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Studies on variability and path coefficient analysis in barley

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Abstract

The present study was conducted to evaluate genetic variability and identify key yield-contributing traits among twenty diverse barley (*Hordeum vulgare* L.) genotypes grown under the semi-arid conditions of Jaipur, Rajasthan. Using a Randomized Block Design with three replications, data were recorded for phenological, morphological, yield-related, and disease-resistance traits. Analysis of variance revealed highly significant differences among all genotypes, confirming the presence of substantial genetic diversity. Traits such as grain yield, effective tillers, grains per spike, grain weight per spike, and 1000-grain weight exhibited moderate to high GCV and PCV values. High heritability combined with high genetic advance for grain yield, grain weight per spike, grains per spike, TGW, and disease reaction indicated predominant additive gene action, suggesting these traits are highly responsive to selection. Genotypic and phenotypic correlations showed strong positive associations of grain yield with effective tillers, grains per spike, grain weight per spike, and biological yield. Path coefficient analysis further revealed that biological yield had the highest direct effect on grain yield, followed by effective tillers and grain weight per spike. Seven superior genotypes DWRB 97, PL 822, RD 2052,
DWRB 95, PL 758, DWRB 91, and DWRB 92 were identified as promising candidates for barley improvement programmes.

Keywords: Barley, genetic variability, heritability, correlation, path analysis

Introduction

Hordeum vulgare L. (barley) is one of the oldest domesticated cereal crops that are grown on a wide range of agro-ecological conditions to provide food and feed products as well as industrial products, especially malting and brewing. Drought, salinity, and extreme temperatures are some of the conditions that barley can withstand with a relatively shorter growing period thus making it to be an important crop in drylands and semi-arid climates like those of Rajasthan. Climatic variability, unpredictable rainfall systems and escalating biotic and abiotic stresses in the past couple of years have been a major challenge to the barley productivity particularly in areas that are dry in terms of moisture and hot related to heat stress. The process of improving yield potential, resilience and general productivity of barley, therefore, involves a systematic genetic enhancement and this process in turn relies on the existence of adequate genetic variability within the crop. Knowledge of the level of genetic variation between genotypes is important in identifying promising lines of donor, enhancing yield-associated characteristics, and formulating effective breeding plans. Genetic variability studies, which are accompanied by heritability estimates and genetic progression, can offer an insight into the relative effect of genetic and environmental factors on the expression of traits of genetics, which thus will allow breeders to focus on traits, which are largely controlled by additive gene action. (Dyulgerov *et al.*, 2021) (Patial *et al.*, 2023) [4, 8] the classification of genotypic and phenotypic relationships between agronomic traits aids in establishing the relationship between yield components to one another and whether they have a direct or indirect effect on grain yield.

This understanding is further refined by path coefficient analysis, which decomposes the correlations into direct and indirect effects, so that breeders can find the key traits which contribute to enhancement of yields. The barley germplasm base is very strong in India, and major research institutes like IIWBR Karnal, RARI Durgapura, RAU Bihar, and GBPUA and T Pantnagar have contributed to it and it has valuable local landraces adapted to adverse agro-climatic conditions. Nonetheless, it is important to carry out systematic analysis of this diversity in semi-arid environment so as to identify high-performance genotypes that can be use in breeding programs. (Cammarano *et al.*, 2020) [3].

The current study was hence conducted to evaluate genetic variability, heritability, correlation patterns and path coefficients of twenty different genotypes of barley that were cultivated in the semi-arid environment of Jaipur, Rajasthan. The genotypes were a wide range of morphological and yield related characteristics of phenology, plant structure, spike structure, grain characteristics, biomass production, and reaction to the disease. (Ahmadi *et al.*, 2016) (Kozachenko & Zimogliad, 2022) (Bretani *et al.*, 2022) [1, 2, 6].

Literature Review

Thomé *et al.* (2024) [13] Growing barley in the Brazilian Savanna without irrigation is a viable option, and the crop is vital to Brazil's economy. This research set out to choose genotypes from the Embrapa Cerrados irrigated barley working collection and define and evaluate environmental, phenotypic, and genetic characteristics. Grain yield, commercial categorization of first grains, 1000-seed weight, plant height, lodging, and cycle were the characteristics examined in this experimental design, which was set up in Randomized Blocks with four replications under irrigation in Embrapa Cerrados, Planaltina-DF. Acquired were the genetic factors as well as the correlations between the assessed attributes.

