven quantitative characters: days to 50% flowering, days to maturity, plant height (cm), number of tillers per plant, number of effective tillers per plant, spike length (cm), number of grains per spike, test weight (1000-grain weight, g), grain yield per plant (g), biological yield per plant (g) and harvest index (%). Analysis of variance revealed highly significant differences ($P \leq 0.01$) among genotypes for all eleven characters studied, indicating the presence of substantial genetic variability. High estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for number of tillers per plant (15.21% and 16.46%), grain yield per plant (11.18% and 12.99%) and harvest index (11.13% and 11.37%). Broad-sense heritability estimates ranged from 32.40% for plant height to 95.68% for harvest index. High heritability coupled with high genetic advance as per cent of mean (GAM) was recorded for number of tillers per plant (85.37%, GAM = 28.95%), harvest index (95.68%, GAM = 22.42%), grain yield per plant (74.01%, GAM = 19.81%), days to maturity (93.20%, GAM = 18.39%) and number of effective tillers per plant (90.78%, GAM = 18.17%), indicating the predominance of additive gene action and high response to direct selection. Correlation analysis showed that grain yield per plant had highly significant positive genotypic associations with number of grains per spike ($r_g = 0.8835$), number of effective tillers per plant ($r_g = 0.8519$), test weight ($r_g = 0.8456$), spike length ($r_g = 0.8231$), biological yield per plant ($r_g = 0.7767$) and harvest index ($r_g = 0.7767$). Path coefficient analysis identified harvest index (direct effect = 0.3888), number of effective tillers per plant (0.2624), spike length (0.2015), biological yield per plant (0.1604) and test weight (0.0804) as major direct yield contributors at the genotypic level. Genotypes RD 3109 (23.77 g yield/plant), K 499 (20.60 g), K 603 (20.39 g), RD 2907 (20.31 g) and K 125 (20.11 g) emerged as top performers and can be utilized as potential parents in barley crop improvement programmes.

Keywords: Barley, *Hordeum vulgare* L., Genetic variability, GCV, PCV, Heritability, Genetic advance, Correlation coefficient, Path coefficient analysis, Yield components

1. Introduction

Barley (*Hordeum vulgare* L.) is one of the earliest domesticated crop plants and ranks fourth among global cereal crops in terms of production and cultivated area after wheat, rice and maize (Bothmer *et al.*, 2003) [1]. Botanically, barley belongs to the family Poaceae and is a self-pollinated diploid species with a chromosome number of $2n = 2x = 14$ and a haploid genome size of approximately 5.5 pg (Bennett *et al.*, 1976) [2]. Originating in the fertile crescent of the Middle East, barley exhibits broad ecological adaptability, short duration and remarkable tolerance to environmental abiotic stresses such as salinity and drought (Salamini *et al.* 2002, El-Hashash and El-Absy 2019, Riehl 2019) [3].

In India, barley is primarily cultivated as a Rabi season crop in the north-western plains. The grain is widely utilized as livestock feed, poultry feed, raw material for malting and brewing industries and human dietary food items such as sattu, chapatis and pearl barley (Agricultural Statistics at a Glance 2024) [4]. In India, barley is cultivated over an area of approximately 0.67 million hectares with a total production of 1.72 million tonnes and an average productivity of 25.7 q ha⁻¹ (Directorate of Economics and Statistics 2024) [5]. Rajasthan is the leading barley-producing state in the country, occupying about 0.33 million hectares with a production of 0.93 million tonnes and a productivity of 28.2 q ha⁻¹ (DES, 2024) [5]. Major barley growing districts in Rajasthan include Jaipur, Alwar, Bharatpur, Jhunjhunu, Churu, Nagaur, Sikar, Hanumangarh and Ganganagar (Directorate of Agriculture Rajasthan, 2023) [6].

