



Selection strategies for yield enhancement in barley (*Hordeum vulgare* L.)

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Received: 13 Jan 2024; Received in revised form: 19 Feb 2024; Accepted: 28 Feb 2024; Available online: 07 Mar 2024

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Abstract— A field experiment with 42 genotypes of barley was conducted in order to select key components and promising genotypes for yield enhancement. The experiment was laid in randomized block design with four replications during 2022-23 at Barley Research Area, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. The genotypic correlation estimates showed significant positive association of grain yield with days to maturity, spike length and 1000-grain weight. The trait viz., days to maturity exhibited the highest positive direct effect on grain yield followed by 1000 grain weight and spike length. Hence, these traits could be considered as suitable selection criterion for the development of high yielding barley varieties. Cluster analysis assigned all the genotypes into four distinct clusters. Cluster I, contained 14 genotypes recorded with shortest plant height having highest number of effective tillers per meter. Cluster II consisted of 8 genotypes, characterized by long spikes and high 1000-grain weight. Cluster III had 11 genotypes with highest grain yield. Cluster IV comprised of nine early maturing genotypes. The average inter-cluster distance was found to be highest between the cluster I and III followed by between cluster I and IV while the lowest inter-cluster distance was observed between clusters III and IV. The improvement in six rowed barley could be achieved through the use genotypes assigned in clusters III, whereas the genotypes which contained in cluster II might be considered as potential parents for two rowed barley to obtain high heterotic response and consequently better segregants for grain yield.



Keywords— Barley, Cluster, Correlation, Direct Effects, Genetic divergence

I. INTRODUCTION

Barley is a coarse cereal, which is being utilized for human food, livestock feed and as well as for malting and brewing purposes. The barley cultivation requires low inputs in terms of fertilizers and irrigation and has better adaptability to harsh environments. Barley offers many health benefits and has a huge potential to be a future staple cereal substituting wheat and rice in diet for diabetic and people suffering from high cholesterol. It has low glycemic index as well as low amount of anti-nutritional factor *i.e.* phytate along with high beta glucan, that offers many health benefits. In India, the area under barley is about 0.62 m ha with the production and productivity of 1.69 m t and 27.33 kg/ha, respectively. Barley was cultivated on 15,300

hectares with a grain production of 53,300 tons in Haryana which ranks second in average productivity (34.86 q/ha) after Punjab (36.54 q/ha) during 2022-23 [1].

Genetic reconstruction of a plant type is essential for development of high yield potential genotypes by selection and incorporation of yield components. The evaluation of breeding material for genetic variability is vital for present as well as for future crop improvement approaches. The extent and nature of interrelationship among different characters and their contribution towards yield helps in formulating the efficient scheme of multiple trait selection. Genetic diversity is one of the important mechanism of stability of biological systems and is always remained the key parameter of plant breeding [2]. Hence,

their information facilitates the plant breeders in isolation of trait specific superior donors for commencing targeted hybridization programme, as heterotic expression is believed to be associated with genetic divergence among the genotypes used as parents. In addition, appropriate utilization of genotypes requires screening of genetic potential under specific environmental condition for which the breeding programme is designed. The Bioversity International as well as International Union for the Protection of New Varieties of Plants recommended the morphological characterization as criterion to identify accessions for the assessment of genetic diversity [3]. Some findings on genetic diversity of barley have also focused on importance of morphological traits [4, 5]. Several approaches are available to examine genetic diversity in the breeding material. Often cluster analysis has widely been used in order to identify the traits specific donors to be used in a fresh breeding programme for meaningful achievement.

Keeping in view the above, the present investigation was therefore undertaken to identify the key yield components and to select the trait specific promising genotypes for inclusion in yield enhancement strategies in barley under timely sown irrigated conditions.

II. MATERIALS AND METHODS

A total of 42 barley genotypes comprised of two and six row types were grown in a randomized block design with three replications during 2022-23 at Barley Research Area, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. The experimental location is

situated between 29°10'N latitude, 75°46'E longitude and at an altitude of 215.2 m above mean sea level in subtropical region of North Western Plain Zone of India. Each genotype was consisted of 6 rows of 5.0 m length grown under timely sown irrigated condition, with spacing of 23 cm between rows. The observations were recorded for eight morphological traits *viz.*, days to heading, days to maturity, plant height (cm), effective tillers per meter, spike length (cm), number of grains per spike, 1000-grain weight (g) and grain yield (q/ha). The crop was raised following recommended package of practices. For recording data, five randomly selected competitive plants in each replication were chosen for all the traits under study except of days to heading and maturity, and grain yield which were recorded on plot basis. The mean performance of each genotype was subjected to statistical analysis using statistical software R Studio [6].