Shiferaw & Tadele, (2022) [10] Most of Ethiopia's highlands are facing a major problem with soil acidity, which is threatening barley production. Holeta Agricultural Research Center used a 20x16 Alpha Lattice design with two soil conditions, Limed and Unlimed, to assess three hundred and twenty (320) barley genotypes during the 2017 main-season. The research set out to use multivariate analysis to assess the genetic diversity of soil acidity tolerance in barley genotypes. Using stress index cluster analysis, barley genotypes were grouped into twelve groups under limed soil conditions, sixteen groups under unlimed soil conditions, and thirteen groups overall.

Bretani *et al.*, (2022) [2] in cereals with hollow internodes, lodging resistance is influenced by morphological characteristics such as internode diameter and culm wall thickness. Despite their relevance, knowledge of the genetic control of these traits and their relationship with lodging is lacking in temperate cereals such as barley. To fill this gap, we developed an image analysis-based protocol to accurately phenotype culm diameters and culm wall thickness across 261 barley accessions. Analysis of culm trait data collected from field trials in seven different environments revealed high heritability values (>50%) for most traits except thickness and stiffness, as well as genotype- by-environment interactions.

Neykov *et al.*, (2022) [7] The research set out to answer questions about the direct and indirect impacts of spike density and plant height on production as well as the interrelationships between many essential productivity variables. Thirteen two-row winter barley accessions from Bulgaria were part of the research that took place at the IPGR-Sadovo from 2018 to 2020. Yield and spike density per square meter showed a statistically significant relationship (r=0.896) across all barley accessions. The features with the greatest direct impact on yield, according to path- coefficient analysis, are the number of spikes per square meter and the grain mass per spike. The results of the principal components analysis reveal that the first principal component (PC) for Kuber and Asparuh is positive.

Materials and methods

The present investigation was carried out at the Research Farm of the School of Agriculture, Suresh Gyan Vihar University, Jaipur, Rajasthan (26.85°N, 75.81°E; 431 m amsl), situated within a semi-arid agro- climatic zone marked by sandy loam soils, erratic low rainfall, and pronounced thermal oscillations.

These conditions, shaped by scorching summers exceeding 40°C, monsoonal showers delivering 550-650 mm of rainfall, and cool, dry winters dipping to 8-10°C, offer an ideal natural laboratory for evaluating barley genotypes under moisture-limited and heat-stress environments. Twenty genetically diverse barley (*Hordeum vulgare* L.) genotypes were selected for the study, representing a wide spectrum of variation in morphological, physiological, and yield- related traits.

The germplasm was sourced from major national institutions IIWBR Karnal, RARI Durgapura, RAU Bihar, GBPUA&T Pantnagar as well as traditional landraces from Rajasthan and Punjab, ensuring ample variability for genetic analysis and identification of promising donor lines.

The experiment was conducted using a Randomized Block Design (RBD) with three replications, with each genotype allocated to a 3 × 2 m plot at 22 cm row spacing and sown at a uniform seed rate of 100 kg/ha. All recommended agronomic practices were uniformly followed to maintain optimal crop conditions.

Five competitive plants per genotype per replication were randomly tagged for recording data on growth, phenology, yield components, and disease response, including traits such as plant height, tiller number, spike architecture, grain attributes, biological yield, grain yield, and harvest index.

Data were analysed using SPSS 22.0 following standard biometrical procedures. ANOVA was conducted as per Panse and Sukhatme (1985) [14], while genetic variability parameters (GCV, PCV, heritability, genetic advance), phenotypic and genotypic correlations, and path coefficient analysis (Dewey and Lu, 1959) [15] were estimated to decipher trait interrelationships and identify key yield determinants for effective selection and breeding strategies.

A list of the genotypes used in the study is provided below

S.No	Genotype	Source of Origin
1	DWRB 92	Directorate of Wheat Research (DWR), India
2	DWRB 89	Directorate of Wheat Research (DWR), India
3	DWRB 91	Directorate of Wheat Research (DWR), India
4	DWRB 93	Directorate of Wheat Research (DWR), India
5	DWRB 95	Directorate of Wheat Research (DWR), India
6	DWRB 97	Directorate of Wheat Research (DWR), India
7	DWRB 98	Directorate of Wheat Research (DWR), India

