

## Morphological Trait based Genetic Divergence and Correlation in Barley Genotypes for Drought Tolerance

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### ABSTRACT

An experiment was conducted to explore the genetic diversity for the selection and utilization of drought-tolerant barley genotypes in future breeding approaches for yield enhancement. The experimental material comprised thirty barley genotypes planted at the Barley Research Area, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar, under drought conditions during 2015-16 and 2016-17. All the genotypes were classified into four distinct clusters. Cluster IV occupied the maximum number of genotypes, i.e. 17, followed by cluster I with eight genotypes. Cluster II and III possessed three and two genotypes, respectively. The average inter-cluster distance was found to be highest between clusters II and III (261.7), followed by clusters III and IV (188.1), while the lowest inter-cluster distance was observed between clusters II and IV (73.8). Cluster I, comprised of eight genotypes, exhibited maximum germination per cent. Cluster II consisted of three genotypes, characterized by high initial vigour, early heading and minimum plant height. Two genotypes from cluster III exhibited minimum internode length, longest spike, and maximum number of tillers per meter and were also found promising for the traits viz., culm thickness, number of grains per spike, 1000-grain weight and grain yield per plot. Cluster IV, being the largest one, had 17 genotypes with the characteristic features of early maturity. Number of effective tillers per meter showed significant positive correlation with grain yield per plot. This trait could be used as a key component in the screening and selection of drought-tolerant genotypes. The improvement in barley could be achieved through the use of genotypes namely JB 481 and Lakhan assigned in clusters III. These genotypes might be considered as potential parents to obtain high heterotic response and accordingly better segregant for grain yield under drought condition.

**Key words:** Barley, Cluster analysis, Correlation, Drought, Genetic diversity.

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## INTRODUCTION

Barley (*Hordeum vulgare* L.) is one of the earliest domesticated cereal crops, currently ranking fourth in the world cereal production after rice, wheat and maize (USDA, 2023). This is truly a diploid ( $2n=14$ ) species that belongs to the genus *Hordeum* of *Poaceae* family in the tribe *Triticeae*. Barley is a nutrient-rich cereal and occupies an area of 0.62 million hectares, producing 1.69 million tonnes of grain with productivity of 27.33 q/ha at the national level. It was cultivated on 15,300 hectares with a production of 53,300 tons in Haryana state and ranked second in average productivity (34.86 q/ha) after Punjab (36.54 q/ha) during 2022-23 (ICAR-IIWBR, 2023). Barley cultivation requires less input in fertilizer, irrigation and insecticides, and it can grow well under harsh environments. Barley has gained importance owing to its increased use in health tonics, multigrain blends, malting and brewing industries (Kaur *et al.*, 2018). Barley offers many health benefits and has a huge potential to be a future staple cereal, substituting wheat and rice in the diet for diabetics and people suffering from high cholesterol. It has a low glycemic index as well as a low amount of anti-nutritional factors, *i.e.* phytate, along with high beta-glucan, which offers many health benefits.

Grain yield is affected by different environmental factors; one is being deficient soil moisture, influencing the plant growth and interaction of these factors with genotypes. The best strategy for yield improvement under drought conditions is to develop drought-tolerant crop varieties. Understanding plant responses to drought is important and a fundamental part of crop breeding tolerant to drought stress. Genetic diversity is an important mechanism of biological system stability and has always remained the key component of plant breeding (Khajavi *et al.*, 2014). The information about the existing genetic diversity in available germplasm, its proper management and utilization is a prerequisite and key factor for selecting parents with diverse genetic backgrounds and making crop improvement more efficient.

Information on the nature and degree of divergence among the genotypes facilitates the plant breeders in isolation of trait-specific superior donors for commencing targeted hybridization programme, as the heterotic expression is believed to be associated with genetic divergence among the genotypes used as parents. Therefore, systematic evaluation of germplasm must be included into plant breeding programmes to diversify the parental material. Morphological traits have remained the means of studying genetic variations for a long time in plant breeding populations. The International Plant Genetic Resources Institute (now known as Bioversity International), as well as the International Union for the Protection of New Varieties of Plants, also recommended morphological characterization as a criterion to identify accessions for the assessment of genetic diversity (Kaur *et al.*, 2018). Some findings on the genetic diversity of barley have focused on the significance of morphological and quantitative traits (Mekonnen *et al.*, 2014; & Yadav *et al.*, 2015b). Several approaches are available to examine genetic diversity in the breeding material. Often, cluster analysis has been widely used in large germplasm lines to identify the key characters to be used in a fresh breeding programme for meaningful achievement.

