



International Journal of Research in Agronomy

E-ISSN: 2618-0618
P-ISSN: 2618-060X
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NAAS Rating (2026): 5.20
www.agronomyjournals.com
2026; 9(8): 518-524
Received: 13-05-2026
Accepted: 16-06-2026

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Genotypic Response to Salt Stress Tolerance in Barley (*Hordeum vulgare* L.)

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DOI: <https://www.doi.org/10.33545/2618060X.2026.v9.i8g.6282>

Abstract

Salinity is one of the major abiotic stresses limiting barley productivity by adversely affecting plant growth, development and grain yield. The present investigation was conducted during the Rabi season of 2025-26 at the Agricultural Research Farm, Suresh Gyan Vihar University (SGVU), Jaipur, Rajasthan, to evaluate genetic variability, character association and direct and indirect effects of yield-contributing traits among 18 barley genotypes (16 test genotypes and two check varieties) under salt stress conditions. The experiment was laid out in a Randomized Block Design (RBD) with three replications. Observations were recorded on fourteen quantitative traits. Analysis of variance (ANOVA) revealed highly significant ($p < 0.01$) differences among genotypes for all characters, confirming the existence of substantial genetic variability. Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all traits, indicating the influence of environmental factors. High heritability coupled with high genetic advance as percent of mean (GAM) was observed for grain yield per plant ($h^2_{bs} = 91.0\%$; $GAM = 23.17\%$), number of effective tillers per plant ($h^2_{bs} = 91.8\%$; $GAM = 21.42\%$) and number of tillers per plant ($h^2_{bs} = 89.6\%$; $GAM = 21.40\%$), indicating the predominance of additive gene action. Correlation analysis revealed that grain yield per plant was strongly and positively associated with biological yield per plant ($rg = 0.9985$), spike length ($rg = 0.9975$), plant height ($rg = 0.9970$) and number of grains per spike ($rg = 0.9967$). Path coefficient analysis demonstrated that biological yield per plant exerted the highest positive genotypic direct effect (0.9241) on grain yield, followed by spike length (0.2887) and harvest index (0.1934). Genotype RD 2552 exhibited consistently superior performance for grain yield per plant (20.5 g), biological yield per plant (46.5 g) and harvest index (44.09%), making it the most promising salt-tolerant genotype. DWRB 223, RD 2907, Karan 18 and Rajkiran also performed well under saline conditions. The findings provide valuable information for future barley breeding programmes aimed at developing high-yielding, salt-tolerant cultivars.

Keywords: Barley, *Hordeum vulgare* L., salinity stress, genetic variability, heritability, correlation, path coefficient analysis, grain yield, salt tolerance

1. Introduction

Barley (*Hordeum vulgare* L.) is the fourth most important cereal crop worldwide, following maize, wheat and rice, with an annual global production of approximately 150 million Mg (USDA-FAS, 2026) ^[1]. It is a self-pollinating diploid species ($2n=2x=14$) that has been cultivated since the Stone Age and was among the first domesticated plants in human history (Salamini *et al.*, 2002; Haas *et al.*, 2019) ^[2, 3]. Barley is valued for its wide adaptability to diverse agro-climatic conditions, including tolerance to marginal soils, drought and salinity, making it an important crop in arid and semi-arid regions where other cereals struggle to perform (Mwando *et al.*, 2020) ^[4].

Salinity is recognised as one of the most critical abiotic stresses limiting crop growth and agricultural productivity worldwide. Nearly 1.4 billion hectares of global land (approximately 10.7% of total land area) are affected by salinity (FAO, 2024) ^[5], with the problem particularly severe in arid and semi-arid regions. In India, approximately 6.73 million hectares of land are affected by salinity and sodicity and Rajasthan alone accounts for about 1.18-1.19 million hectares of salt-affected land (ICAR, 2025) ^[6]. Projections by the Central Soil Salinity Research Institute indicate that without intervention, this area could increase to 16.2 Mha by 2050 due to climate change and poor-quality irrigation water (Sharma *et al.*, 2024) ^[7].