III. RESULTS AND DISCUSSION

Correlation coefficient analysis measures the natural relation between various plant characters and determines the component traits on which selection can be used for yield enhancement. The genotypic correlation coefficients between studied traits are depicted in Table 1. The results revealed significant positive correlation of grain yield with days to maturity, spike length and 1000-grain weight. These finding are in accordance with result of Kumar *et al.* [7] for days to maturity and 1000-grain weight. The positive correlation of grain yield with these traits signifies that improvement in one or more of these traits could result in higher grain yield in barley.

Table 1: Estimates of genotypic correlation coefficients for different traits in barley

Traits	DH	DM	PH	ET/m	SL	G/S	TGW	GY
DH	1.00	0.732**	0.300	0.101	0.215	-0.034	0.20	0.143
DM		1.00	0.245	0.139	0.341*	-0.187	0.437**	0.385*
PH			1.00	-0.387*	0.312*	0.369*	-0.174	0.135
ET/m				1.00	-0.452**	-0.619**	0.226	-0.132
SL					1.00	0.245	0.223	0.307*
G/S						1.00	-0.606**	-0.047
TGW							1.00	0.322*

DH: Days to heading, DM: Days to maturity, PH: Plant height, ET/m: Effective tillers per meter, SL: Spike length, G/S: Number of grains per spike, TGW: 1000-Grain weight, GY: Grain yield, *, ** Significant at 0.05 and 0.01 level, respectively

Plant height showed positive and significant correlation with spike length and number of grains per spike. However, it registered significant negative correlation with effective tillers per meter. Further, the results of correlation coefficient implied the significant

positive association for days to maturity with days to heading, spike length and 1000-grain weight. Kumar *et al.* [7] also reported positive but non-significant correlation of days to maturity with 1000-grain weight. Similarly, significant negative correlation was found for spike length

and number of grains per spike with effective tillers per meter; and number of grains per spike with 1000-grain weight, thereby indicating that these traits could not be improved simultaneously. Some authors also reported significant positive correlation for days to heading with maturity [8], plant height with spike length [9], days to maturity with days to maturity and spike length; plant height with spike length and number of grains per spike [10]. The negative and significant relation of effective tillers per meter with plant height and number of grains per spike; 1000-grain weight with number of grains per spike also corroborated with the findings of Devi *et al.* [10] under different environments. The negative but non-significant association between spike length and effective tillers per meter was also confirmed by Kumar *et al.* [7] in barley.

Path coefficient presents an effective way of finding direct and indirect sources of correlation. Direct and indirect effects of these components determined on

grain yield at genotypic level are presented in Table 2. The results of path coefficient analysis revealed that days to maturity (0.477) exerted the highest positive direct effect on grain yield followed by 1000-grain weight (0.218), spike length (0.060), plant height (0.041) and number of grains per spike (0.040), which support the findings of Devi *et al.* [10] except for number of tillers per meter however, Kumar *et al.* [9] in their findings mentioned positive direct effect of number of tillers per meter on grain yield. Therefore, these traits could be considered as main components for selection in a breeding program for higher grain yield. Path analysis further revealed that though effective tillers per meter had negative direct effect (-0.154) but it highly contributed to grain yield *via* number of grains per spike and spike length. In addition, days to heading contribute *via* number of grains per spike to grain yield as this traits also showed high negative direct effect (-0.257).

Table 2: Direct and indirect effects of different traits on grain yield in barley

Traits	DH	DM	PH	ET/m	SL	G/S	TGW	rg with GY
DH	-0.257	-0.188	-0.077	-0.026	-0.055	0.009	-0.052	0.143
DM	0.349	0.477	0.117	0.066	0.163	-0.089	0.209	0.385*
PH	0.012	0.010	0.041	-0.016	0.013	0.015	-0.007	0.135
ET/m	-0.016	-0.021	0.059	-0.154	0.070	0.095	-0.035	-0.132
SL	0.013	0.020	0.019	-0.027	0.060	0.015	0.013	0.307*
G/S	-0.001	-0.008	0.015	-0.025	0.010	0.040	-0.024	-0.047
TGW	0.044	0.095	-0.038	0.049	0.049	-0.132	0.218	0.322*

DH: Days to heading, DM: Days to maturity, PH: Plant height, ET/m: Effective tillers per meter, SL: Spike length, G/S: Number of grains per spike, TGW: 1000-Grain weight, GY: Grain yield, rg: Genotypic correlation, *, ** Significant at 0.05 and 0.01 level, respectively; **Residual effect=0.259**

