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Unravelling variability, heritability, and genetic advance for yield and its component traits in Indian barley (*Hordeum vulgare* L.) Landraces and diallelic lines

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Abstract
Indian barley (*Hordeum vulgare* L.) is a vital cereal and fodder crop, known for its wide adaptability to various agro-climatic conditions. The study encapsulates the genetic parameters persuading yield and contributing traits in barley as a major thrust. A phenotypic evaluation study to explore heritability and genetic advancements was conducted with diallel set of 45 hybrids developed from 10 barley genotypes. The experiment followed a randomized block design with three replications, assessing fifteen characters across the F_1 and F_2 generations. Accordingly, the high magnitude of heritability was observed for the characters, days to maturity, and number of spikelets per spike. The genetic advance was high for days to maturity, plant height, number of spikelets per spike, number of grains per spike, peduncle length, and harvest index. This research provides valuable insights for future barley improvement programs, promoting genetic diversity and superior genotype development. Additionally, a comprehensive analysis of genetic variability, heritability, and genetic advancement in barley using diallel crosses will enhance breeding strategies for sustainable yield improvements. This study will provide actionable insights for future crop development programs in India.

Keywords: Barley, diallelic lines, genetic variability, heritability, genetic advance

Introduction
Barley (*Hordeum vulgare* L.), is a vital cereal crop in India, extensively used for food, fodder, and malt production. It belongs to a member of the Poaceae family (Kling and Hayes, 2004) [10], and is one of the oldest cultivated cereals, playing a vital role in global agriculture. Known for its adaptability to diverse agro-climatic conditions, barley thrives in marginal soils and under limited water availability, making it a crucial crop for regions prone to abiotic stresses (Kumar *et al.*, 2012) [11]. Barley is a cereal crop that is cultivated during the summer season in temperate regions and in the winter season in tropical regions. In India, barley is grown in several states, including Rajasthan, Uttar Pradesh, Madhya Pradesh, Haryana, Punjab, Bihar, Himachal Pradesh, Uttarakhand, and Jammu & Kashmir. It is the fourth largest cereal produced in the world, following maize, wheat, and rice. Barley is a resilient crop and can thrive in challenging soil conditions, such as saline, alkaline, drought-affected, and flood-prone areas. In addition to its uses as human food and animal feed, barley has potential applications as a health tonic, featured in products like Horlicks, Maltova, and barley syrups, as well as in the production of malt and beer (Katiyar, *et. al.*, 2020) [9]. The genetic improvement of barley has historically focused on enhancing yield, stress tolerance, and nutritional quality. However, the low productivity of barley in regions like India is attributed to factors such as limited genetic diversity, suboptimal cultural practices, and inadequate breeding efforts. Variability in traits such as grain yield, spike length, and biological yield provides the raw material for selection and hybridization in breeding programs (Sood *et al.*, 2019) [15]. Heritability and genetic advancement are key parameters in understanding the inheritance of traits and predicting the response to selection. High heritability, coupled with substantial genetic advancement, indicates the predominance of

additive genetic variance, facilitating the development of superior genotypes (Dabholkar,1992) [6]. With growing global concerns about food security and climate resilience (Chandra *et al*., 2020) [5], enhancing barley yield and stress tolerance has become a priority. Understanding genetic variability, heritability, and genetic advance is essential for improving traits through effective breeding programs. The use of diallel crosses provides valuable insights into the genetic makeup of breeding lines by allowing comprehensive analysis of genetic parameters. This approach helps in identifying parental lines with desirable traits, understanding gene actions, and predicting potential genetic gains (Raghunandan *et al.*, 2022) [12]. Henceforth, this study aims to explore these genetic parameters in barley to guide effective breeding strategies for yield and adaptation improvement. The work was carried out under the following objectives, a) estimate genetic variability for yield and its contributing traits, b) determine heritability and genetic advance for key characteristics, and c) provide insights into the selection of promising genotypes for breeding perspectives.