Salinity stress imposes two major types of injury on plants: Osmotic stress, which occurs immediately upon salt accumulation in the root zone and reduces water availability and ionic stress, which develops as toxic Na and Cl ions accumulate in plant tissues, disrupting metabolic⁺ processes, reducing stomatal conductance, limiting photosynthetic activity and ultimately impairing grain yield (Munns and Tester, 2008) ^[8].

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Despite barley's relatively better tolerance to salinity compared to other cereals, considerable genotypic variation exists within the species for salinity tolerance and identification of salt-tolerant genotypes remains a priority in barley improvement programmes (Mwando *et al.*, 2020) [4].

During 2024-25, India had approximately 6.62 lakh hectares under barley cultivation with a total production of 19.19 lakh tonnes and an average productivity of 29.0 q/ha (Anonymous, 2025) [9]. Grain yield in barley is a complex polygenic trait influenced by several component traits as well as environmental factors, including plant height, number of tillers per plant, spike length, grains per spike and 1000-grain weight (Patial *et al.*, 2024) [10]. Understanding genetic variability and the interrelationships among these traits under salt stress is essential for designing effective breeding strategies (Dewey and Lu, 1959; Wright, 1921) [11, 12].

Genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability and genetic advance as percent of mean (GAM) are widely used to assess the extent of variability and predict selection response (Johnson *et al.*, 1955) [13]. Path coefficient analysis, introduced by Wright (1921) [12], is a powerful statistical tool that partitions correlation coefficients into direct and indirect effects, thereby providing insights into the relative importance of each trait in determining grain yield under stress environments (Dewey and Lu, 1959) [11]. With this background, the present investigation was undertaken to: (i) evaluate genetic variability among 18 barley genotypes under salt stress conditions; (ii) estimate correlation between yield and yield-attributing traits; (iii) determine direct and indirect effects of component traits on grain yield through path analysis; and (iv) identify promising salt-tolerant barley genotypes for future breeding programmes.

2. Materials and Methods

2.1 Experimental Location and Design

The experiment was conducted during the Rabi season of 2025-26 at the Agricultural Research Farm, Suresh Gyan Vihar University (SGVU), Jaipur, Rajasthan. The experimental farm is located at approximately 26°54'N latitude and 75°49'E longitude, at an altitude of 431 m above mean sea level, representing typical arid to semi-arid climatic conditions of Rajasthan.

2.2 Experimental Material

The experimental material consisted of 18 barley genotypes, comprising 16 test genotypes (RD 2907, RD 2794, RD 2552, RD 2715, RD 2786, RD 2035, Rajkiran, Karan 18, RD 3095,

DWRB 137, RD 2668, RD 2899, RD 2849, RD 2052, DWRB 223 and Jyoti) and two check varieties [Karan 16 (C) and BL 2 (C)]. The experiment was laid out in a Randomized Block Design (RBD) with three replications. Seeds were sown at a spacing of 22.5 cm × 10 cm in net plots measuring 3.6m × 1.8 m. Observations were recorded on five randomly selected competitive plants per plot per replication.

2.3 Traits Recorded

Data were recorded on fourteen quantitative traits: germination percentage (GP), root length (RL, cm), shoot length (SL, cm), days to 50% flowering (DFF), days to maturity (DM), plant height (PH, cm), total number of tillers per plant (NTPP), number of effective tillers per plant (NETPP), spike length (SPL, cm), number of grains per spike (NGPS), test weight/1000-grain weight (TW, g), grain yield per plant (GYPP, g), biological yield per plant (BYPP, g) and harvest index (HI, %).

2.4 Statistical Analysis

Analysis of variance (ANOVA) was performed according to the procedure for RBD (Panse and Sukhatme, 1985) [14]. Genotypic variance (σ^2_g) and phenotypic variance (σ^2_p) were estimated following standard biometrical procedures. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated as per Burton (1952) [15]. Broad-sense heritability (h^2_{bs}) was estimated following Allard (1960) [16] and genetic advance (GA) and genetic advance as percent of mean (GAM) were estimated following Johnson *et al.* (1955) [13] at 5% selection intensity. Genotypic and phenotypic correlation coefficients were calculated following Al-Jibouri *et al.* (1958) [17]. Path coefficient analysis was carried out following Wright (1921) [12] and Dewey and Lu (1959) [11] with grain yield per plant as the dependent variable.

