

International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2026): 5.29
IJABR 2026; 10(6): 1239-1243
www.biochemjournal.com
Received: 26-04-2026
Accepted: 29-05-2026

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Study of genetic variability and divergence in barley for grain yield

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DOI: <https://www.doi.org/10.33545/26174693.2026.v10.i6o.9017>

Abstract

The experiment was conducted in Augmented Block Design having 5 blocks and checks were repeated after nine germplasm each. The data recorded on these characters were utilized for estimation of mean, range, genetic variability and genetic divergence. The present study, 45 genotypes and three checks, exotic and indigenous lines of barley, showing wide spectrum of variation for various characters, were evaluated in irrigated conditions during Rabi, 2021-22. A wide range of variation for different characters and comparison of means of germplasm lines using least significant differences, indicated existence of very high degree of variability for all the characters in the germplasm collections. The most promising lines showing highest seed yield with high mean performance for other yield contributing characters were identified as IBYT-HI-2021-5, IBON-HI-2021-94, 8th GSBYT-2021-16, IBYT-HI-2021-13, IBON-HI-2021-16. The superior lines identified for seed yield and other characters may be used as donor parents in hybridization programme for the characters to which they showed high mean performance. The Non-Hierarchical Euclidean cluster analysis grouped 48 and indigenous lines of germplasm into three distinct and non-overlapping clusters. The discrimination of germplasm into so many direct clusters suggested presence of high degree of genetic diversity in the material evaluated. Presence of substantial genetic diversity among the germplasm lines screened in the present study indicated that this material might serve as good source for selecting the diverse parents for hybridization programme aimed at isolating desirable segregates for grain yield as well as the important characters.

Keywords: Genetic variability, heritability, genetic advance, genetic diversity

1. Introduction

Barley (*Hordeum vulgare* L.), a winter-friendly crop that originated in the Middle East, is belonging to the Poaceae (Gramineae) family. Cultivated barley is a self-pollinating diploid species ($2n = 2x = 14$). Barley the genus *Hordeum* consists of 32 species and 45 taxa with a basic chromosome number $x = 7$. Globally, barley ranks fourth among cereal crops after wheat, maize and rice is among the top ten crop plants in the world. Globally, barley will cover 51.36 million hectares in 2020-21, with a production of 159.41 million tonnes (USDA 2020-21). India has roughly 0.65-0.70 million hectares of land available in 2020-21, with a production of 1.6-1.8 million tonnes and a productivity of 24.16 q/ha. Barley was grown on 1.78 lakh ha in Uttar Pradesh, with a total yield of 5.10 lakh tonnes and a productivity of 27.01q/ha (Ministry of Agriculture and Farmers Welfare 2020-21). It is a major winter cereal crop farmed in India's northern plains, which include the states of Uttar Pradesh, Bihar, Haryana, Rajasthan, Punjab, Madhya Pradesh, Himachal Pradesh, and Uttarakhand, which account for around 80% of the country's total acreage. The crop, which looks like white berries, is said to be ideal for drought-like circumstances as well as perfectly adapted in soil salinity. It is a primary feed crop in Asia, Africa, and South America's semi-arid regions. Barley is typically grown in arid and semi-arid climates. Iran is positioned in the world's desert belt and is classified as arid and semi-arid. It is a drought-tolerant crop with characteristics such as green pastures during the tillers stage, grain output and use in the food sector, and cropping systems in arid regions of the world. Generally, the Cultivated barley is grown for animal feed, especially for pigs, for malting and brewing in the manufacture of beer, and distilling in whisky manufacture (Gashaw Abebaw (2021) [3].