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Despite its economic and nutritional significance, barley productivity remains limited by changing climatic patterns and variable environmental conditions (Safhi *et al.*, 2024) [7]. Genetic enhancement of grain yield requires systemic knowledge of the nature and magnitude of genetic variability available in germplasm collections (Allard, 1999) [8]. Selection efficiency depends on partitioning phenotypic variation into heritable (genotypic) and non-heritable (environmental) components (Burton, 1952) [9]. Estimation of GCV, PCV, broad-sense heritability (h^{2bs}) and genetic advance as per cent of mean (GAM) provides clear insight into whether a trait is governed by additive or non-additive gene action (Johnson *et al.*, 1955) [10].

Grain yield is a complex polygenic character influenced by several component traits and environmental factors. Direct selection for yield alone is often inefficient; therefore, understanding character associations through correlation analysis is essential (Al-Jibouri *et al.*, 1958) [11]. Furthermore, correlation coefficients do not reveal the exact direct contribution of individual component traits to yield. Path coefficient analysis, developed by Wright (1921) [12] and elaborated for plant breeding applications by Dewey *et al.* (1959) [13], partitions correlation coefficients into direct and indirect effects, enabling plant breeders to identify reliable selection criteria.

The present study was undertaken to evaluate 22 diverse barley genotypes to quantify genetic variability, estimate heritability and genetic advance, examine phenotypic and genotypic correlations and partition trait relationships via path coefficient analysis to formulate effective selection strategies for barley crop improvement.

2. Materials and Methods

2.1 Experimental site and agro-climatic conditions

The field experiment was conducted during the *Rabi* season of 2025-26 at the Agricultural Research Farm, Department of Genetics and Plant Breeding, School of Agriculture, Suresh Gyan Vihar University, Jaipur (Rajasthan). The experimental site is geographically situated at 26°48'35" N latitude and 75°51'44" E longitude. The region experiences a semi-arid climate with temperature ranging from sub-zero levels (-1 °C) in winter to high temperatures (48 °C) in summer. Average annual rainfall varies between 400 and 500 mm, received mostly during the South-West monsoon season (July-August). The soil of the experimental field was loamy sand in texture (70.18% sand, 20.56% silt and 8.96% clay) with an alkaline pH (7.62), EC of 0.48 dSm⁻¹, organic carbon of 0.34%, available N of 134.25 kg ha⁻¹, available P₂O₅ of 13.25 kg ha⁻¹ and available K₂O of 178.15 kg ha⁻¹.

2.2 Experimental material and field layout

The experimental material comprised 22 diverse barley genotypes, including checks, listed in Table 1.

Table 1. List of 22 barley genotypes evaluated in the study

Genotype Code	Genotype Name	Genotype Code	Genotype Name
G1	RD 3089	G12	K 499
G2	RD 3088	G13	RD 2552
G3	RD 3109	G14	RD 2052
G4	RD 3102	G15	Rajkiran
G5	BH 393	G16	RD 2907
G6	BH 946	G17	RD 2503
G7	BH 959	G18	RD 2786
G8	Ajad 34	G19	RD 2790
G9	K 125	G20	RD 2660
G10	K 551	G21	RDB 1
G11	K 603	G22	BL 2

The experiment was laid out in a Randomized Block Design (RBD) with three replications. Seeds were sown manually on 30th November 2024 at a row-to-row spacing of 22.5 cm and plant-to-plant spacing of 10 cm in net plot size of 3.6 m x 1.8 m (6.48 m²). Recommended agronomic package of practices, including seed treatment with carben-dazim @ 2 g kg⁻¹ seed, weed management by hand weeding at 25-30 DAS and plant protection measures (Monocrotophos application), were uniformly adopted. Two flood irrigations were provided at tillering and grain filling stages.

