

STUDY OF GENETIC DIVERSITY OF ECONOMIC TRAITS IN BARLEY (*HORDEUM VULGARE* L.)

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SUMMARY

A number of forty five genotypes of barley and six checks were evaluated in augmented design. The non-hierarchical Euclidean cluster analysis grouped the genotypes including checks into seven different clusters. Maximum number of genotypes were centered in cluster VI and VII, nine each. Clusters III, IV and V collected eight genotypes in each group. Lowest number of genotypes were studied to be in cluster II *i.e.* four. The highest intra-cluster distance was recorded for cluster II, indicating the existence of higher genetic variability within this cluster. The maximum inter cluster distance was recorded between cluster IV and cluster V, pointing to the higher genetic diversity for genotypes included in these clusters. The genotypes *viz.*, IBYT-18-4, IBYT-18-21, IBYT-18-8, IBON-18-46 and 5th GSBYT-18-6 were scored to be promising for their further exploitation in barley breeding programmes.

Key words: Barley, clusters, euclidean distance, genetic divergence

Barley, one of the primarily cultivated crops of ancient era, is followed by wheat, rice and maize in grain production in world scenario. In India, barley occupied an area of 0.59 mha with 1.72 mt production and 2920 kg/ha average productivity. In Haryana, it is cultivated on an area of 12,120 ha with a production of 46,500 tonnes and average productivity of 3837 kg/ha (ICAR-IIWBR, 2020). Compared to other cereal crops its ability to survive and grow under adverse climatic conditions and also grown over a wide range of soil, barley is the most suitable one cereal crop (Saied and Ashraf, 2014). Barley is widely used for malting, human consumption as well as for animal feed includes production of soup, stews, bread and many healthy products.

The extent of genetic variability existing in a material determines the success of a breeding programme. Therefore, the evaluation and use of genetic variability to get expected results is essential in any crop improvement programme. Isozyme markers besides the quantitative characters determining grain yield being co-dominant in nature having simple inheritance and detect diversity at functional gene level even with a small sample size of plant material are also used to assess the variability among genotypes. Genetic variability gives wider scope for selection making it the primary requirement for crop improvement. The present study aimed at

studying genetic variability pattern and to categorise trait specific promising genotypes which may be utilized in plant breeding programmes.

MATERIALS AND METHODS

The experimental material for the present investigation consisted of forty five barley genotypes and six check varieties (BH 946, BH 959, BHS 400, RD 2715, DWRB 101, HUB 113) was grown during *rabi* season 2018-19 in augmented design at Barley Research area of Department of Genetics and Plant Breeding, CCS HAU, Hisar. The soils of the farm is mainly sandy loam and rainfall received during the crop season was 44.1 mm with mean monthly minimum and maximum temperatures of 10.43°C and 26.37°C, respectively during 2018-19.

Each plot consisted of two rows of 2.5m length with 30 cm spacing. All the recommended package of practices was adopted. Five plants from each genotype were taken randomly from each block for recording of observations for ten morphological traits. Statistical analysis carried out on average data of five plants. The data were recorded for ten morphological traits *viz.* Days to heading, Days to maturity, Plant height (cm), Number of effective tillers/meter, Spike length (cm), Number of grains/spike, 1000 grain weight (g), Grain yield/plot (g), Biological

yield/plot (g), Harvest index (%), and two biochemical characters *viz.* dehydrogenase activity and peroxidase enzyme. Genetic divergence of barley genotypes was calculated on the basis of Euclidean cluster analysis as suggested by Spark (1973).

RESULTS AND DISCUSSION

The analysis of variance revealed significant variations among the genotypes.

Genetic divergence

The genetic diversity was studied by Ward’s minimum method of Euclidean cluster analysis for different traits. Fifty-one genotypes were grouped into seven non-overlapping clusters as depicted in Table 1 and dendrogram showing clustering pattern in Fig. 1 and Mahalanobis Euclidean distances in all genotypes in Fig. 2. Highest number of genotypes (nine) in cluster VI and cluster VII was recorded followed by cluster III, cluster IV and cluster V having eight genotypes each, cluster I had five genotypes and cluster II had minimum number of genotypes four (Table 1 and Fig. 1). Similar results for cluster analysis were also reported by Muhe and Assefa (2011), Singh *et al.* (2013), Sunil *et al.* (2017), Hagenblad *et al.* (2019) and Dido *et al.* (2020).