The major component of barley kernel is starch that may amount to over 70% of the dry weight (FAOSTAT. (2017) ^[13]. Therefore, it may be expected that the quality of barley-based food/feed products can be much affected by the starch properties. Barley has been gaining the attention towards value addition to make various “healthy” food products such as pasta and bread (Edeogu *et al* 2007) ^[12]. The beans are roasted, ground, and utilized in the preparation of “Sattu.” The strong grain can also be roughly milled and used in soups like pearl barley. It is a morning meal in several European countries. It is easier to digest than wheat because it has less gluten and more water-soluble fiber. According to archaeological evidence, the sacred barley known as “Indra Jau” was formerly the most popular sacred grain in all religious rites. Barley is considering for good source of essential nutrients such as dietary fiber and a good nutritional source of Iron, Calcium, Magnesium, Selenium, Copper, Boron, Zinc, Molybdenum, and a better source of Protein, Carbohydrates, and Lipids (Gujral *et al.*, 2013) ^[4]. It consists good source of both soluble and insoluble dietary fibers and in particular, the beta-glucan. The beta-glucan content of cereals ranges from 1% in wheat grains, 3-7% in oats, and 5-11% in barley. Beta-glucan is principally found in the aleurone layer and endosperm in barley. Compared to insoluble fiber such as cellulose, beta-glucan is more flexible, soluble, and viscous. It confers many health benefits including reducing the risk of heart disease, lowering blood cholesterol levels, increasing insulin response in diabetics, and preventing obesity and cancer. The barley grain consists of-Starch-65-68% Protein-10-13.6% β -Glucan-4-9% Lipids-2-3% Minerals-1.5-2.5% Total dietary fiber-11-34% Soluble dietary fiber-3-20%. Grain yield is a complex of component qualities that is influenced by a variety of environmental factors. Grain yield is influenced by a variety of physiological and morphological characteristics. Each of these genetic systems is responsible for one of these component qualities. Furthermore, environmental variables have an impact on these yield components. Thus, using genetic characteristics such as phenotypic and genotypic coefficients of variation, heritability, and genetic gain, it is necessary to divide total variation into non-heritable and heritable components. Statistical relationships between agronomic and morphological variables and grain yield have been found in a large number of barley grain production studies and its improvement.

2. Materials and Methods

The present investigation was conducted during Rabi 2021-22 at Genetics & Plant Breeding Research Farm of “Acharya Narendra Deva University of Agriculture & Technology Kumarganj, Ayodhya”. The experimental materials consist of 48 germplasm of barley including 3 checks viz. BHS400, BH946 and HUB113. These genotypes were evaluated in Augmented Block Design. The experimental field was divided into 5 blocks and all the three checks were repeated in each block possessing nine genotypes. The observations were recorded on five randomly selected plants in each row except 50% flowering and days to maturity, where data were recorded on plot basis recorded for the following quantitative characters.: Days to 50% flowering, Days to maturity, Plant height (cm), Tillers/plant, Flag Leaf area (cm²), Spike length (cm), Biological yield per plant (g), 1000-seed weight (g), Harvest

index, Grain yield per plant (g): The analysis of variance for different characters in Augmented Block Design was done following Federer (1956) ^[7]. Genetic divergence among 48 genotypes planted in augmented design was studied through Non-hierarchical Euclidean cluster analysis (Beale, 1969) ^[5].

3. Results and Discussion

The present investigation was carried out with 48 genotypes along with 3 check varieties viz., BH946, HUB113 and BHS400. The results of various analyses on various aspects examined under the present investigation have been described in the following subtitles:

- Analysis of variance.
- Mean performance of genotypes
- Coefficient of variation
- Heritability and genetic advance in percentage of mean
- Genetic divergence analysis

3.1 Analysis of variance

The analysis of variance for the Augmented Block Design with respect to 10 characters is shown in Table 1. The fluctuations due to the blocks were highly significant for days to 50% flowering (heading), plant height (cm), test weight (g), and biological yield/plant (g). The differences among the checks varieties were found to be highly significant for all the studied characters except biological yield per plant (g) was non-significant.

3.2 Mean performance of genotypes

The mean performance of forty-eight indigenous barley genotypes with including three checks of ten characters are presented for evaluation and comparison of genotypes in Table .2.

3.3 Coefficient of variation

The success of selection in improving plant characters depends mainly on presence of substantial genetic variability and nature of heritability and gene action. The phenotypic and genotypic coefficients of variation can be used to evaluate and compare the nature and extent of variability present in breeding materials for various traits. The phenotypic and genotypic coefficient of variation for all the 10 characters has been given in Table 2.