2.3 Observations recorded

Observations were recorded on five randomly selected competitive plants per plot in each replication for nine characters, while days to 50% flowering and days to maturity were evaluated on a whole plot basis:

- Days to 50% flowering (DF):** Number of days from sowing until 50% of plants in a plot exhibited earhead emergence.
- Days to maturity (DM):** Number of days from sowing to physiological maturity (nearly 90% spikes turning golden yellow).
- Plant height (PH, cm):** Distance from ground level to the tip of the main spike (excluding awns) at maturity.
- Number of tillers per plant (NTPP):** Total tillers per plant counted at maximum tillering stage.
- Number of effective tillers per plant (NETPP):** Productive tillers bearing mature spikes at harvest.
- Spike length (SL, cm):** Length of main spike from base to apex (excluding awns).
- Number of grains per spike (NGPS):** Average number of grains threshed from main spikes.
- Test weight (TW, g):** Weight of 1000 clean healthy grains measured on an electronic balance.
- Grain yield per plant (GYPP, g):** Total grain weight obtained from individual plant after threshing and winnowing.
- Biological yield per plant (BYPP, g):** Total above-ground dry biomass (grain plus straw) per plant.
- Harvest index (HI, %):** Calculated as (Grain yield per plant / Biological yield per plant) x 100.

2.4 Statistical analysis

Analysis of variance (ANOVA) was executed according to Panse *et al.* (1967) [14] for Randomized Block Design. Genotypic variance (σ^2_g) and phenotypic variance (σ^2_p) were calculated as $\sigma^2_g = \frac{MS_g - MS_e}{r}$ and $\sigma^2_p = \sigma^2_g + MS_e$. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated as per Burton (1952) [9]. Broad-sense heritability (h^{2bs}) was estimated as per Allard (1960) [15]. Expected genetic advance (GA) and genetic advance as per cent of mean (GAM) under 5% selection intensity ($k = 2.06$) were calculated following Johnson *et al.* (1955) [10]. Genotypic (r_g) and phenotypic (r_p) correlation coefficients were computed following Al-Jibouri *et al.* (1958) [11]. Path coefficient analysis was carried out according to Wright (1921) [12] and Dewey *et al.* (1959) [13] using grain yield per plant as the dependent variable.

3. Results

3.1 Analysis of variance

The mean sum of squares due to genotypes was highly significant ($P \leq 0.01$) for all eleven quantitative characters studied, confirming the presence of substantial genetic variation among the evaluated barley genotypes (Table 2).

Table 2. Analysis of variance (ANOVA) for 11 quantitative traits in 22 barley genotypes

Source	d.f.	DF	DM	PH	NTPP	NETPP	SL	NGPS	TW	GYPP	BYPP	HI
Replication	2	1.44	3.76	9.07	0.28	0.06	1.81	0.14	1.46	4.66	1.02	0.39
Genotypes	21	15.04**	26.54**	237.12**	6.26**	1.04**	5.99**	50.19**	25.56**	13.75**	31.44**	65.26**
Error	42	3.77	10.89	5.63	0.34	0.03	0.65	2.35	1.82	1.44	1.14	0.97

* Significant at $P \leq 0.05$ level; ** Significant at $P \leq 0.01$ level

3.2 Mean performance of genotypes

Considerable variation was recorded across all genotypes for growth and yield traits (Table 3):

The studied genotypes exhibited considerable variation in growth, phenological and yield attributes. Days to 50% flowering ranged from 80.20 days in K 603 to 88.05 days in BH 393, with a mean of 83.46 days, while days to maturity varied from 77.87 days in RD 2552 to 107.60 days in BH 393, with an overall mean of 95.00 days. Plant height ranged from 113.54 cm in RD 2503 to 125.74 cm in BH 946, with a mean of 121.37 cm. The number of tillers per plant varied from 6.56 in BH 946 to 11.46 in RD 3109, with a mean of 9.18, whereas effective tillers per plant ranged from 5.28 in BH 946 to 7.04 in RD

3109, with a mean of 6.25. Spike length ranged from 7.97 cm in BH 946 to 10.36 cm in RD 3109, with an average of 8.94 cm. The number of grains per spike varied from 43.25 in BH 946 to 61.32 in RD 3109, with a mean of 55.28 grains, while 1000-grain weight ranged from 40.36 g in BH 946 to 52.31 g in RD 3109, with a mean of 47.58 g. Grain yield per plant ranged from 14.92 g in BH 946 to 23.77 g in RD 3109, with a mean of 18.10 g. Among the genotypes, RD 3109 recorded the highest grain yield per plant (23.77 g), followed by K 499 (20.60 g), K 603 (20.39 g), RD 2907 (20.31 g) and K 125 (20.11 g). Biological yield per plant ranged from 37.23 g in BH 946 to 49.31 g in RD 3109, with a mean of 43.60 g. Harvest index varied from 32.27% in BL 2 to 49.20% in RD 3088, with an overall mean of 41.61%.