Intra and inter cluster distances

The calculated intra and inter-cluster distances for seven clusters are presented in Table 2. The highest intra-cluster distance value was found for cluster II (4.183) followed by cluster VII (3.906), cluster V (3.856), cluster VI (3.841), cluster III (3.671), cluster

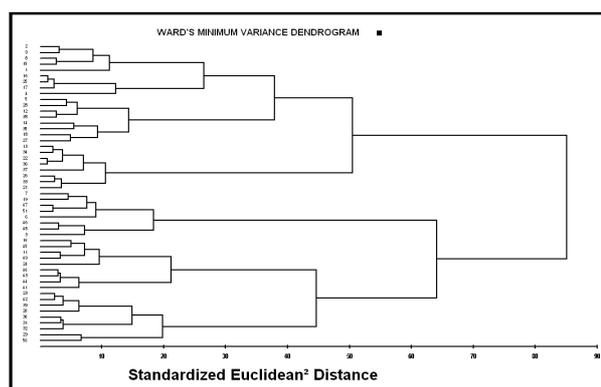


Fig. 1. Dendrogram showing the clustering pattern of 51 barley genotypes.

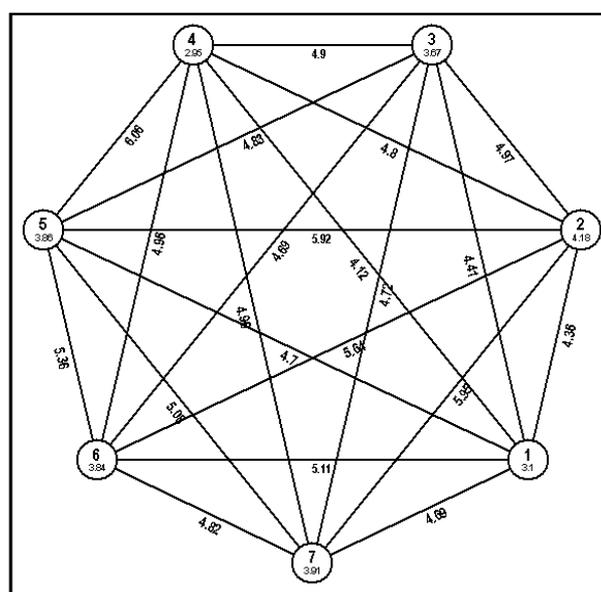


Fig. 2. Mahalanobis Euclidean distances in all genotypes.

I (3.099) and cluster IV (2.951). The maximum inter cluster distance value was recorded between cluster IV and V (6.063) followed by cluster II and VII

TABLE 1
Euclidean clustering arrangement of 51 barley genotypes for twelve parameters

Clusters	No. of genotypes	Genotypes
I	5	IBYT-18-5, IBYT-18-21, IBYT-18-18, INBYT-HI-18-22, IBYT-18-4
II	4	5th GSBYT-18-3, IBON-18-46, 5th GSBYT-18-4, IBYT-18-8
III	8	IBYT-18-9, IBON-18-60, INBYT-HI-18-11, INBON-HI-18-55, INBYT-HI-18-18, INBON-HI-18-26, 5th GSBYT-18-6, IBON-18-59
IV	8	INBYT-HI-18-13, INBON-HI-18-11, 5th GSBYT-18-19, INBON-HI-18-48, INBON-HI-18-49, IBON-18-47, INBON-HI-18-7, 5th GSBYT-18-16
V	8	IBYT-18-16, 5th GSBYT-18-7, BH 959, HUB 113, IBYT-18-12, BH 946, BHS 400, IBYT-18-6
VI	9	INBYT-HI-18-3, 5th GBSON-18-114, INBYT-HI-18-9, RD 2715, 5th GSBYT-18-22, 5th GBSON-18-79, 5th GBSON-18-104, 5th GBSON-18-109, 5th GBSON-18-84
VII	9	5th GSBYT-18-21, 5th GBSON-18-94, 5th GBSON-18-65, 5th GSBYT-18-15, IBON-18-97, IBON-18-100, IBON-18-108, IBON-18-82, DWRB 101