Materials and Methods

Experimental Materials

The study was conducted at the Agriculture Research Farm, B.R.D (P.G). College, Deoria (Uttar Pradesh), during the *Rab*i season (2020-2021). A diallel set of 45 hybrids (F_1) was developed by crossing 10 barley genotypes: NDB-302, NDW-1173, UB-307, DWRB-137, NDW-1459, RD-2804, NDB-1609, NDB-1490, HUB-240, and RD-2772. Selfed seeds of F_1 hybrids were used to develop F_2 populations. Details of the Indian barley genotypes, lineages, and diallelic crossed lines used in the study are presented in Table 1.

Experimental Design and data collection

The experiment comprised 100 treatments (45 F_1 hybrids, 45 F_2 populations, and 10 parents including one check variety) arranged in a randomized block design with three replications. Each plot consisted of double rows of 4 m in length with a spacing of 22.5 cm between rows and 5 cm between plants. The observations were recorded through ten randomly selected plants for all fifteen characters *viz*., days to 50% flowering, days to 90% physical maturity, Plant height (cm), number of effective tillers per plant, flag leaf area (cm²), spike length (cm), peduncle length (cm), number of spikelets per spike, number of grains per spike, grain yield per spike (g), 1000-grain weight (g), grain yield per plant (g), biological yield per plant (g), harvest index (%), and protein content (%) (Table 2).

Statistical Analysis

The statistical analysis including range, average, standard deviation (SD), coefficient of variation (CV), and analysis of variance of the recorded quantitative traits datasets were calculated using the OPSTATE package (Sheoran *et al*., 1998; Chandra *et al*., 2022) [4]. Furthermore, the heritability (in the narrow sense) in F_1 generation was calculated by the formula proposed by Crumpacker and Allard, (1962), which is as follows:

$$\text{Heritability } (\hat{h}^2) = (1/4)\hat{D} / [(1/4)\hat{D} + (1/4)\hat{H}_1 - (1/4)\hat{F} + \hat{E}]$$

Heritability in F_2 generation was calculated according to the methodology proposed by Verhalen and Murray (1969).

$$(\hat{h}^2) = (1/4)\hat{D} / [(1/4)\hat{D} + (1/16)\hat{H}_1 - (1/8)\hat{F} + \hat{E}]$$

Or

1/2D/VP

Where,
$\hat{h}^2$ =Estimates of heritability coefficient and $\hat{D}$, $\hat{H}_1$, $\hat{F}$ and $\hat{E}$ are the same as explained earlier.
D = additive genetic variance
VP = phenotypic variance

The estimates of heritability and genetic advance were arbitrarily categorized in three classes by Robinson (1966):
Heritability (%) = Heritability coefficient X 100
Genetic advance: The genetic advance was calculated by the formula given by Robinson *et al.* (1949) as:

$$\text{Genetic advance (GA)} = (k) \times (\hat{h}^2) \times (\sigma ph),$$

Or

$$(GA) = (k) \times (V_P) \times ½\, v_g / v_p, \text{ and}$$

Genetic advance over the mean of the character

$$[GA (\%)] = \frac{GA}{\bar{x}} \times 100$$

Where,
GA=Estimate of genetic advance
K =Selection differential at 5% selection intensity, *i.e*. 2.06
Σph=Phenotypic standard deviation
$\hat{h}^2$=Heritability coefficient in a narrow sense
$\bar{X}$=Mean of the character concerned
Vp=Phenotypic variance
Gp=Genotypic variance

Results and Discussion

Barley (*Hordeum vulgare*) is one of the most important cereal crops in India, valued for its use in food, fodder, and malt production. In recent years, enhancing barley yield and stress resilience has been a key focus of breeding programs. Studies of genetic variability, heritability, and genetic advancement are crucial for identifying traits amenable to selection and breeding improvements. Heritability estimates play a critical role in crop improvement programs, serving as an essential selection criterion for identifying desirable traits that can be passed from parents to offspring. These estimates quantify the proportion of variation in a particular trait attributable to genetic factors, allowing researchers and breeders to understand the potential for these traits to be inherited. By utilizing heritability estimates, crop improvement initiatives can efficiently select parental lines with favourable characteristics, ultimately enhancing the genetic quality and yield of future generations of crops. Accordingly, a high magnitude of heritability (over 30%) was observed for the characters, days to maturity, and the number of spikelets per spike showed high heritability in the F_1 generation (Figure 1). At the same time, a moderate magnitude of heritability (30-10%) was observed only for the characters days to 50% flowering, plant height, number of grains per spike, 1000-grain weight, flag leaf area, peduncle length, biological yield per plant, and harvest index in F_1 generation (Table 2). Similar estimates were also reported by Abebe *et al.*, (2023) [1], for plant height (Dinsa *et al.*, 2018) [7] for grain weight per spike; high heritability estimates were due to the contribution of additive genetic component. It indicates that a widely adopted genotype could be developed if these characters are subjected to progeny and any other selection scheme for exploiting fixable genetic variance. Selection pressure should be exercised in early generations.