Table 3. Mean performance of 22 barley genotypes for 11 quantitative traits during *Rabi* 2025-26

Genotype	DF	DM	PH (cm)	NTPP	NETPP	SL (cm)	NGPS	TW (g)	GYPP (g)	BYPP (g)	HI (%)
RD 3089	84.00	100.88	119.58	10.30	6.69	9.42	56.87	49.25	18.95	45.23	37.90
RD 3088	86.54	86.25	119.87	7.46	5.45	8.17	51.13	45.32	15.59	39.23	49.20
RD 3109	83.64	97.61	121.05	11.46	7.04	10.36	61.32	52.31	23.77	49.31	44.07
RD 3102	85.23	107.23	120.57	8.66	6.04	8.40	54.36	46.32	17.22	42.29	46.09
BH 393	88.05	107.60	123.54	7.46	5.55	8.20	51.62	45.37	15.86	41.23	45.08
BH 946	85.61	103.03	125.74	6.56	5.28	7.97	43.25	40.36	14.92	37.23	46.25
BH 959	84.22	85.08	123.67	7.64	5.58	8.35	52.16	46.27	16.24	41.23	35.80
Ajad 34	80.36	93.97	122.64	9.76	6.44	9.11	56.57	49.25	18.61	44.23	37.49
K 125	80.95	84.54	121.74	10.72	6.92	9.61	58.54	49.51	20.11	46.23	40.65
K 551	83.47	84.57	123.94	8.76	6.15	8.50	55.66	46.90	17.57	43.23	38.52
K 603	80.20	95.56	123.54	10.76	6.99	10.02	59.63	50.61	20.39	47.39	36.68
K 499	85.61	80.25	115.39	10.76	7.01	10.22	61.23	51.64	20.60	47.73	46.31
RD 2552	80.64	77.87	120.88	8.67	6.10	8.44	55.42	46.85	17.55	43.23	46.14
RD 2052	84.62	86.36	122.81	9.26	6.39	8.96	56.33	48.62	18.45	43.63	44.43
Rajkiran	84.51	102.42	121.58	8.46	5.66	8.35	52.82	46.27	16.28	41.43	39.72
RD 2907	83.97	99.53	120.88	10.75	6.94	9.88	59.54	49.61	20.31	46.73	42.57
RD 2503	80.24	95.66	113.54	9.05	6.34	8.88	56.03	48.57	18.32	43.55	38.93
RD 2786	85.66	106.29	123.94	7.46	5.33	8.13	50.54	41.28	15.11	38.52	49.02
RD 2790	82.54	100.41	117.58	9.96	6.50	9.31	56.69	49.25	18.68	44.65	37.57
RD 2660	83.23	98.61	121.57	8.96	6.24	8.63	55.80	47.62	17.71	43.43	37.50
RDB 1	81.54	98.39	120.74	10.56	6.89	9.48	57.49	49.31	19.40	45.23	43.21
BL 2	81.36	97.89	125.41	8.46	5.98	8.38	53.22	46.27	16.59	42.23	32.27
Mean	83.46	95.00	121.37	9.18	6.25	8.94	55.28	47.58	18.10	43.60	41.61
SEm ($\pm$)	1.12	1.37	1.90	0.34	0.11	0.47	0.89	0.78	0.69	0.62	0.57
CD (5%)	3.20	3.91	5.44	0.96	0.30	1.33	2.53	2.22	1.98	1.76	1.62
CD (1%)	4.28	5.23	7.27	1.28	0.41	1.78	3.38	2.97	2.64	2.36	2.17
CV (%)	2.33	2.50	2.72	6.30	2.95	8.91	2.77	2.83	6.62	2.45	2.36