TABLE 2
Estimated average intra (diagonal) and inter (above diagonal) cluster distances of seven clusters

Clusters	I	II	III	IV	V	VI	VII
I	3.099	4.356	4.415	4.125	4.700	5.108	4.687
II		4.183	4.974	4.798	5.916	5.642	5.955
III			3.671	4.904	4.831	4.693	4.724
IV				2.951	6.063	4.958	4.962
V					3.856	5.357	5.075
VI						3.841	4.824
VII							3.906

Intra-cluster distance indicated by bold figures.

(5.955). The inter-cluster distance values amongst cluster II and V (5.916), cluster II and VI (5.642), cluster V and VI (5.357), cluster I and VI (5.108) and cluster V and VII (5.075) were also high. The minimum inter-cluster distance were recorded between cluster I and IV (4.125), followed by cluster I and II (4.356), cluster I and III (4.415), clusters III and VI (4.693) and cluster I and VII (4.687).

Mean values of different clusters

The cluster mean performance for all the traits are presented in Table 3. The maximum cluster mean for grain yield per plot was noted for cluster II ($X = 677.00$) showing that the genotypes with high grain yield per plot were focused in this cluster, followed by cluster V ($X = 646.750$). The genotypes of low grain yield were assembled in cluster IV ($X = 403.750$). Taking mean values as a reference, the genotypes in high yielding cluster group gave higher mean of grain yield per plot, biological yield per plot, number of grains per spike and spike length. In contrast, the genotypes in low yielding clusters were characterized

by higher mean values of plant height and number of effective tillers per meter and lower harvest index. Similar findings were also stated by different authors like Mekonnen *et al.* (2015), Dyulgerova *et al.* (2016), Hailu *et al.* (2016), Khalid and Hamid (2017) and Saroei *et al.* (2017).

Contribution of different characters towards divergence

The main characters which highly contribute towards divergence were biological yield per plant, grain yield per plant, number of grains per spike, number of effective tillers per meter (Table 4). Alam *et al.* (2007) concluded that 1000 grain weight, days to maturity and grains per spike were main characters offering diversity in barley. Nessa *et al.* (1998) also concluded that spike length, plant height and tiller's number were such characters contributing to diversity

TABLE 4
Contribution of different characters towards divergence in Barley

S. No.	Source	Contribution towards divergence (%)
1.	Days to heading	1.02
2.	Days to maturity	0.16
3.	Plant height (cm)	1.23
4.	Number of effective tillers per meter	6.16
5.	Spike length (cm)	0.28
6.	Number of grains per spike	11.02
7.	1000 grain weight (g)	2.92
8.	Grain yield per plot (g)	21.92
9.	Biological yield per plot (g)	46.90
10.	Harvest index (%)	2.01
11.	DHA	3.09
12.	POD	3.29

TABLE 3
Cluster mean performance of seven clusters for twelve characters in genotypes of barley

Clusters	DH	DM	PH	NET/M	SL	NG/S	1000GW	GY/P	BY/P	HI	DHA	POD
I	98.250	142.750	106.750	104.500	8.400	58.750	41.500	573.750	2560.000	22.585	0.609	0.655
II	97.400	142.800	111.600	102.800	10.340 ^H	74.600 ^H	37.520 ^L	677.000 ^H	2838.000 ^H	23.960	0.329	1.093
III	90.250	138.375	109.000	81.125 ^L	8.925	73.875	38.512	410.000	1762.500	23.445	0.385	0.835
IV	101.375 ^H	143.750 ^H	115.125 ^H	110.250 ^H	10.162	30.000	41.200	403.750 ^L	1923.750	21.131 ^L	0.286	0.829
V	90.200	139.000	101.250	89.750	7.588	62.463	39.450	646.750	991.912 ^L	31.317 ^H	0.652 ^H	0.637 ^L
VI	88.467 ^L	137.156 ^L	109.478	91.867	9.000	38.156	47.078 ^H	471.556	1555.289	26.667	0.325	1.193 ^H
VII	97.311	140.533	94.900 ^L	86.133	7.233 ^L	37.478 ^L	42.600	416.222	1511.100	24.620	0.263 L	0.809