The phenotypic coefficient of variation was greater than the genotypic coefficient of variations for all traits. The highest estimate of the phenotypic (PCV) and genotypic (GCV) coefficient of variation was observed for the tillers per plant (PCV = 12.36% & GCV = 9.47%), followed by flag leaf area (PCV = 9.46% & GCV = 5.45%), spike length (PCV = 9.42% & GCV = 5.96%), grain yield per plant (g) (PCV = 8.45% & GCV = 6.96%), harvest index (%) (PCV = 7.97% & GCV = 1.63), respectively and lowest for days to maturity i.e. (PCV = 1.90% & GCV = 1.36%). (Eshghi *et al.*, 2012) ^[6] reported the similar results indicated that the higher GCV and PCV value in characters, tillers per plant followed by flag leaf area, spike length and grain yield per plant.

3.4 Heritability and genetic advance in percentage of mean

In a broad sense, heritability is the ratio of fixable additive genetic variance to total phenotypic variance, but in a narrow sense, it is the proportion of heritable genetic

variance to total phenotypic variance. The estimate of broad sense heritability (h^2_b) and genetic advance in percentage of mean (GA) for different character are given in Table 2. The highest estimate of heritability in broad sense was recorded in test weight (72.99%) followed by grain yield per plant (67.79%), biological yield per plant (67.24%), days to 50% flowering (66.21%), tillers per plant (58.70%) and least in the harvest index (%) (4.18%). The highest genetic advance as percentage was observed for tillers per plant (14.94) followed by grain yield per plant (11.80), biological yield per plant (8.98), spike length (7.77), flag leaf area (6.47), 1000 grain weight (4.41), days to 50% flowering (3.86), plant height (2.73), days to maturity (2.01) and harvest index (0.69). The highest heritability coupled with high genetic advance was observed for both grain yield per plant as well as biological yield per plant. The similar result for both heritability and genetic advance was reported by (Hailu *et al.* 2016) [8].

3.5 Genetic divergence analysis

The basic material of a plant breeding programme is genetic diversity, which is used to generate superior genotypes through selection. The Non-hierarchical Euclidean cluster analysis was employed to study the genetic divergence existing among 48 barley germplasm collections on the basis of 10 quantitative characters. The quasi-Fisher-test (F-test) showed that three clusters provisions were most appropriate for grouping the forty-eight genotypes. Therefore, the 48 genotypes were accepted to be grouped in to 3 non-overlapping clusters. The study also reveals the percentage of contribution of these characters towards total divergence, clustering pattern and intra-cluster and inter-cluster distance. The dendrogram and cluster diagram were prepared through the Tocher's method and Mahalanobis Euclidean distance method, respectively. Several workers (Alam *et al.*, 2007; Ali *et al.*, 2007 and Mishra *et al.*, 2009) [7, 2, 8] have emphasized importance of genetic diversity in plant breeding. The distribution of 48 barley lines in 3 clusters is presented in Table 3.

3.5.1 Group constellation

Cluster (II) emerged with highest number of entries as it was constituted by 23 genotypes entries followed by cluster (I) having 15 genotypes and least in the cluster (III) having 10 genotypes respectively.

3.5.2 Intra and Inter-cluster distances

The inter and intra cluster distance are presented in Table no 4. The largest intra-cluster distance was observed in cluster III (2.793), followed by cluster II (2.624). The lowest intra-cluster value was observed for cluster I (2.422). The highest inter-cluster distance was observed between cluster III and cluster II (3.354), followed by cluster II and cluster I (3.006). The minimum inter-cluster distance was observed between cluster III and cluster I (2.931).