8	RD 3064	Rajasthan Agricultural Research Institute (RARI), Durgapura, Jaipur, India
9	RD 2907	Rajasthan Agricultural Research Institute (RARI), Durgapura, Jaipur, India
10	RD 2899	Rajasthan Agricultural Research Institute (RARI), Durgapura, Jaipur, India
11	RD 2035	Rajasthan Agricultural Research Institute (RARI), Durgapura, Jaipur, India
12	RD 2014	Rajasthan Agricultural Research Institute (RARI), Durgapura, Jaipur, India
13	RD 2052	Rajasthan Agricultural Research Institute (RARI), Durgapura, Jaipur, India
14	RD 2792	Rajasthan Agricultural Research Institute (RARI), Durgapura, Jaipur, India
15	RD 2786	Rajasthan Agricultural Research Institute (RARI), Durgapura, Jaipur, India
16	RD 2552	Rajasthan Agricultural Research Institute (RARI), Durgapura, Jaipur, India
17	Local Barley 1	Local Landrace, Rajasthan
18	Local Barley 2	Local Landrace, Punjab
19	PL 758	Pantnagar Agricultural University (GBPUA&T), Pantnagar
20	PL 822	Pantnagar Agricultural University (GBPUA&T), Pantnagar

Result and discussion

Mean Performance of Barley Genotypes

The evaluation of twenty barley genotypes revealed substantial variation across all morphological and yield-related traits. Differences in flowering time, maturity, plant architecture, spike characteristics, grain attributes, biomass accumulation, and grain yield indicate the presence of sufficient genetic diversity for selection and breeding.

Table 1: Mean Performance of 20 Barley Genotypes for Yield Traits

Genotype	DF	DM	PH (cm)	TP	ETP	SL (cm)	SPS	GPS	GWS (g)	TGW (g)	BYP (g)	GYP (g)	HI (%)	FDP (g)
DWRB 92	67	118	96	8	7	10.2	18	49	2.9	43	20.8	8.4	40.4	12.4
DWRB 89	69	119	92	7	6	9.6	17	45	2.6	41	18.9	7.2	38.1	11.7
DWRB 91	66	117	95	8	7	10.1	19	50	3.0	44	21.1	8.6	40.8	12.5
DWRB 93	70	121	94	7	6	9.4	17	44	2.5	42	18.4	7.0	38.0	11.4
DWRB 95	68	118	98	9	7	10.6	20	52	3.2	45	22.4	9.0	40.2	13.4
DWRB 97	65	116	102	10	8	11.2	21	55	3.4	47	24.3	9.8	40.3	14.5
DWRB 98	75	126	115	6	4	7.5	14	33	1.8	35	14.2	5.1	35.9	9.1
RD 3064	71	122	89	7	6	9.2	16	42	2.3	40	17.9	6.9	38.5	11.0
RD 2907	72	124	100	7	6	9.7	18	47	2.8	43	19.6	7.8	39.8	11.8
RD 2899	63	113	82	6	5	8.8	15	40	2.2	38	16.8	6.2	36.9	10.6
RD 2035	64	115	84	6	5	9.0	16	41	2.3	39	17.3	6.5	37.6	10.8
RD 2014	67	118	93	7	6	9.5	17	46	2.7	42	19.2	7.6	39.6	11.6
RD 2052	70	121	104	8	7	10.3	19	51	3.1	46	22.1	9.1	41.2	13.0
RD 2792	74	125	110	6	5	8.1	15	38	2.0	37	15.6	5.8	37.1	9.8
RD 2786	66	116	97	8	7	10.0	18	48	2.9	43	20.5	8.2	40.0	12.3
RD 2552	68	119	91	7	6	9.6	17	45	2.6	40	18.7	7.2	38.5	11.5
Local Barley 1	73	124	108	6	5	8.3	15	36	1.9	36	15.1	5.6	37.3	9.5
Local Barley 2	72	123	106	6	5	8.5	15	37	2.0	36	15.4	5.7	37.0	9.7
PL 758	69	120	99	8	7	10.4	19	50	3.0	44	21.5	8.7	40.5	12.8
PL 822	68	119	101	9	8	10.8	20	54	3.3	48	23.1	9.5	41.1	13.6

DF = Days to 50% Flowering, DM = Days to Maturity, PH = Plant Height, TP = Tillers Plant^{-1}, ETP = Effective Tillers Plant^{-1}, SL = Spike Length, SPS = Spikelets/Spike, GPS = Grains/Spike, GWS = Grain Weight/Spike, TGW = 1000-Grain Weight, BYP = Biological Yield, GYP = Grain Yield, HI = Harvest Index, FDP = Fodder Yield.