Therefore, the present study was designed and conducted with 30 barley genotypes to assess genetic diversity and identify key traits that may contribute as probable donors for their future exploitation in developing drought-tolerant barley varieties.

## MATERIALS AND METHODS

A field experiment with 30 genotypes of barley (Table 1) was carried out at the Barley Research Area of the Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar, which is situated in the semi-arid subtropics at 29°10' N latitude and 75°46' E longitude with an altitude of 215.2 m AMSL. The experimental location is predominantly having sandy loam type of soil. The experimental material was planted in three

replications using randomized block design (RBD). Each genotype was sown in four rows of 2.5 m length by maintaining 23 cm spacing between rows. The experiment was conducted for two successive cropping seasons *i.e.*, *rabi* 2015-16 and 2016-17. The recommended package of practices (cultural and agronomic) was followed to raise the crop. A total of 12 morphological traits *viz.*, Germination (%), initial vigour, days to heading, days to maturity, plant height (cm), culm thickness (mm), internode length (cm), number of effective tillers per meter, spike length (cm), number of grains per spike, 1000 grain weight (g) and grain yield per plot (g) were recorded at appropriate stages of the crop growth. Culm thickness and internode length were measured on the 2<sup>nd</sup> basal internode with the help of vernier caliper and measuring scale, respectively. The five plants were randomly selected for recording observations of each genotype, except for days to heading and maturity, germination (%), initial vigour and grain yield, which were recorded at plot level.

All the recorded data was pooled over two years (2015-16 and 2016-17) and was subjected to cluster and correlation analysis using statistical software SPSS (SPSS Statistics v. 20.0).

## RESULTS AND DISCUSSION

The distribution of thirty genotypes of barley into different diverse clusters is depicted in Table 1. All the genotypes were classified into four distinct clusters. The clustering pattern of genotypes recognized cluster IV as largest one with 17 genotypes, followed by cluster I with eight genotypes. Cluster II and III possessed three and two genotypes, respectively. Kumar et al. (2020) studied and classified 87 barley genotypes into different clusters based on 10 qualitative traits and also selected the promising genotypes for future barley breeding program. The genetic distances between different clusters are presented in Table 2. The results also revealed that cluster II is the most distantly placed from cluster III which is the maximum (261.66) among all cluster combinations, followed by clusters III

and IV (188.09). However, cluster II is most closely placed to cluster IV which is minimum distance (73.81) among inter cluster distances. It is well documented that the higher the distance between clusters, the greater the genetic diversity between the genotypes. Therefore, highly diverse genotypes would produce segregants in successive generations, enabling further selection and trait improvement. Ebrahim et al. (2015), Sarkar et al. (2014) and Hailu et al. (2016) also reported the existence of enough genetic diversity in their findings in barley crops.

Almost all clusters exhibited substantial differences in mean performance for the characters under study (Table 3). Cluster I exhibited the maximum percentage of germination among all the clusters. Cluster II was characterized by early heading and short plant height stature; and also illustrated high initial vigour. Cluster III was found promising for the traits *viz.*, culm thickness, initial vigour, internode length, number of effective tillers per plant, spike length, number of grains per spike, 1000-grain weight and grain yield per plot. Cluster VI illustrated with early maturing genotypes. Several studies have been conducted for the assessment of genetic diversity in barley based on different quantitative characteristics for selecting genetically diverse genotypes for hybridization (Sharma et al., 2014; & Dyulgerova et al., 2016).

The estimates of correlation coefficients among different characters are depicted in Table 4. Number of effective tillers per meter showed significant positive correlation with grain yield. The same result corroborates with the findings of Devi et al. (2019) in barley. Pal et al. (2010) conducted an experiment with 158 barley genotypes and also reported positive association of grain yield with tillers per plant. The significant positive association was also recorded for days to heading with days to maturity; plant height with spike length and 1000-grain weight; culm thickness with spike length and 1000-grain weight, indicating that these traits may be improved simultaneously. Some authors also

reported a significant positive correlation for days to heading with maturity (Yadav et al., 2015a), plant height with 1000-grain weight and spike length (Kumar et al., 2018). Significant negative correlation was observed in germination percent with initial vigour; and

internode length with spike length. The present correlation study revealed that the number of effective tillers might be considered key while selecting promising genotypes for drought tolerance.