The distribution of forty two genotypes of barley into different diverse clusters and their genetic distances are depicted in Table 3. All the genotypes were classified into four distinct clusters (Fig. 1). The clustering pattern of genotypes recognized cluster I as largest one with 14 genotypes, followed by cluster III with eleven genotypes. Cluster II and IV possessed eight and nine genotypes, respectively. Kumar *et al.* [11] studied and classified 87 barley genotypes into different clusters based on 10 qualitative traits and also selected the promising genotypes for future barley breeding strategies. The estimates of intra-cluster distances showed highest genetic distance in cluster I (120.20) followed by clusters II with genetic distance of 61.57. The results also revealed that cluster I is the most

distantly placed from cluster III which is the maximum (154.12) among all cluster combinations, followed by clusters I and IV (152.32). However, cluster III is most closely placed to cluster IV which is minimum distance (55.25) among inter cluster distances. It is well known that higher the distance between clusters, more the genetic diversity would be between the genotypes. Therefore, highly diverse genotypes would produce better segregants in the following generations enabling further selection and trait improvement. Sarkar *et al.* [12], Ebrahim *et al.* [13], Hailu *et al.* [14] and Devi *et al.* [15] also reported the existence of adequate genetic diversity in their findings in barley crop.

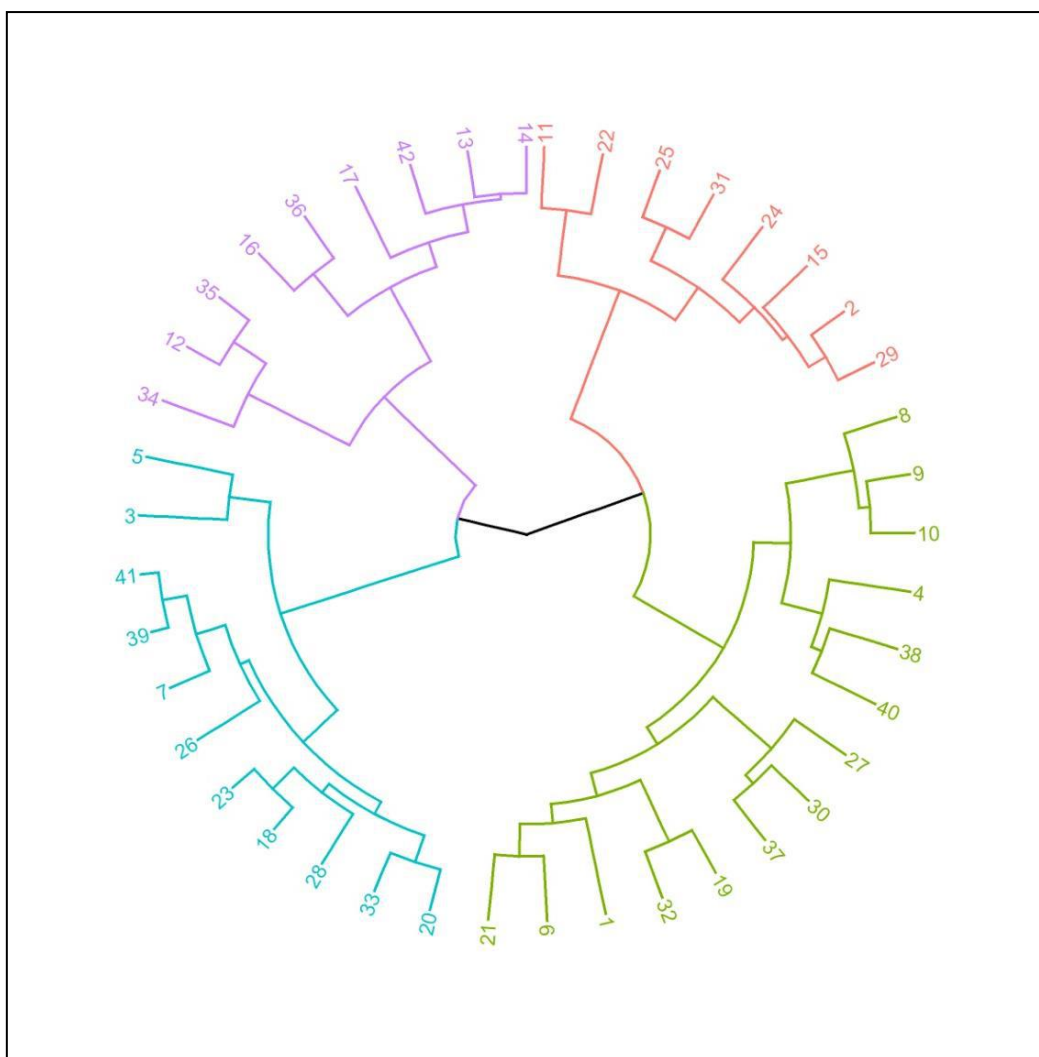


Fig. 1. Dendrogram showing the clustering pattern of 42 genotypes of barley

Table 3: Distribution of 42 genotypes into different clusters and their genetic distances