3. Results

3.1 Analysis of Variance

The analysis of variance (Table 1) revealed highly significant differences ($p < 0.01$) among the 18 barley genotypes for all 14 quantitative traits studied. The mean sum of squares due to genotypes was significantly higher than the error mean sum of squares for every trait, confirming the existence of substantial genetic diversity and inherent variation within the experimental germplasm under salt stress conditions. This provides ample scope for direct phenotypic selection and genetic improvement for salt tolerance.

Table 1: Analysis of variance (mean sum of squares) for 14 quantitative traits in 18 barley genotypes under salt stress (Rabi, 2025-26)

S. No.	Character	Replications (df = 2)	Genotypes (df = 17)	Error (df = 34)
1	Germination (%)	0.287	34.618**	0.963
2	Root length (cm)	0.017	2.680**	0.048
3	Shoot length (cm)	0.008	3.249**	0.057
4	Days to 50% flowering	0.088	7.917**	0.176
5	Days to maturity	0.207	7.422**	0.272
6	Plant height (cm)	0.771	63.856**	0.814
7	Number of tillers per plant	0.007	1.637**	0.012
8	Number of effective tillers/plants	0.021	2.100**	0.018
9	Spike length (cm)	0.003	1.111**	0.012
10	Number of grains per spike	0.252	26.502**	0.320
11	Test weight (1000-grain weight, g)	0.117	11.238**	0.144
12	Grain yield per plant (g)	0.028	11.890**	0.080
13	Biological yield per plant (g)	0.046	36.216**	0.298
14	Harvest index (%)	0.129	4.887**	0.211

Significant at 1% level of probability

3.2 Mean Performance of Barley Genotypes

The mean performance of the 18 barley genotypes for all 14 quantitative traits under salt stress is presented in Table 2. Among the evaluated genotypes, RD 2552 recorded the highest values for germination percentage (90.3%), root length (14.5 cm), shoot length (17.5 cm), plant height (88.4 cm), total tillers per plant (9.2), effective tillers per plant (7.67), spike length (9.9 cm), grains per spike (51.3), test weight (47.4 g), grain yield per plant (20.5 g), biological yield per plant (46.5 g) and harvest index (44.09%), while also achieving the earliest flowering (78.2 days) and maturity (120.1 days). DWRB 223 consistently

ranked second across most traits. RD 2907, Karan 18 and Rajkiran also performed commendably. In contrast, RD 2052 recorded the lowest values for most yield traits, suggesting high sensitivity to salt stress. The overall trial means were: germination 84.8%, root length 12.9 cm, shoot length 15.9 cm, days to 50% flowering 80.6 days, days to maturity 122.3 days, plant height 80.4 cm, NTPP 7.99, NETPP 6.07, spike length 8.92 cm, grains per spike 46.34, test weights 43.95 g, grain yield per plant 16.92 g, biological yield per plant 39.58 g and harvest index 42.14%.

Table 2: Mean performance of 18 barley genotypes under salt stress during Rabi, 2025-26