The estimates of heritability were low (below 10%) for the character number of productive tillers, spike length, grain weight per spike, protein content, and grain yield per plant in F_1 generation (Figure 1). A similar result was observed by Jalata *et. al.*, (2011) [8]. The expected genetic advance expressed as a percentage over the mean ranged from 0.12 for grain weight per spike to 32 for days to maturity in the F_1 generation. The genetic advance was high for days to maturity, plant height, number of spikelets per spike, number of grains per spike, peduncle length, and harvest index in F_1. The genetic advance was medium for days to 50% flowering, 1000-grain weight, flag leaf area, and biological yield per plant in F_1 (Figure 1, Table 2). It indicated that the manifestation of these traits was primarily governed by additive, fixable genetic effects, and the desired selection gain could be achieved in early generations (Aidun *et al.*, 1990) [3]. This information revealed the presence of both additive and non-additive genetic effects; therefore, the selection should be followed in later generations. The moderate genetic advance was reported by Riaz and Chowdhry, (2003)., for the number of grains per spike and biological yield; Raikwar *et. al.*, (2014) [13] for biological yield and productive tillers per plant. Low genetic advance was observed for productive tillers, spike length, grain weight per spike, protein content, and grain yield per plant, which exhibited low values of genetic advance in both the generation and protein content in the F_2 generation. Thus, the selection of material would not be effective for these traits in early generations (Katiyar *et. al.*, 2020) [9]. Heritability coupled with high genetic advance was observed for characters biomass per plant, grain yield, and number of tillers per plant indicating that selection for these characters could be more effective due to additive gene action (Addisuand Shumet,2015). Overall, this study revealed substantial genetic variability among barley genotypes in India, with significant potential for selection in breeding programs (Figure 2). Traits with high heritability and genetic advancement, such as tillering capacity and plant height, offer promising targets for genetic improvement. Future research should integrate molecular tools and multi-location trials to enhance selection accuracy and stability.

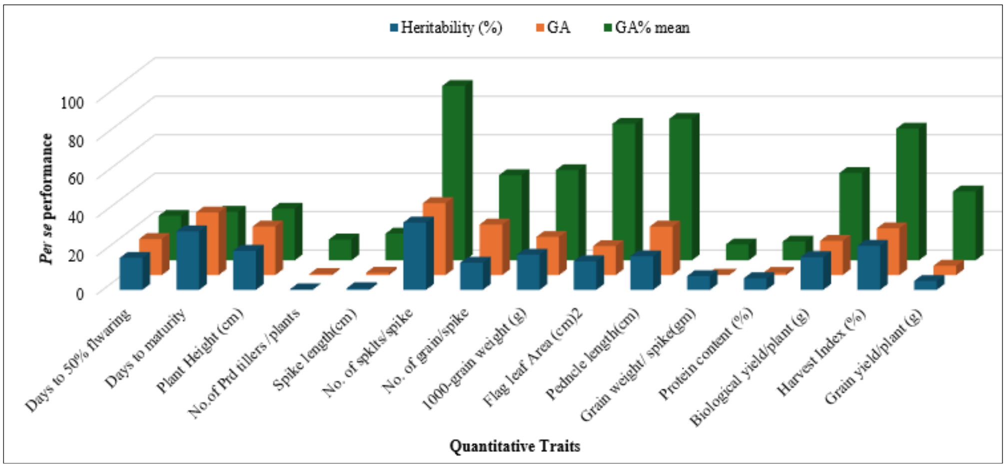

Fig 1: Percent heritability and genetic advance of the derived diallelic lines for the 15 different quantitative traits.