Genotypes	No. of Genotypes	Cluster Number	Genetic distances between clusters			
			1	2	3	4
BH 21-02 (1), BH 21-01 (4), DWRB 101 (6), BH 21-28 (8), BH 21-37 (9), BH 21-21 (10), BH 21-23 (19), DWRB 182 (21), BH 20-15 (27), BH 20-16 (30), BH 885 (32), DWRB 92 (37), BH 21-33 (38), BH 20-38 (40)	14	1	120.20	123.05	154.12	152.32
BH 21-09 (2), DWRB 160 (12), BH 21-05 (15), BH 20-13 (22), BH 20-09 (24), BH 20-10 (25), BH 20-02 (29), BH 20-11 (31)	8	2	123.05	61.57	97.48	95.49
BH 21-06 (3), BH 21-22 (5), BH 21-38 (7), BH 21-03 (18), BH 21-12 (20), BH 21-35 (23), BH 22-27 (26), BH 21-26 (28), BH 946 (33), BH 20-40 (39), BH 21-24 (41)	11	3	154.12	97.48	51.30	55.25
BH 21-07 (11), BH 21-31 (13), BH 21-10 (14), BH 393 (16), BH 21-36 (17), BH 22-28 (34), BH 22-29 (35), DWRB 137 (36), BH 21-11 (42)	9	4	152.32	95.49	55.25	50.60

Values in parenthesis indicates the serial number of genotypes

Almost all of the clusters exhibited substantial variation in mean performance for the characters under study (Table 4). Cluster I possessed genotypes with short plant height having highest effective tillers per meter. Cluster II was characterized by genotypes with long spikes and with high 1000-grain weight. Cluster III was found promising for the traits *viz.*, number of grains per spike and grain yield. Cluster VI illustrated with early maturing

genotypes. Most diverse and promising genotypes for specific traits selected from different clusters and are shown in Table 5. For improvement of a particular component trait, the promising donors thus identified which plunged in different clusters could be used in crossing programme to obtain high heterotic response and thus better segregants in subsequent generations for yield enhancement in barley. Several studies have also been conducted for assessment of genetic diversity in barley based on different morphological characters for selecting genetically diverse genotypes for hybridization [16, 17, 18].

Table 4: Average performance of clusters for different traits in barley

Traits	Clusters			
	1	2	3	4
Days to heading	85	88	88	82
Days to maturity	128	131	130	124
Plant height (cm)	99	101	111	101
Effective tillers per meter	156	117	96	90
Spike length (cm)	7.4	8.6	8.5	7.9
Number of grains per spike	26	25	65	64
1000-Grain weight (g)	47.9	57.6	44.9	39.8
Grain yield (q/ha)	43.6	49.2	50.3	39.8

Table 5: Trait specific promising barley genotypes in different clusters

Trait	Promising donors
Days to heading (≤ 80 Days)	BH 21-10, BH 393, BH 21-36, BH 885, DWRB 137, BH 21-11
Days to maturity (≤ 125 Days)	BH 21-31, BH 21-10, BH 393, BH 21-36, BH 885, DWRB 137, BH 21-11
Plant height (≤ 90 cm)	DWRB 182, BH 20-11, DWRB 137
Effective tillers per meter (>150)	BH 21-02, DWRB 101, BH 21-37, BH 21-21, BH 21-23, DWRB 182, BH 20-16, BH 20-11, BH 885, DWRB 92, BH 21-33
Spike length (>8.5 cm)	BH 21-22, DWRB 160, BH 21-09, BH 21-06, BH 21-10, BH 21-03, BH 21-35, BH 20-09, BH 20-10, BH 21-26, BH 20-11
Number of grains per spike	Six rowed: BH 21-06, BH 21-22, BH 22-29, BH 21-24, BH 21-11
Six rowed (≥ 70)	Two rowed: BH 21-09, BH 21-37, DWRB 160
Two rowed (≥ 27)	
1000 grain weight (>55.0 g)	DWRB 160, BH 21-05, BH 20-13, BH 20-09, BH 20-10, BH 20-16, BH 20-11, DWRB 92
Grain yield (>50 q/ha)	Six rowed: BH 21-06, BH 21-38, BH 21-03, BH 21-12, BH 21-35, BH 22-27, BH 21-24
	Two rowed: BH 21-09, BH 20-09, BH 20-10, BH 20-15, BH 20-16, BH 20-11, BH 21-33

IV. CONCLUSION

From this study, it can be concluded that the improvement in six rowed barley could be achieved through the use of genotypes assigned in clusters III, whereas the genotypes which contained in cluster II might be considered as potential parents for two rowed barley keeping days to maturity, spike length and 1000-grain weight traits as suitable selection criterion for the development of high yielding barley varieties under timely sown irrigated conditions.

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