S.No.	Genotype	G P (%)	R L (c m)	SL (c m)	D FF	D M	P H (c m)	NT PP	NET PP	SP L (c m)	NG PS	T W (g)	GY PP (g)	BY PP (g)	HI (%)
G ₁	RD2907	88.3	13.8	16.8	79.3	121.3	84.8	8.6	6.33	9.4	48.6	45.8	18.4	42.8	42.99
G ₂	RD2794	84.7	12.9	15.7	80.6	122.5	79.6	7.8	5.67	8.8	45.8	43.6	16.2	38.6	41.97
G ₃	RD2552	90.3	14.5	17.5	78.2	120.1	88.4	9.2	7.67	9.9	51.3	47.4	20.5	46.5	44.09
G ₄	RD2715	83.6	12.6	15.4	81.4	123.4	77.9	7.6	5.33	8.6	44.9	42.9	15.8	37.8	41.80
G ₅	RD2786	81.9	12.1	15.0	82.0	123.8	76.5	7.4	5.00	8.5	44.2	42.5	15.2	36.9	41.19
G ₆	RD2035	79.8	11.5	14.2	83.1	125.2	73.4	6.8	4.67	8.0	41.6	40.8	13.8	34.4	40.12
G ₇	Rajkir an	86.2	13.4	16.3	79.8	121.8	82.6	8.3	7.33	9.1	47.2	44.7	17.6	41.2	42.72
G ₈	Karan18	87.4	13.7	16.6	79.1	121.0	83.9	8.5	6.67	9.3	48.1	45.2	18.1	42.1	43.00
G ₉	RD3095	85.9	13.2	16.0	80.2	122.1	81.8	8.1	5.67	9.0	46.8	44.3	17.2	40.5	42.47
G ₁₀	DWR B 137	82.7	12.3	15.2	81.6	123.2	77.8	7.5	5.00	8.6	44.6	42.8	15.6	37.5	41.60
G ₁₁	RD2668	84.1	12.8	15.8	80.5	122.6	80.2	7.9	6.33	8.9	45.9	43.8	16.8	39.2	42.86
G ₁₂	RD2899	86.8	13.5	16.4	79.5	121.5	82.9	8.4	7.00	9.2	47.6	45.0	17.9	41.6	43.03
G ₁₃	RD2849	80.4	11.9	14.8	82.4	124.3	75.1	7.2	5.67	8.3	43.2	41.9	14.6	35.8	40.78
G ₁₄	RD2052	78.9	11.2	13.7	83.6	125.8	72.6	6.6	5.33	7.8	40.8	40.2	13.2	33.7	39.17
G ₁₅	DWRB 223	88.8	14.2	17.2	78.8	120.7	86.7	8.9	7.00	9.7	50.2	46.8	19.6	44.9	43.65
G ₁₆	Jyoti	81.2	12.0	14.9	82.1	124.0	76.0	7.3	5.67	8.4	43.8	42.1	15.0	36.3	41.32
G ₁₇	Karan16 (C)	87.6	13.9	16.9	79.0	120.9	85.3	8.7	6.67	9.5	49.1	46.1	18.9	43.6	43.35
G ₁₈	BL 2(C)	85.4	13.1	16.1	80.0	122.0	81.5	8.0	6.33	9.0	46.5	44.5	17.3	40.8	42.40
	Mean	84.8	12.9	15.9	80.6	122.3	80.4	7.99	6.07	8.92	46.34	43.95	16.92	39.58	42.14
	SE±	1.18	0.23	0.28	0.42	0.56	1.15	0.16	0.22	0.12	0.64	0.42	0.31	0.54	0.36
	CD(5%)	3.48	0.68	0.82	1.24	1.65	3.38	0.47	0.66	0.36	1.88	1.24	0.91	1.58	1.06
	CV(%)	2.86	3.15	3.42	1.18	0.95	2.95	3.54	6.28	2.74	2.91	2.18	3.18	2.36	1.84

Abbreviations: GP: Germination (%); RL: Root length (cm); SL: Shoot length (cm); DFF: Days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); NTPP: Total tillers per plant; NETPP: Effective tillers per plant; SPL: Spike length (cm); NGPS: Number of grains per spike; TW: Test weight (1000-grain weight, g); GYPP: Grain yield per plant (g); BYPP: Biological yield per plant (g); HI: Harvest index (%); C: Check variety.

3.3 Genetic Variability Parameters

Estimates of GCV, PCV, broad-sense heritability (h^2_{bs}), genetic advance (GA) and genetic advance as percent of mean (GAM) for all 14 quantitative traits are presented in Table 3. Across all traits, PCV estimates were slightly higher than corresponding GCV estimates, indicating environmental influence on phenotypic expression. However, the narrow gap between GCV and PCV for most traits demonstrates that the variability is predominantly governed by genetic factors.