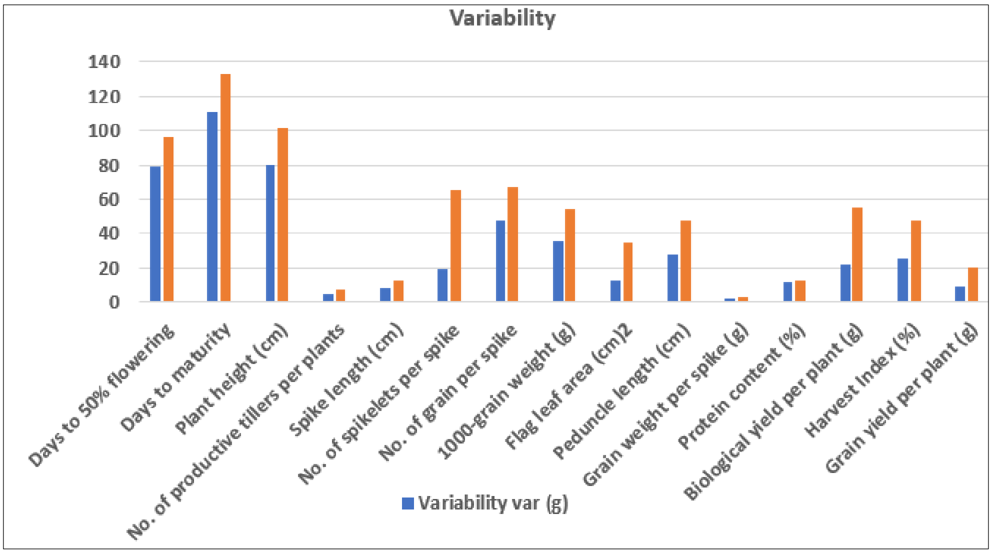

Fig 2. Genotypic and phenotypic variability across the derived diallelic lines for the 15 different quantitative traits.

Table 1: Details of the Indian barley genotypes, lineages, and diallelic crossed lines used in the study.

S. No.	Parental lines	S. No.	Breeding lines developed through diallelic crosses						
1.	NDB -302	1.	NDB -302 X NDB-1173	13.	NDB-1173 X NDB-1490	25.	DWRB-137 X NDW-1459	37.	RD-2804 X RD-2772
2.	NDB -1173	2.	NDB -302 X HUB-307	14.	NDB-1173 X HUB-240	26.	DWRB-137 X RD-2804	38.	RD-2804 X NDB-1609
3.	HUB-307	3.	NDB -302 X RD-2772	15.	NDB-1173 X NDB-1609	27.	DWRB-137 X RD-2772	39.	RD-2804 X HUB-240
4.	DWRB-137	4.	NDB -302 X NDB-1490	16.	NDB-1173 X DWRB-137	28.	DWRB-137 X HUB-240	40.	NDB-1609 X NDB-1490
5.	NDB-1459	5.	NDB -302 X RD-2804	17.	NDB-1173 X RD-2804	29.	DWRB-137 X NDB-1490	41.	NDB-1609 X HUB-240
6.	RD-2804	6.	NDB -302 X NDB-1609	18.	HUB-307 X DWRB-137	30.	DWRB-137 X NDB-1609	42.	NDB-1609 X RD-2772
7.	NDB-1609	7.	NDB -302 X DWRB-137	19.	HUB-307 X NDB-1490	31.	NDB-1459 X RD-2772	43.	NDB-1490 X RD-2772
8.	NDB-1490	8.	NDB -302 X HUB-240	20.	HUB-307 X NDB-1459	32.	NDB-1459 X NDB-1490	44.	NDB-1490 X HUB-240
9.	HUB-240	9.	NDB -302 X NDB-1459	21.	HUB-307 X HUB-240	33.	NDB-1459 X RD-2804	45.	HUB-240 X RD-2772
10.	RD-2772	10.	NDB-1173 X NDB-1449	22.	HUB-307 X RD-2804	34.	NDB-1459 X HUB-240		
		11.	NDB-1173 X HUB-307	23.	HUB-307 X RD-2772	35.	NDB-1459 X NDB-1609		
		12.	NDB-1173 X RD-2772	24.	HUB-307 X NDB-1609	36.	RD-2804 X NDB-1490		

Table 2: Estimates of variability, heritability, and genetic advance of Indian barley landraces and diallelic lines for yield and its component traits.