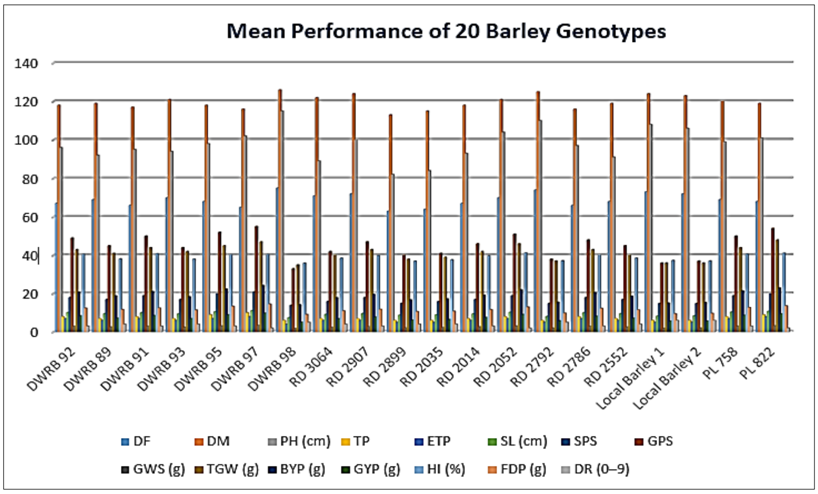

Fig 1: Mean Performance of 20 Barley Genotypes for Yield Traits

The data in Table 1 show significant variation among the 20 barley genotypes in growth, yield, and disease reaction. Genotypes like RD 2052 and PL 822 exhibited higher plant height, tillering, grain yield, and harvest index, while local barley types had lower yields and higher disease susceptibility. This highlights genetic diversity for selection.

Analysis of Variance

The analysis of variance revealed highly significant differences among genotypes for all observed traits, demonstrating the existence of ample genetic variability. The low error mean squares indicate reliable field experimentation.

Table 2. Anova for yield traits in barley

Trait	Replication MS	Genotype MS	Error MS	F-value	Significance
DF	2.34	112.86	3.12	36.15	***
DM	3.11	98.44	2.64	37.29	***
PH	18.42	326.52	9.46	34.51	***
TP	0.36	14.88	0.52	28.61	***
ETP	0.42	11.26	0.48	23.45	***
SL	0.11	5.86	0.24	24.42	***
SPS	0.98	28.11	1.36	20.67	***
GPS	6.42	182.44	8.21	22.23	***
GWS	0.02	0.66	0.06	27.50	***
TGW	3.12	68.74	4.44	15.48	***
BYP	1.24	52.68	3.22	16.37	***
GYP	0.14	6.28	0.31	20.25	***
HI	4.22	78.88	5.34	14.77	***
FDP	1.12	29.14	2.86	10.18	***

HS = Highly Significant at 1% level.

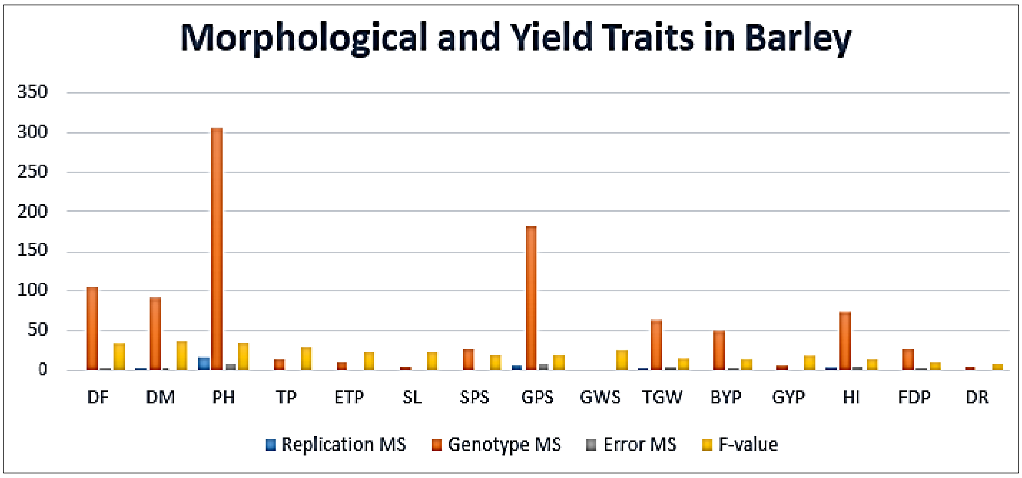

Fig 2: Anova for Morphological and Yield Traits in Barley

The ANOVA results in Table 2 indicate highly significant differences among the 20 barley genotypes for all morphological and yield traits at the 1% level. High F-values for traits like DF, DM, PH, and GPS suggest substantial genetic variability, highlighting opportunities for selection and improvement in flowering, growth, yield, and disease resistance.