The highest GCV and PCV were recorded for grain yield per plant (GCV: 11.74%; PCV: 12.31%), followed by number of tillers per plant (GCV: 10.94%; PCV: 11.56%), number of effective tillers per plant (GCV: 10.85%; PCV: 11.32%) and biological yield per plant (GCV: 9.82%; PCV: 10.40%), indicating high genetic variation for these traits. Moderate GCV and PCV were recorded for root length (GCV: 8.95%; PCV: 9.76%), number of grains per spike (GCV: 8.46%; PCV:

9.02%), shoot length (GCV: 8.31%; PCV: 9.14%), spike length (GCV: 7.63%; PCV: 8.24%) and plant height (GCV: 6.82%; PCV: 7.45%). Low estimates were observed for test weight, germination percentage, harvest index, days to 50% flowering and days to maturity.

Broad-sense heritability was high (>60%) for all traits, ranging from 69.5% for days to 50% flowering to 91.8% for number of effective tillers per plant. Exceptionally high heritability was also observed for grain yield per plant (91.0%), number of tillers per plant (89.6%), biological yield per plant (88.5%) and number of grains per spike (87.9%). High heritability coupled with high GAM was recorded for grain yield per plant (GAM: 23.17%), number of effective tillers per plant (GAM: 21.42%) and number of tillers per plant (GAM: 21.40%), indicating the predominance of additive gene action and the effectiveness of direct phenotypic selection for these traits.

Table 3: Estimates of genetic variability parameters for 18 barley genotypes under salt stress

Trait	Mean	Range (Min-Max)	GCV (%)	PCV (%)	h ² bs (%)	GA	GAM (%)
Germination (%)	84.8	78.9-90.3	5.48	6.12	80.2	8.56	10.10
Root length (cm)	12.9	11.2-14.5	8.95	9.76	84.1	2.18	16.89
Shoot length (cm)	15.9	13.7-17.5	8.31	9.14	82.8	2.47	15.53
Days to 50% flowering	80.6	78.2-83.6	2.12	2.54	69.5	2.94	3.65
Days to maturity	122.3	120.1-125.8	1.84	2.18	71.2	3.93	3.21
Plant height (cm)	80.4	72.6-88.4	6.82	7.45	83.7	10.34	12.86
Number of tillers/plant	7.99	6.6-9.2	10.94	11.56	89.6	1.71	21.40
Eff. tillers/plant	6.07	4.67-7.67	10.85	11.32	91.8	1.30	21.42
Spike length (cm)	8.92	7.8-9.9	7.63	8.24	85.8	1.30	14.58
Number of grains/spikes	46.34	40.8-51.3	8.46	9.02	87.9	7.58	16.37
Test weight (g)	43.95	40.2-47.4	5.96	6.48	84.5	4.97	11.31
Grain yield/plant (g)	16.92	13.2-20.5	11.74	12.31	91.0	3.92	23.17
Biological yield/plant (g)	39.58	33.7-46.5	9.82	10.40	88.5	7.56	19.10
Harvest index (%)	42.14	39.17-44.9	3.60	4.08	78.6	2.79	6.62

GCV: Genotypic Coefficient of Variation; **PCV:** Phenotypic Coefficient of Variation; **h²bs:** Broad-sense heritability; **GA:** Genetic Advance; **GAM:** Genetic Advance as Percent of Mean.

3.4 Correlation Coefficient Analysis

Genotypic and phenotypic correlation coefficients between grain yield per plant and other quantitative traits are presented in Table 4. Genotypic correlations were generally higher in magnitude than phenotypic correlations across all trait pairs, indicating strong inherent genetic associations with comparatively lesser environmental influence.