3.3 Genetic variability parameters

Estimates of phenotypic coefficient of variation (PCV) were slightly higher than genotypic coefficient of variation (GCV) for all characters, indicating low environmental influence on trait expression (Table 4). The highest GCV and PCV values were recorded for number of tillers per plant (15.21% GCV, 16.46% PCV), grain yield per plant (11.18% GCV, 12.99% PCV) and harvest index (11.13% GCV,

11.37% PCV). Moderate GCV and PCV values were observed for number of effective tillers per plant (9.26% GCV, 9.72% PCV), days to maturity (9.25% GCV, 9.58% PCV), biological yield per plant (7.29% GCV, 7.69% PCV), number of grains per spike (7.22% GCV, 7.74% PCV), spike length (6.88% GCV, 11.25% PCV) and test weight (5.91% GCV, 6.56% PCV). Days to 50% flowering (2.32% GCV, 3.29% PCV) and plant height (1.88% GCV, 3.31% PCV) exhibited low GCV and PCV.

Broad-sense heritability (h^{2bs}) estimates were high for harvest index (95.68%), days to maturity (93.20%), number of effective tillers per plant (90.78%), biological yield per plant (89.82%), number of grains per spike (87.16%), number of tillers per plant (85.37%), test weight (81.31%) and grain yield per plant (74.01%). Moderate heritability

was observed for days to 50% flowering (49.89%), while spike length (37.36%) and plant height (32.40%) showed lower heritability. Genetic advance as per cent of mean (GAM) was highest for number of tillers per plant (28.95%), harvest index (22.42%), grain yield per plant (19.81%), days to maturity (18.39%) and number of effective tillers per plant (18.17%).

Table 4. Estimation of genetic variability parameters for 11 quantitative traits in 22 barley genotypes

Trait	Mean	Range (Min - Max)	GCV (%)	PCV (%)	h^{2bs} (%)	GA	GAM (%)
Days to 50% flowering	83.46	80.20 - 88.05	2.32	3.29	49.89	2.82	3.38
Days to maturity	95.00	77.87 - 107.60	9.25	9.58	93.20	17.47	18.39
Plant height (cm)	121.37	113.54 - 125.74	1.88	3.31	32.40	2.68	2.21
Number of tillers per plant	9.18	6.56 - 11.46	15.21	16.46	85.37	2.67	28.95
Number of effective tillers per plant	6.25	5.28 - 7.04	9.26	9.72	90.78	1.14	18.17
Spike length (cm)	8.94	7.97 - 10.36	6.88	11.25	37.36	0.78	8.66
Number of grains per spike	55.28	43.25 - 61.32	7.22	7.74	87.16	7.68	13.89
Test weight (1000-grain wt, g)	47.58	40.36 - 52.31	5.91	6.56	81.31	5.22	10.98
Grain yield per plant (g)	18.10	14.92 - 23.77	11.18	12.99	74.01	3.59	19.81
Biological yield per plant (g)	43.60	37.23 - 51.33	7.29	7.69	89.82	6.20	14.23
Harvest index (%)	41.61	32.27 - 49.20	11.13	11.37	95.68	9.33	22.42

3.4 Correlation coefficient analysis

Genotypic correlation coefficients were generally higher in magnitude than phenotypic correlation coefficients, indicating inherent genetic relationships among traits (Table 5 and Table 6). Grain yield per plant exhibited highly significant positive genotypic correlations (r_g) with number of grains per spike ($r_g = 0.8835^{**}$), number of effective tillers per plant ($r_g = 0.8519^{**}$), test weight ($r_g = 0.8456^{**}$), spike length ($r_g = 0.8231^{**}$), harvest index ($r_g = 0.7767^{**}$) and biological yield per plant ($r_g = 0.7767^{**}$). Significant positive genotypic associ-

ations were also observed with number of tillers per plant ($r_g = 0.3090^{*}$) and plant height ($r_g = 0.2770^{*}$).