3.5.3 Cluster means analysis for distances

The cluster means for 10 characters are presented in Table 5. The highest cluster mean for days to 50% flowering was recorded for cluster III (84.70) the lowest cluster mean for days to 50% flowering was found in case of cluster I (77.88), while remaining cluster had moderate means for days to 50% flowering. The highest cluster mean for days to maturity was recorded in case of cluster III (125.60 cm) the lowest cluster mean for days to maturity was found in case of cluster II (71.90 cm). The highest cluster mean for plant height was recorded in case of cluster I (89.53) the lowest cluster mean for plant height was found in case of cluster II (87.42). The cluster I was responsible for highest cluster mean for tillers per plant (7.02), the genotypes with lowest tillers per plant was found in cluster II (5.35). The highest cluster mean for flag leaf area was recorded in case of cluster III (18.18 cm²) the lowest cluster mean for flag leaf area was found in case of cluster I (15.29 cm²). The highest cluster mean for spike length was recorded in case of cluster III (7.46 cm) the lowest cluster mean for spike length was found in case of cluster I (6.73 cm). The highest cluster mean for test weight was recorded in case of cluster III (39.94 g) t lowest cluster mean for test weight was found in case of cluster I (38.15 g). The highest cluster mean for biological yield per plant was recorded in case of cluster III (31.47 g) and lowest cluster mean for biological yield per plant was found in case of cluster II (25.80 g). The highest cluster mean for harvest index was recorded in case of cluster III (34.99%) the lowest cluster mean for harvest index was found in case of cluster II (31.63%). The highest cluster mean for grain yield per plant was found in case of cluster III (10.99 g) the lowest cluster mean for grain yield per plant was observed in case of cluster II (8.16 g). Several researchers also reported significant genetic divergences in barley material (Sharma *et al.*, 2005; Singh *et al.*, 2006; Alam *et al.*, 2007, Ali *et al.*, 2007; Mishra *et al.*, 2009) [11, 10, 1, 2, 8].

Table 1: Analysis of variance of Augmented Block Design for 10 characters in barley (*Hordeum vulgare* L.)

Source of variation	D.F.	Days to 50% flowering	Days to maturity	Plant height (cm)	Tillers per plant	Flag leaf area (cm ²)	Spike length (cm)	Test weight (g)	Biological yield per plant (g)	Harvest index (%)	Grain yield per plant (g)
Blocks	4	4.27**	2.43	25.30**	0.43	1.65	0.76*	2.89**	3.34**	8.78	0.26
Checks	2	5.60**	6.20**	44.02**	1.57**	32.24**	2.12**	3.67**	2.86	45.67**	1.36**
ERROR	8	1.77	2.62	4.86	0.24	1.69	0.26	0.35	1.11	6.72	0.21

*, ** significant at 5% and 1% level, respectively

Table 2: Range, mean, coefficient of variation and least significant differences for 10 character of barley genotypes

Characters	G mean	Range		Coefficient of variations		Heritability (%)	GA	GA mean 5 %
		Max	Min	GCV%	PCV%			
Days to 50% flowering	80.71	74.00	90.00	2.31	2.83	66.21	3.12	3.86
Days to maturity	121.88	116.00	130.00	1.36	1.90	51.28	2.45	2.01
Plant height(cm)	88.08	76.80	98.95	2.08	3.25	40.77	2.40	2.73
Tillers/plant	6.12	3.80	8.36	9.47	12.36	58.70	0.92	14.94
Flag leaf area (cm ²)	16.80	12.88	20.86	5.45	9.46	33.19	1.09	6.47
Spike length (cm)	6.99	5.40	9.10	5.96	9.42	40.05	0.54	7.77
1000-grain weight (g)	38.87	36.05	44.25	2.51	2.93	72.99	1.71	4.41
Biological yield per plant (g)	28.40	23.45	34.73	5.32	6.48	67.24	2.55	8.98
Harvest index (%)	33.23	26.95	40.01	1.63	7.97	4.18	0.23	0.69
Grain yield/plant	9.47	7.15	12.00	6.96	8.45	67.79	1.12	11.80

PCV = phenotypic coefficient of variance. GCV = genotypic coefficient of variance.