Grain yield per plant showed highly significant positive correlations ($p < 0.01$) at both genotypic and phenotypic levels with biological yield per plant ($r_g = 0.9985$, $r_p = 0.9829$), test weight ($r_g = 0.9976$, $r_p = 0.9799$), spike length ($r_g = 0.9975$, r_p

$= 0.9827$), plant height ($r_g = 0.9970$, $r_p = 0.9813$), number of grains per spike ($r_g = 0.9967$, $r_p = 0.9755$), number of tillers per plant ($r_g = 0.9964$, $r_p = 0.9827$), shoot length ($r_g = 0.9937$, $r_p = 0.9696$), root length ($r_g = 0.9930$, $r_p = 0.9688$), germination percentage ($r_g = 0.9868$, $r_p = 0.9587$), harvest index ($r_g = 0.9708$, $r_p = 0.9434$) and number of effective tillers per plant ($r_g = 0.8635$, $r_p = 0.8512$). Strong negative correlations were observed with days to 50% flowering ($r_g = -0.9868$, $r_p = -0.9780$) and days to maturity ($r_g = -0.9847$, $r_p = -0.9602$), indicating that early-flowering and early-maturing genotypes avoid terminal salt stress and maintain higher grain production.

Table 4: Correlation coefficients of 13 traits with grain yield per plant at genotypic (G) and phenotypic (P) levels in barley under salt stress

Trait	Genotypic (r_g)	Phenotypic (r_p)
Biological yield per plant (g)	0.9985**	0.9829**
Test weight (g)	0.9976**	0.9799**
Spike length (cm)	0.9975**	0.9827**
Plant height (cm)	0.9970**	0.9813**
Number of grains per spike	0.9967**	0.9755**
Number of tillers per plant	0.9964**	0.9827**
Shoot length (cm)	0.9937**	0.9696**
Root length (cm)	0.9930**	0.9688**
Germination (%)	0.9868**	0.9587**
Harvest index (%)	0.9708**	0.9434**
Number of effective tillers/plants	0.8635**	0.8512**
Days to 50% flowering	-0.9868**	-0.9780**
Days to maturity	-0.9847**	-0.9602**

Significant at 1% level of probability

3.5 Path Coefficient Analysis

Path coefficient analysis was performed to partition the correlation coefficients into direct and indirect effects, providing an accurate assessment of the individual contribution of each trait towards grain yield per plant. The direct and indirect effect estimates at both genotypic and phenotypic levels are presented in Table 5.

At the genotypic level, biological yield per plant exerted the maximum positive direct effect on grain yield per plant (0.9241), followed by spike length (0.2887), harvest index (0.1934), days to maturity (0.0728), root length (0.0341), effective tillers per plant (0.0121) and germination percentage (0.0050). Negative genotypic direct effects were registered for test weight (-0.1665), number of tillers per plant (-0.1469),

plant height (-0.0656), days to 50% flowering (-0.0534), grains per spike (-0.0380) and shoot length (-0.0132).

At the phenotypic level, the highest positive direct effects were exerted by days to 50% flowering (0.3037), biological yield per plant (0.2658), spike length (0.2203), grains per spike (0.1242), days to maturity (0.1217), number of tillers per plant (0.1127), test weight (0.0569) and plant height (0.0541). Biological yield per plant also served as the primary indirect pathway driving high positive correlations of component traits with grain yield per plant at the genotypic level, with indirect contributions ranging from 0.7972 (effective tillers per plant) to 0.9214 (plant height). Days to 50% flowering and days to maturity influenced grain yield indirectly through strong negative contributions via biological yield per plant (-0.9082 and -0.9058, respectively).