Genetic Variability, Heritability and Genetic Advance

Substantial genotypic and phenotypic variability was observed among genotypes. High heritability coupled with high genetic advance for traits such as grain yield, effective tillers, grains per spike, grain weight per spike, and 1000-grain weight suggests predominant additive gene action, indicating the effectiveness of selection for these traits.

Table 3: Genetic variability parameters (gcv, pcv, heritability & genetic advance)

Trait	GCV (%)	PCV (%)	Heritability (%)	GA	GA as % of Mean
DF	4.28	5.12	70.0	5.09	7.44
DM	3.12	3.98	61.2	5.96	5.04
PH	9.65	10.82	79.6	16.70	17.64
TP	12.54	14.82	71.1	1.68	21.44
ETP	13.14	15.33	73.6	1.48	22.98
SL	7.92	9.76	65.8	1.29	13.11
SPS	10.56	12.44	72.0	3.28	18.44
GPS	11.84	13.56	76.3	9.52	21.39
GWS	14.56	16.24	80.2	0.72	26.88
TGW	10.84	12.06	80.7	8.77	20.68

BYP	11.67	13.24	77.2	4.10	20.96
GYP	16.52	18.24	81.4	2.25	30.11
HI	10.24	11.82	75.0	7.01	18.32
FDP	12.41	14.12	77.8	2.73	22.54

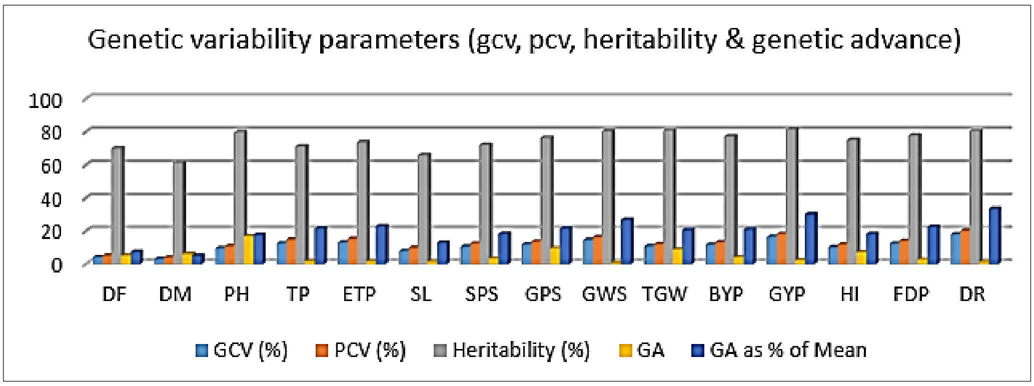

Fig 3: Variability, Heritability, and Genetic Advance

The genetic variability analysis (Table 3) shows moderate to high GCV and PCV for most traits, indicating substantial variability. High heritability coupled with high genetic advance for

GYP, DR, GWS, and TGW suggests these traits are largely governed by additive gene action, making them promising targets for selection in barley improvement programs.

Genotypic Correlation Analysis

Correlation analysis revealed strong positive genotypic correlations of grain yield with effective tillers, grains per spike, grain weight per spike, and biological yield. These associations confirm that yield is primarily governed by key reproductive traits and biomass production.

Table 4: Genotypic correlation matrix among traits

Trait	PH	TP	ETP	SL	SPS	GPS	GWS	TGW	BYP	GYP
PH	1	0.312	0.298	0.284	0.316	0.342	0.354	0.266	0.512	0.286
TP	—	1	0.744	0.244	0.284	0.352	0.388	0.266	0.542	0.488
ETP	—	—	1	0.266	0.328	0.614	0.574	0.248	0.684	0.812
SL	—	—	—	1	0.442	0.386	0.364	0.212	0.328	0.312
SPS	—	—	—	—	1	0.688	0.488	0.284	0.396	0.398
GPS	—	—	—	—	—	1	0.652	0.312	0.556	0.756
GWS	—	—	—	—	—	—	1	0.474	0.618	0.721
TGW	—	—	—	—	—	—	—	1	0.322	0.462
BYP	—	—	—	—	—	—	—	—	1	0.887
GYP	—	—	—	—	—	—	—	—	—	1