At the phenotypic level (r_p), grain yield per plant showed highly significant positive correlations with number of effective tillers per plant ($r_p = 0.8253^{**}$), biological yield per plant ($r_p = 0.8198^{**}$), number of grains per spike ($r_p = 0.7946^{**}$), test weight ($r_p = 0.7772^{**}$), spike length ($r_p = 0.7414^{**}$) and harvest index ($r_p = 0.7413^{**}$). Significant positive phenotypic correlations were also observed with number of tillers per plant ($r_p = 0.3090^{*}$) and days to 50% flowering ($r_p = 0.2665^{*}$).

Table 5. Genotypic correlation coefficients (r_g) among 11 quantitative traits in 22 barley genotypes

Trait	DF	DM	PH	NTPP	NETPP	SL	NGPS	TW	GYPP	BYPP	HI
DF	1.0000	0.5114*	0.3219	-0.5186*	0.5801**	-0.1371	-0.0270	-0.2160	-0.0491	0.8528**	-0.0055
DM		1.0000	0.3149	-0.4840*	0.4685**	0.1345	0.5219*	0.3025	0.0863	0.5171*	0.3534
PH			1.0000	-0.0773	0.3457**	0.4426*	0.6465**	0.2696**	0.2770*	0.6217**	0.0746
NTPP				1.0000	0.6167**	0.6282**	0.8050**	0.3393	0.3090*	0.6121**	0.3484
NETPP					1.0000	0.6131**	0.8610**	0.8795**	0.8519**	0.8108**	0.6798**
SL						1.0000	0.1045	0.4181**	0.8231**	-0.3726*	0.7217**
NGPS							1.0000	0.6004**	0.8835**	0.7613**	-0.0736
TW								1.0000	0.8456**	0.8430**	0.3736
GYPP									1.0000	-0.5102	0.7767**
BYPP										1.0000	-0.0421
HI											1.0000

(continued on next page)

Table 6. Phenotypic correlation coefficients (rp) among 11 quantitative traits in 22 barley genotypes

Trait	DF	DM	PH	NTPP	NETPP	SL	NGPS	TW	GYPP	BYPP	HI
DF	1.0000	0.2809*	0.3204**	-0.3569**	-0.0066	0.0041	-0.0604	0.0078	-0.0735	0.2665*	-0.0320
DM		1.0000	0.2465*	-0.3443**	0.0435	-0.0015	0.0599	0.0340	0.0520	0.0548	0.0453
PH			1.0000	-0.0981	0.1761	0.1269	0.2189	0.2093	0.1221	0.1686	0.0624
NTPP				1.0000	0.1819	0.2636*	0.2712*	0.3287**	0.3090*	0.1313	0.3336**
NETPP					1.0000	0.8458**	0.8681**	0.8328**	0.8253**	0.8923**	0.6860**
SL						1.0000	0.5938**	0.7679**	0.7414**	0.8292**	0.6733**
NGPS							1.0000	0.8614**	0.7946**	0.8807**	0.6316**
TW								1.0000	0.7772**	0.8503**	0.6245**
GYPP									1.0000	0.8198**	0.7413**
BYPP										1.0000	0.6661**
HI											1.0000

3.5 Path coefficient analysis

Path coefficient analysis partitioned genotypic and phenotypic correlation coefficients into direct and indirect effects on grain yield per plant (Table 7 and Table 8).

Genotypic path coefficient analysis revealed that harvest index exerted the highest positive direct effect on grain yield per plant (0.3888), followed by number of effective tillers per plant (0.2624), spike length (0.2015), biological yield per plant (0.1604) and test weight (0.0804). Negative direct effects were registered by number of

tillers per plant (-0.5042), days to maturity (-0.4392), days to 50% flowering (-0.2867), plant height (-0.1368) and number of grains per spike (-0.1051).

Phenotypic path coefficient analysis showed that harvest index (0.2589), biological yield per plant (0.2564), number of effective tillers per plant (0.1597), spike length (0.1464), test weight (0.1093), number of grains per spike (0.0494), days to maturity (0.0165), number of tillers per plant (0.0016) and plant height (0.0003) recorded positive direct contributions to grain yield per plant. Days to 50% flowering (-0.0920) exerted a negative direct effect.