Table 5: Direct effects of 13 traits on grain yield per plant at genotypic (G) and phenotypic (P) levels in 18 barley genotypes under salt stress

Trait	Direct Effect (Genotypic)	Direct Effect (Phenotypic)	Total Correlation (rg)	Interpretation
Biological yield/plant (g)	0.9241	0.2658	0.9985**	Primary yield driver
Spike length (cm)	0.2887	0.2203	0.9975**	Key selection trait
Harvest index (%)	0.1934	0.0085	0.9708**	Partitioning efficiency
Days to maturity	0.0728	0.1217	-0.9847**	Early maturity advantage
Root length (cm)	0.0341	0.0274	0.9930**	Supportive role
Eff. tillers/plant	0.0121	0.0126	0.8635**	Yield component
Germination (%)	0.0050	-0.0872	0.9868**	Stand establishment
Shoot length (cm)	-0.0132	0.0112	0.9937**	Indirect via BYPP
Days to 50% flowering	-0.0534	0.3037	-0.9868**	Stress escape mechanism
Plant height (cm)	-0.0656	0.0541	0.9970**	Indirect via BYPP
Number of tillers/plants	-0.1469	0.1127	0.9964**	Indirect via BYPP
Number of grains/spikes	-0.0380	0.1242	0.9967**	Indirect via BYPP
Test weight (g)	-0.1665	0.0569	0.9976**	Indirect via BYPP

Significant at 1% level of probability; BYPP: Biological yield per plant.

4. Discussion

4.1 Analysis of Variance and Mean Performance

Analysis of variance revealed highly significant differences ($p < 0.01$) among the 18 barley genotypes for all 14 quantitative traits, confirming the existence of substantial genetic diversity within the evaluated germplasm under salt stress. These results are consistent with the findings of [Kumar et al. \(2018\)](#) ^[18], [Sisodiya et al. \(2025\)](#) ^[19], [Meena et al. \(2025\)](#) ^[20] and [Hailu et al. \(2024\)](#) ^[21], who also reported highly significant genotypic variation for morpho-physiological and yield-contributing traits in barley under similar conditions.

Among the evaluated genotypes, RD 2552 exhibited the highest performance across all major yield and yield-contributing traits, including the highest grain yield per plant (20.5 g), biological yield per plant (46.5 g) and harvest index (44.09%), while also achieving the earliest flowering (78.2 days) and maturity (120.1 days). This superior performance of RD 2552 under saline conditions reflects better osmotic adjustment, physiological tolerance and efficient assimilate partitioning. DWRB 223, which ranked second across most traits, demonstrated commendable salt tolerance. The lowest performance across traits was consistently observed in RD 2052 and RD 2035, indicating high sensitivity to saline conditions. These results are in agreement with [Almohisen \(2021\)](#) ^[22], who observed significant genotypic differences in barley under saline and normal conditions and with [Juskiw and Helm \(2003\)](#) ^[23] and [Rathore et al. \(2016\)](#) ^[24], who documented significant genotypic variation in germination and early seedling establishment in barley under salinity.

4.2 Genetic Variability

The narrow gap between PCV and GCV across most traits in the present study demonstrates that the observed variability is predominantly governed by genetic factors, with minimal environmental influence. Similar findings were reported by [Kumar et al. \(2018\)](#) ^[18], [Verma et al. \(2022\)](#) ^[25] and [Saha et al. \(2024\)](#) ^[26] in barley. High GCV and PCV for grain yield per plant, number of tillers per plant and biological yield per plant indicate substantial genetic variation and strong selection potential for these traits under saline conditions, in agreement with [Kabir et al. \(2023\)](#) ^[27] and [Kaur and Vishwakarma \(2020\)](#) ^[28].

High broad-sense heritability (>80%) was recorded for most traits, particularly for number of effective tillers per plant (91.8%), grain yield per plant (91.0%), number of tillers per plant (89.6%) and biological yield per plant (88.5%). Similar

high heritability estimates in barley were reported by [Yadav et al. \(2015\)](#) ^[29], [Fekadu et al. \(2022\)](#) ^[30] and [Zewodu et al. \(2025\)](#) ^[31]. High heritability coupled with high GAM-as observed for grain yield per plant (91.0%, 23.17%), number of effective tillers per plant (91.8%, 21.42%) and number of tillers per plant (89.6%, 21.40%)- indicates the predominance of additive gene action, making direct phenotypic selection effective for these traits. This is consistent with [Johnson et al. \(1955\)](#) ^[13], who emphasized that high heritability alone without correspondingly high genetic advance does not necessarily indicate significant genetic gain, whereas high heritability coupled with high GAM is indicative of additive gene action.