L Lowest value, H Highest value

DH: Days to heading, DM: Days to maturity, PH: Plant height, NE/T: Number of effective tillers/meter, SL: Spike length, NG/S: Number of grains/spike, 1000GW: 1000 grain weight (g), GY/P: Grain yield per plot (g), BY/P: Biological yield per plot (g), HI: Harvest index (%), DHA: Dehydrogenase activity, POD: Peroxidase activity.

TABLE 5
Promising genotypes in different clusters based on yield and its associated characters

Clusters	Promising genotypes	Characters
I	IBYT-18-4, IBYT-18-21	1000GW, GY/P, BY/P, HI
II	IBYT-18-8, IBON-18-46	1000GW, GY/P, BY/P, HI
III	5th GSBYT-18-6, IBON-18-59, INBYT-HI-18-11	1000GW, GY/P, BY/P, HI
IV	INBON-HI-18-49, 5th GSBYT-18-19, INBON-HI-18-48	1000GW, GY/P, BY/P, HI
V	5th GSBYT-18-7, IBYT-18-12, IBYT-18-16	1000GW, GY/P, BY/P, HI
VI	5th GBSON-18-84, 5th GBSON-18-22, 5th GBSON-18-109, INBYT-HI-18-3	1000GW, GY/P, BY/P, HI
VII	5th GSBYT-18-21, 5th GBSON-18-65, IBON-18-108	1000GW, GY/P, BY/P, HI

for yield. Ram and Singh (1989) reported that grain weight, spike length and grains per spike highly presented diversity for yield to barley genotypes. All these results determined that these traits for corresponding clusters were best for selection for crop improvement to bring higher yield.

Diverged and promising genotypes selected

The promising diversified genotypes selected on the basis high performance of 1000 grain weight, grain yield per plant, biological yield per plant and harvest index showed superiority for their utilization in plant breeding programmes. These genotypes were selected in addition to the other genotypes showing higher mean than the general mean and cluster mean for different traits. Promising genotypes were also identified by Kumar *et al.* (2021) in barley based on genetic divergence.

CONCLUSIONS

The maximum inter cluster distance was recorded between cluster IV and cluster V, pointing to the higher genetic diversity for genotypes included in these clusters. Therefore, genotypes from these clusters would be selected for the recombination breeding programmes. The minimum inter-cluster distance values was obtained between cluster I and IV. Highest contribution towards genetic divergence was presented by biological yield per plot followed by grain yield per plot, number of grains per spike and number of effective tillers per meter.

The genotypes namely, IBYT-18-4, IBYT-18-21, IBYT-18-8, IBON-18-46, 5th GSBYT-18-6, IBON-18-59, INBYT-HI-18-11, INBON-HI-18-49, 5th GSBYT-18-19, INBON-HI-18-48, 5th GSBYT-18-7, IBYT-18-12, IBYT-18-16, 5th GBSON-18-84, 5th GBSON-18-84, 5th GBSON-18-109, INBYT-HI-18-3, 5th GSBYT-18-21, 5th GBSON-18-65, 5th GBSON-18-

65 were evaluated and selected on the basis of general mean values, inter-cluster distance values and cluster means from all the clusters along with other superior traits. These genotypes evaluated were found to be very important to use in different breeding programmes for their further exploitation of barley crossing. Genotypes selected in this study may be utilised into elite barley breeding programmes to have transgressive segregants as well.

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