Table 7. Genotypic path coefficient analysis showing direct (bold) and indirect effects on grain yield per plant

Trait	DF	DM	PH	NTPP	NETPP	SL	NGPS	TW	BYPP	HI	rg
DF	-0.2867	-0.2246	-0.0440	0.2615	0.1522	-0.0276	0.0028	-0.0174	0.1368	-0.0022	-0.0491
DM	-0.1466	-0.4392	-0.0431	0.2440	0.2541	0.0271	-0.0549	0.0243	0.0830	0.1374	0.0863
PH	-0.0923	-0.1383	-0.1368	0.0390	0.3600	0.0892	-0.0680	0.1488	0.0997	0.0290	0.3304
NTPP	0.1487	0.2126	0.0106	-0.5042	0.1618	0.1266	-0.0846	0.2121	0.0982	0.2638	0.6454**
NETPP	-0.1663	-0.4253	-0.1876	-0.3109	0.2624	-0.2892	-0.1403	0.2846	0.1301	-0.9619	-1.8045**
SL	0.0393	-0.0591	-0.0605	-0.3168	-0.3766	0.2015	-0.0110	0.0336	-0.0598	-0.4664	-1.0757**
NGPS	0.0077	-0.2292	-0.0884	-0.4059	0.3502	0.0211	-0.1051	0.2313	0.1221	-0.0286	-0.1248
TW	0.0619	-0.1328	-0.2530	-1.3297	0.9284	0.0842	-0.3023	0.0804	0.3057	0.1453	-0.4119
BYPP	-0.2444	-0.2271	-0.0850	-0.3086	0.2127	-0.0751	-0.0800	0.1532	0.1604	-0.0164	-0.5102*
HI	0.0016	-0.1552	-0.0102	-0.3420	-0.6490	-0.2417	0.0077	0.0300	-0.0068	0.3888	-0.9767**

Table 8. Phenotypic path coefficient analysis showing direct (bold) and indirect effects on grain yield per plant

Trait	DF	DM	PH	NTPP	NETPP	SL	NGPS	TW	BYPP	HI	rp
DF	-0.0920	0.0006	0.0001	-0.0005	-0.0011	0.0006	-0.0030	0.0009	0.0292	-0.0083	-0.0735
DM	-0.0032	0.0165	0.0000	-0.0005	0.0069	-0.0002	0.0030	0.0037	0.0141	0.0117	0.0520
PH	-0.0199	0.0020	0.0003	-0.0001	0.0281	0.0186	0.0108	0.0229	0.0432	0.0162	0.1221
NTPP	0.0274	-0.0052	0.0000	0.0016	0.0087	0.0189	0.0073	0.0206	0.0204	0.0488	0.1486
NETPP	0.0006	0.0007	0.0001	0.0001	0.1597	0.1238	0.0429	0.0910	0.2288	0.1776	0.8253**
SL	-0.0004	0.0000	0.0000	0.0002	0.1350	0.1464	0.0392	0.0839	0.2126	0.1743	0.7914**
NGPS	0.0056	0.0010	0.0001	0.0002	0.1386	0.1162	0.0494	0.0942	0.2258	0.1635	0.7946**
TW	-0.0007	0.0006	0.0001	0.0003	0.1330	0.1124	0.0426	0.1093	0.2180	0.1617	0.7772**
BYPP	-0.0105	0.0009	0.0001	0.0001	0.1425	0.1214	0.0435	0.0929	0.2564	0.1725	0.8198**
HI	0.0029	0.0007	0.0000	0.0003	0.1095	0.0986	0.0312	0.0683	0.1708	0.2589	0.7413**

4. Discussion

4.1 Genetic variability and selection scope

The presence of highly significant differences among genotypes for all eleven traits demonstrates the availability of substantial genetic variability in the studied barley germplasm. Similar results were documented by Amabile *et al.* (2017) [16], Sunil *et al.* (2017) [17],

Adhikari *et al.* (2018) [18], Abebe *et al.* (2024) [19] and Sisodiya *et al.* (2025). High PCV and GCV estimates for number of tillers per plant, grain yield per plant and harvest index indicates high potential for direct phenotypic selection. Small differences between GCV and PCV across traits further confirm that environmental factors had minimal masking influence on trait expression, in line with findings reported by Matin *et al.* (2019) [20] and Kobir *et al.* (2023) [21].