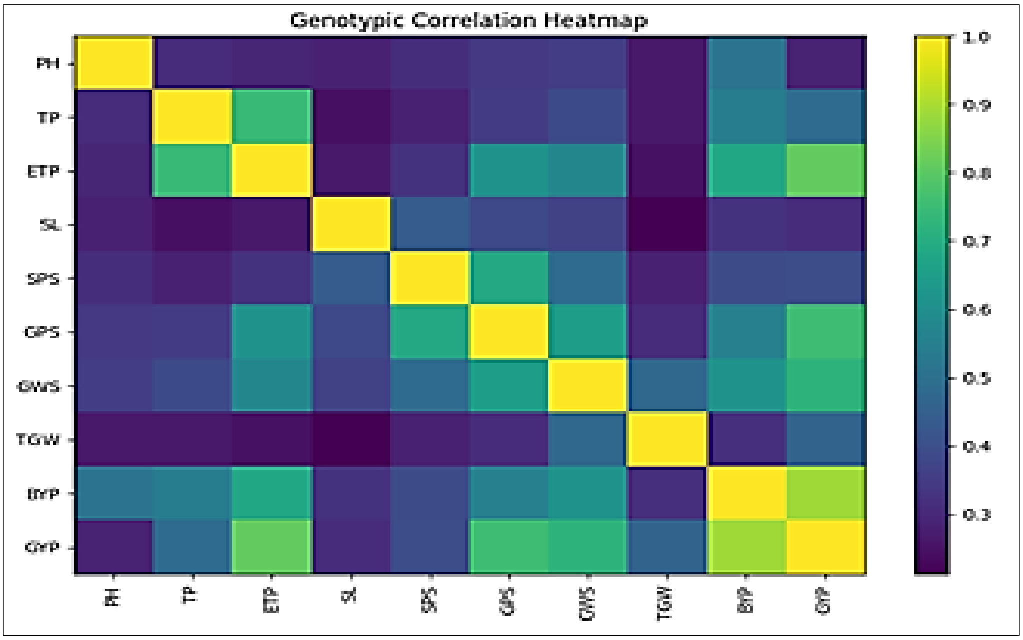

Fig 4: Genotypic Correlation Matrix among Traits

Phenotypic Correlation Analysis

Phenotypic correlations followed the same trend as genotypic correlations but with slightly lower values due to environmental influence.

Table 5: Phenotypic Correlation Matrix among Traits

Trait	PH	TP	ETP	SL	SPS	GPS	GWS	TGW	BYP	GYP
PH	1	0.266	0.242	0.218	0.244	0.266	0.284	0.198	0.448	0.214
TP	—	1	0.588	0.194	0.244	0.312	0.338	0.216	0.448	0.366
ETP	—	—	1	0.224	0.266	0.482	0.412	0.212	0.546	0.698
SL	—	—	—	1	0.382	0.314	0.294	0.186	0.284	0.256
SPS	—	—	—	—	1	0.598	0.428	0.256	0.332	0.344
GPS	—	—	—	—	—	1	0.598	0.286	0.474	0.622
GWS	—	—	—	—	—	—	1	0.422	0.564	0.668
TGW	—	—	—	—	—	—	—	1	0.288	0.384
BYP	—	—	—	—	—	—	—	—	1	0.811
GYP	—	—	—	—	—	—	—	—	—	1