Table 3: Clustering pattern of 48 barley genotypes on the basis of non-hierarchical Euclidean cluster analysis for 10 characters

Clusters	No. of genotypes	Genotypes
I	15	IBYT-HI-2021-14, IBYT-HI-2021-13, IBYT-HI-2021-5, IBON-HI-2021-15, IBON-HI-2021-16, IBON-HI-2021-97, IBON-HI-2021-20, IBON-HI-2021-49, 8 th GSBYT-2021-18, 8 th GSBYT-2021-20, 8 th GSBYT-2021-3, 8 th GSBYT-2021-13, 8 th GSBYT-2021-62, 8 th GSBYT-2021-9, BHS400
II	23	IBYT-HI-2021-10, IBYT-HI-2021-15, IBYT-HI-2021-6, IBYT-HI-2021-2, IBYT-HI-2021-19, IBYT-HI-2021-11, IBON-HI-2021-32, IBON-HI-2021-91, IBON-HI-2021-112, IBON-HI-2021-19, IBON-HI-2021-22, IBON-HI-2021-42, IBON-HI-2021-17, IBON-HI-2021-87, IBON-HI-2021-3, 8 th GSBYT-2021-19, 8 th GSBYT-2021-21, 8 th GSBYT-2021-67, 8 th GSBYT-2021-42, 8 th GSBYT-2021-17, 8 th GSBYT-2021-92, BH946, HUB113
III	10	IBYT-HI-2021-18, IBYT-HI-2021-9, IBYT-HI-2021-1, IBYT-HI-2021-12, IBON-HI-2021-1, IBON-HI-2021-94, IBON-HI-2021-105, 8 th GSBYT-2021-22, 8 th GSBYT-2021-16, 8 th GSBYT-2021-94

Table 4: Estimates of average intra- and inter-cluster distances for clusters in barley

Clusters	I	II	III
I	2.422	3.006	2.931
II		2.624	3.354
III			2.793

Bold figures indicate the intra-cluster distance

Table 5: Clusters means for 10 characters in barley

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Tillers per plant	Flag leaf area (cm ²)	Spike length (cm)	Test weight (g)	Biological yield per plant (g)	Harvest index (%)	Grain yield per plant (g)
I	77.88	119.21	89.53	7.02	15.29	6.73	38.15	30.36	34.50	10.46
II	80.83	122.00	87.42	5.35	17.17	6.96	38.87	25.80	31.63	8.16
III	84.70	125.60	87.45	6.56	18.18	7.46	39.94	31.47	34.99	10.99

4. Conclusion

- The vast range of variation for multiple features, as well as the comparison of genotype means using the least significant differences, revealed that all traits in alien and indigenous barley lines have a high degree of variability.
- The genotypes IBYT-HI-2021-5, IBON-HI-2021-94, and 8thGSBYT-2021-16 produced higher grain yield per plant and had high to very high mean performance for a variety of other yield components.
- The highest estimate of the phenotypic (PCV) and genotypic (GCV) coefficient of variation was observed for the TPP (PCV = 12.36% & GCV = 9.47%), followed by FLA (PCV = 9.46% & GCV = 5.45%), SL (PCV = 9.42% & GCV = 5.96%), grain yield per plant(g) (PCV = 8.45% & GCV = 6.96%), HI (percent) (PCV = 7.97% & GCV = 1.63), respectively and lowest for DM i.e. (PCV = 1.90% & GCV = 1.36%).
- The non-hierarchical Euclidean cluster analysis classified 48 genotypes into three cluster. This revealed that the germplasm evaluated in this study had a high

level of genetic diversity. Cluster II has the most genotypes, with 23, followed by Cluster I with 15, and Cluster III with 10.

- Cluster III and Cluster II had the greatest inter-cluster distance (3.354), followed by Cluster II and Cluster I (3.006), while Cluster III and I had the smallest (2.931).
- Because high or optimal genetic divergence favored among the parents for hybridization plan for obtaining good segregates belonging to the same cluster is very low. In order to increase the likelihood of isolating good segregates within segregating generations, it would seem natural to try crosses among the many exotic lines belonging to clusters with substantial inter cluster distances in the current study.

Acknowledgement

We thank A.N.D.U.A.T, Kumarganj, Ayodhya for sharing barley germplasm for the study. We are also thankful to Head, Division of Genetics and Plant Breeding for providing the necessary facilities during the course of study.

Compliance with ethical standards

This article does not contain any studies involving human or animal participants performed by any of the authors.

Conflict of interest: No

Author Contributions

The manuscript was written and enriched by VKS, RJ & SK. All authors read, edited & approved the final manuscript.

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