S. No.	Genotypes	Mean	Range		Variability		Heritability (%)	GA	GA% mean
			Min	Max	var (g)	var (p)			
1.	Days to 50% flowering	81.13	79.00	85.33	79.00	96.33	16.63	18.78	23.15
2.	Days to 90% physical maturity	128.83	124.00	132.67	110.67	132.67	30.41	32.55	25.27
3.	Plant height (cm)	94.19	87.00	100.03	79.67	101.72	20.32	25.30	26.86
4.	No. of productive tillers per plants	5.63	5.00	6.67	5.00	7.39	0.28	0.61	10.83
5.	Spike length (cm)	8.99	8.00	10.67	8.00	12.47	0.87	1.25	13.90
6.	No. of spikelets per spike	26.96	20.00	65.67	19.43	65.67	35.02	37.46	90.73
7.	No. of grain per spike	59.40	53.33	67.67	47.47	67.67	14.11	26.30	44.28
8.	1000-grain weight (g)	42.30	38.33	46.33	35.99	54.57	18.28	19.85	46.93
9.	Flag leaf area $(cm)^2$	21.29	15.86	34.45	12.58	34.45	14.88	15.12	71.02
10.	Peduncle length (cm)	34.34	27.67	43.83	27.67	47.89	17.43	25.27	73.59
11.	Grain weight per spike (g)	2.53	2.17	2.97	2.17	3.27	7.15	0.21	8.31
12.	Protein content (%)	12.27	11.85	12.81	11.85	12.93	6.05	1.20	9.77
13.	Biological yield per plant (g)	39.24	22.33	55.33	22.33	55.33	17.02	17.84	45.46
14.	Harvest Index (%)	35.57	25.58	43.96	25.58	47.67	22.89	24.37	68.51
15.	Grain yield per plant (g)	13.57	9.40	20.17	9.40	20.17	4.63	4.86	35.81

Note: Data representing the mean of three independent biological replicates. Heritability, GA, Genetic Advance

Conclusion and Future Perspectives

This study highlighted the significance of understanding genetic variability, heritability, and genetic advancement in barley, which is essential for developing effective breeding strategies aimed at enhancing yield and adaptation in diverse agro-climatic conditions. The findings indicated that high heritability estimates for key traits such as grain yield, spike length, and effective tillers suggest a substantial additive genetic variance, which can be leveraged in breeding programs. The estimation of genetic variability among the evaluated barley genotypes revealed promising potential for selection and hybridization. By identifying the traits with high heritability and genetic advances, breeders can make informed decisions when selecting superior genotypes for future breeding efforts. Moreover, the study underscores the need for enhancing genetic diversity in barley through targeted breeding practices to address the challenges of low productivity, particularly in regions like India. Overall, this research provides valuable insights into the genetic parameters governing barley traits, paving the way for the development of resilient and high-yielding barley varieties that can contribute to food security and sustainable agriculture in the face of abiotic stresses. Future breeding programs should focus on integrating these findings to optimize selection processes and improve the overall productivity of barley crops.

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Authors Contribution

Conceptualization of the research (PNS, N, T); Designing of the experiments (KK, PNS, N, SCG); Contribution of experimental materials (PNS, N, UG); Execution of field experiments (KK, UG); Data collection (KK); Statistical analysis of the data (KK, SCG, UG); Preparation and revision of the manuscript (KK, UG, PNS, N, T).

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Data Availability

The current study has not generated any molecular datasets. The analyzed phenotypic data have been presented in the table. If it is required, we can provide detailed data on demand.

Conflict of interest
The authors declare that they have no competing interests.

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