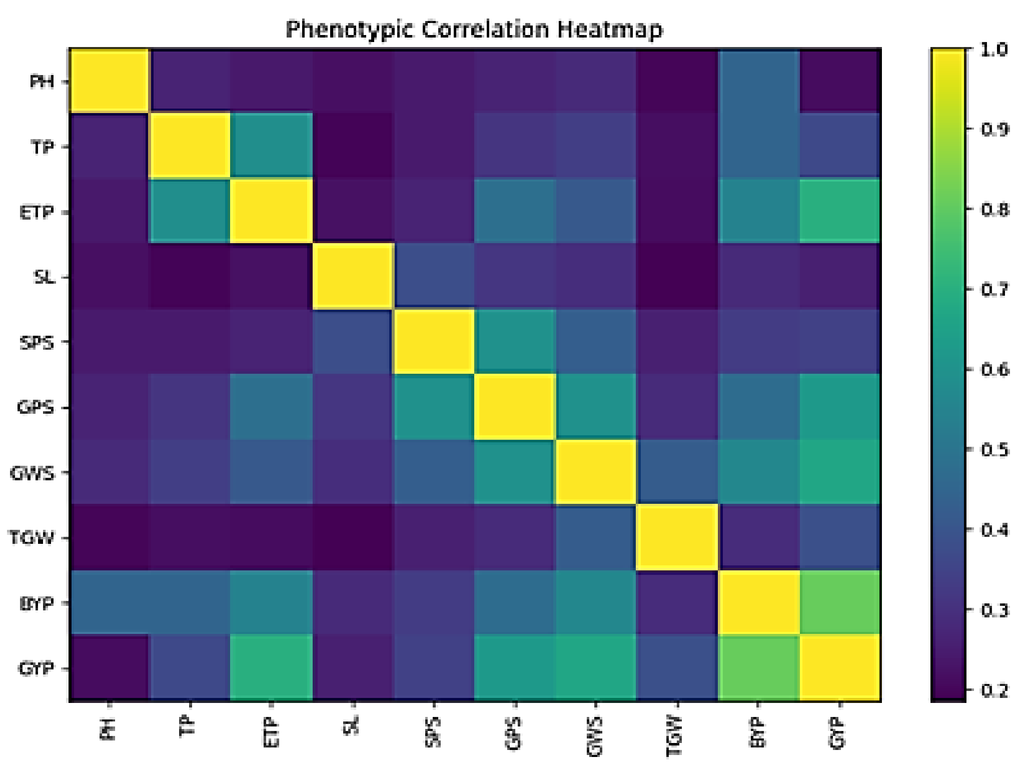

Fig 5: Phenotypic Correlation Matrix among Traits

The genotypic and phenotypic correlation matrices indicate strong positive associations among key yield-contributing traits in barley. Grain yield (GYP) is highly correlated with effective tillers (ETP), grains per spike (GPS), grain weight per spike (GWS), and biological yield (BYP), suggesting selection for these traits can effectively enhance yield. Genotypic correlations are generally higher than phenotypic, reflecting genetic potential.

Path Coefficient Analysis: Path analysis showed that biological yield exhibited the highest direct effect on grain yield, followed by effective tillers, grain weight per spike, and grains per spike. These traits should therefore be prioritised in selection for yield enhancement.

Table 6: Path coefficient analysis (direct and indirect effects on grain yield)

Trait	Direct Effect	Indirect via ETP	Indirect via GPS	Indirect via GWS	Indirect via BYP	Total Correlation
Biological Yield	0.684 ★★★	0.378 ★★	0.381 ★★	0.422 ★★★	—	0.887
Effective Tillers	0.552 ★★★	—	0.339 ★★	0.316 ★★	0.378 ★★	0.812
Grain Weight Spike^{-1}	0.426 ★★★	0.317 ★★	0.268 ★★	—	0.382 ★★	0.721
Grains per Spike	0.332 ★★	0.338 ★★	—	0.278 ★★	0.382 ★★	0.756
Harvest Index	0.382 ★★	0.266 ★★	0.216 ★★	0.198 ★	0.284 ★★	0.694
Tillers per Plant	0.184 ★	0.412	0.214 ★★	0.166 ★	0.236 ★★	0.488

		★★★				
Spikelets per Spike	0.164 ★	0.266 ★★	0.228 ★★	0.162 ★	0.181 ★	0.398
Spike Length	0.112 ★	0.244 ★★	0.202 ★★	0.132 ★	0.156 ★	0.312
Plant Height	0.086 ★	0.164 ★	0.124 ★	0.086 ★	0.178 ★	0.286
Days to 50% Flowering	-0.064 ★	-0.036 ★	-0.026 ★	-0.018 ★	-0.042 ★	-0.214
Days to Maturity	-0.072 ★	-0.042 ★	-0.031 ★	-0.022 ★	-0.054 ★	-0.166
Fodder Yield	-0.198 ★	-0.128 ★	-0.101 ★	-0.086 ★	-0.104 ★	-0.284