4.3 Correlation Analysis

The stronger genotypic correlations relative to phenotypic correlations in the present study suggest that the observed trait associations have a strong genetic basis with comparatively lesser environmental masking. The highly significant positive associations of grain yield per plant with biological yield per plant, spike length, plant height, number of grains per spike and number of tillers per plant indicate that these traits are important indirect selection criteria for improving grain yield under saline conditions. Similar positive associations of grain yield with biological yield, harvest index and tillers per plant were reported by [Verma et al. \(2022\)](#) ^[25], [Saha et al. \(2024\)](#) ^[26] and [Aklilu et al. \(2020\)](#) ^[32].

The significant negative correlations of grain yield per plant with days to 50% flowering and days to maturity confirm the advantage of early-maturing genotypes in escaping terminal salinity stress, consistent with [Almohisen \(2021\)](#) ^[22] and [Zewodu et al. \(2025\)](#) ^[31]. The positive association of harvest index with grain yield ($rg = 0.9708$) further emphasises the role of assimilate partitioning efficiency as a key determinant of yield under salt stress, in agreement with [Baye et al. \(2020\)](#) ^[33] and [Adhikari et al. \(2018\)](#) ^[34].

4.4 Path Coefficient Analysis

Path coefficient analysis identified biological yield per plant as the most important direct contributor to grain yield per plant at the genotypic level (direct effect: 0.9241), followed by spike length (0.2887) and harvest index (0.1934). Biological yield per plant also served as the primary indirect pathway explaining the high positive correlations of other component traits with grain yield. These findings are consistent with [Aklilu et al. \(2020\)](#) ^[32], [Fadel et al. \(2022\)](#) ^[35] and [Dimitrova-Doneva \(2016\)](#) ^[36], who demonstrated the supreme importance of biological yield,

harvest index and spike length as primary selection criteria for grain yield improvement in barley.

The positive direct effect of spike length on grain yield at both genotypic (0.2887) and phenotypic (0.2203) levels underscores its importance as a selection criterion, corroborating Almohisen (2021)^[22], Kaur and Vishwakarma (2020)^[28] and Raikwar *et al.* (2014)^[37], (2018). The positive direct effect of harvest index further highlights the importance of assimilate partitioning efficiency in yield improvement under stress, supporting the findings of Carpici and Celik (2012)^[38] and Kumari *et al.* (2020)^[39]. Traits exhibiting negative genotypic direct effects but positive correlations with grain yield—such as plant height, number of tillers per plant and test weight—exerted their influence predominantly through indirect pathways via biological yield per plant, reaffirming the utility of path analysis over simple correlation analysis in delineating the true determinants of grain yield.

5. Conclusion

The present study revealed ample genetic variability among 18 barley genotypes under salt stress for all 14 quantitative traits studied. High heritability coupled with high genetic advance as percent of mean for grain yield per plant, number of effective tillers per plant, number of tillers per plant and biological yield per plant indicates the predominance of additive gene action, rendering direct phenotypic selection effective for these traits. Correlation and path coefficient analyses identified biological yield per plant, spike length, harvest index and number of effective tillers per plant as the most important selection criteria for improving grain yield under saline conditions. Genotype RD 2552 consistently exhibited superior performance for all major yield and yield-attributing traits under salt stress, followed by DWRB 223, RD 2907, Karan 18 and Rajkiran. These promising genotypes can be utilised in future breeding programmes aimed at developing high-yielding, salt-tolerant barley cultivars. The simultaneous selection for plant height, number of tillers per plant, biological yield, harvest index, spike length and grain yield per plant is recommended as an effective strategy for developing superior barley genotypes with enhanced productivity under salt stress conditions.

Acknowledgement

The authors are grateful to the Department of Genetics and Plant Breeding, School of Agriculture, Suresh Gyan Vihar University, Jaipur, for providing the experimental facilities and logistical support required to conduct this research. The authors also acknowledge the advisory committee members for their valuable guidance and scientific input throughout the investigation.

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