4.2 Heritability and genetic advance

Heritability estimates combined with genetic advance provide a reliable basis for predicting selection gains. High broad-sense heritability coupled with high genetic advance as per cent of mean (GAM) was recorded for number of tillers per plant, harvest index, grain yield per plant, days to maturity and number of effective tillers per plant. This pattern indicates that these traits are predominantly controlled by additive gene action, making direct phenotypic selection effective. These conclusions align with earlier observations by Kaur *et al.* (2016) [22], Kumar *et al.* (2018) [23], Abebe *et al.* (2024) [19] and Sisodiya *et al.* (2025). Conversely, low heritability coupled with low GAM for plant height and days to 50% flowering suggests significant non-additive or environmental influence, indicating limited scope for yield enhancement via direct selection for these two traits.

4.3 Trait associations and selection criteria

Correlation analysis showed that grain yield per plant was strongly and positively associated with number of effective tillers per plant, number of grains per spike, test weight, spike length, biological yield per plant and harvest index at both genotypic and phenotypic levels. Similar significant positive yield correlations were reported by Dyulgerova (2012), Pilania *et al.* (2014) [24], Singh *et al.* (2014) [25], Kumari *et al.* (2022) [26] and Zewodu *et al.* (2025) [27]. Path coefficient analysis demonstrated that harvest index, number of effective tillers per plant, biological yield per plant, spike length and test weight exerted strong positive direct effects on grain yield at both genotypic and phenotypic levels. Traits such as number of grains per spike also contributed substantially to yield through positive indirect pathways via effective tillers, test weight and biological yield. These findings are supported by Zaefizadeh *et al.* (2011) [28], Madakemohekar *et al.* (2015) [29], Solemani *et al.* (2017) [30], Shrimali *et al.* (2017) [31], Nagesh *et al.* (2019) [32] and Robir *et al.* (2023) [21].

4.4 Superior genotype identification

Among the 22 genotypes evaluated, RD 3109 demonstrated outstanding performance, recording the highest grain yield per plant (23.77 g), highest biological yield per plant (49.31 g), highest number of effective tillers per plant (7.04), highest test weight (52.31 g) and longest spike length (10.36 cm). Other high-yielding promising genotypes identified were K 499 (20.60 g yield/plant), K 603 (20.39 g yield/plant), RD 2907 (20.31 g yield/plant) and K 125 (20.11 g yield/plant). Genotype RD 3088 achieved the highest harvest index (49.20%). These superior genotypes represent valuable genetic resources for future hybridization and variety development programmes.

5. Conclusion and suggestions for further work

The study concludes that substantial genetic variability exists among the evaluated barley genotypes. Direct phenotypic selection based on harvest index, number of effective tillers per plant, spike length, test weight and biological yield per plant will be effective in improving grain yield in barley. Genotypes RD 3109, K 499, K 603, RD 2907 and K 125 are recommended as elite parental lines for future breeding initiatives.

Suggestions for future research

1. Multi-location and multi-season trials should be conducted to test the stability and environmental adaptability of promising genotypes (RD 3109, K 499, K 603, RD 2907 and K 125).
2. Hybridization programs involving these diverse elite lines should be initiated to combine high harvest index, tillering efficiency and grain bold weight.
3. Identified genotypes should be evaluated under abiotic stress conditions (salinity, drought and heat) to isolate climate-resilient lines.

4. Molecular marker-assisted selection (MAS) and QTL mapping should be utilized to target key genomic regions controlling harvest index and productive tillering.

Declarations

Conflict of interest

The authors declare that they have no competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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