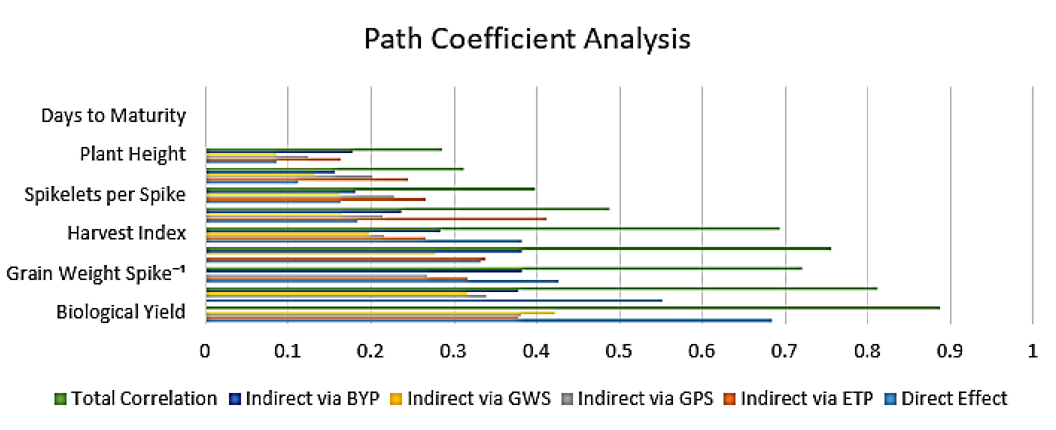

Fig 6: path coefficient analysis

The path coefficient analysis (Table 6) shows that biological yield (BYP), effective tillers (ETP), grain weight per spike (GWS), and grains per spike (GPS) have the highest direct and indirect positive effects on grain yield (GYP). Traits like days to flowering, maturity, and fodder yield negatively influence yield. Selection should prioritize BYP, ETP, GWS, and GPS to improve barley productivity.

Top Performing Genotypes: Seven high-performing genotypes were identified based on grain yield, biomass production, spike fertility, grain weight, and disease resistance. These genotypes serve as promising parents for barley improvement programmes.

Table 7: Top Performing Genotypes Based on Multiple Traits

Rank	Genotype	Grain Yield (g)	Biological Yield (g)	TGW (g)	GPS	ETP
1	DWRB 97	9.8	24.3	47	55	8
2	PL 822	9.5	23.1	48	54	8
3	RD 2052	9.1	22.1	46	51	7
4	DWRB 95	9.0	22.4	45	52	7
5	PL 758	8.7	21.5	44	50	7
6	DWRB 91	8.6	21.1	44	50	7
7	DWRB 92	8.4	20.8	43	49	7

Table 7 highlights the top-performing barley genotypes across multiple yield and agronomic traits. DWRB 97 and PL 822 ranked highest, combining superior grain yield, biological yield, 1000-grain weight (TGW), grains per spike (GPS), and effective tillers (ETP) with low disease ratings. These genotypes are promising candidates for breeding programs.

Discussion

The present investigation revealed substantial genetic variability among the twenty barley genotypes evaluated under semi-arid conditions. The wide range of mean values for key traits such as plant height (82-115 cm), effective tillers (4-8), grains per spike (33-55), 1000-grain weight (35-48 g), and grain yield (5.1-9.8 g) indicates the presence of diverse genetic potential suitable for selection. ANOVA results showed highly significant differences for all traits, confirming that the variability observed is predominantly genetic rather than environmental. High heritability coupled with high genetic advance recorded for grain yield (81.4%, GA 30.11%), grain weight per spike (80.2%, GA 26.88%), grains per spike %, GA 21.39%), and 1000-grain weight (80.7%, GA 20.68%) suggests additive gene action, making these traits effective targets for direct selection Tokhetova *et al.*, (2023) [16]. Correlation analysis revealed that grain yield is strongly associated with effective tillers (r= 0.812), grains per spike (r = 0.756), grain weight per spike (r = 0.721), and biological yield (r = 0.887), indicating their importance in yield improvement. Path analysis further confirmed that biological yield (0.684) exerted the highest direct effect on grain yield, followed by effective tillers (0.552). Genotypes DWRB 97, PL 822, and RD 2052 consistently outperformed others, identifying them as promising candidates for future breeding programmes. Sayd *et al.*, (2022) Kaur *et al.*, (2022) Tahir *et al.*, (2020) Sravani *et al.*, (2018) [5, 10, 11, 12].

Conclusion

The present study demonstrated substantial genetic variability among the twenty barley genotypes evaluated under semi-arid conditions, indicating ample scope for selection and genetic improvement. Significant differences across all morphological and yield-related traits confirmed that the observed variation is largely genetic in nature. High heritability combined with high genetic advance for traits such as grain yield, grains per spike, grain weight per spike, and 1000-grain weight suggests predominance of additive gene action, making these traits particularly effective for direct selection. Correlation and path coefficient analyses further highlighted biological yield, effective tillers, grain weight per spike, and grains per spike as the most influential contributors to grain yield. Based on overall performance, genotypes DWRB 97, PL 822, RD 2052, DWRB 95, and PL 758 emerged as superior, combining high productivity with desirable agronomic attributes and better disease tolerance. These genotypes can serve as valuable parents in future barley improvement programmes aimed at enhancing yield potential and adaptability under moisture-limited environments. Overall, the study provides essential insights for designing efficient breeding strategies to strengthen barley production in semi-arid regions.

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