**Table 1: Distribution of 30 genotypes into different clusters**

Genotypes	No. of Genotypes	Cluster Number
JB 484, JB 485, KB 1317, KB 1401, 2 <sup>nd</sup> GSBSN 28, 2 <sup>nd</sup> GSBYT 02, AZAD, K 560	8	1
PL 890, NDB 2, KB 1302	3	2
JB 481, LAKHAN	2	3
PL 751, NDB 1, NDB 3, BL 1122, BL 1163, JB 482, JB 483, KB 1055, KB 1326, 2 <sup>nd</sup> GSBSN 60, 2 <sup>nd</sup> GSBSN 66, 2 <sup>nd</sup> GSBSN 93, 2 <sup>nd</sup> GSBSN 94, 2 <sup>nd</sup> GSBYT 23, RD 2660, RD 2624, K 603	17	4

**Table 2: Genetic distances between clusters**

Clusters	1	2	3	4
1	-	169.50	92.55	95.94
2	169.50	-	261.66	73.808
3	92.55	261.66	-	188.09
4	95.94	73.81	188.09	-

**Table 3: Cluster performance for different traits in barley**

Traits	Clusters			
	1	2	3	4
Germination (%)	<b>81.0</b>	75.9	77.5	78.0
Initial Vigour	2.33	<b>2.83</b>	<b>2.83</b>	2.81
Days to heading	86	<b>85</b>	88	86
Days to maturity	129	129	134	<b>128</b>
Plant height (cm)	73	<b>69</b>	76	71
Culm thickness (mm)	1.56	1.48	<b>1.65</b>	1.57
Internode length (cm)	11.2	11.0	<b>10.2</b>	10.7
Number of effective tillers per meter	85	73	<b>91</b>	82
Spike length (cm)	6.7	6.6	<b>6.9</b>	6.6
Number of grains per spike	54.8	55.1	<b>61.9</b>	56.5
1000- grain weight (g)	44.8	44.3	<b>45.2</b>	43.3
Grain yield per plot (g)	702	533	<b>794</b>	606

**Table 4: Estimates of Pearson correlation coefficients (above diagonal) and p values (bellow diagonal) among different traits in barley**

Traits	GP	IV	DH	DM	PH	CT	IL	ETM	SL	GPS	TGW	GYP
GP	<b>1.00</b>	<b>-0.675**</b>	0.213	0.210	0.321	0.111	-0.144	0.186	0.181	-0.179	0.324	0.318
IV	<b>0.000</b>	<b>1.00</b>	-0.199	-0.294	-0.278	-0.176	0.034	-0.266	-0.165	-0.017	-0.121	-0.269
DH	0.259	0.293	<b>1.00</b>	<b>0.620**</b>	0.176	-0.051	-0.141	0.126	0.057	-0.015	-0.078	0.239
DM	0.266	0.115	0.000	<b>1.00</b>	0.014	0.111	-0.212	0.207	0.150	-0.135	0.167	0.305
PH	0.084	0.137	0.351	0.941	<b>1.00</b>	0.143	0.233	0.270	<b>0.440*</b>	0.193	<b>0.369*</b>	0.327
CT	0.560	0.351	0.790	0.559	0.449	<b>1.00</b>	-0.182	-0.049	<b>0.463*</b>	-0.055	<b>0.400*</b>	0.101
IL	0.448	0.858	0.457	0.261	0.216	0.336	<b>1.00</b>	-0.066	<b>-0.410*</b>	-0.143	0.050	-0.044
ETM	0.326	0.156	0.508	0.273	0.150	0.796	0.730	<b>1.00</b>	0.054	-0.009	-0.125	<b>0.434*</b>
SL	0.338	0.385	0.765	0.430	0.015	0.010	0.024	0.778	<b>1.00</b>	0.282	0.294	0.165
GPS	0.344	0.927	0.936	0.478	0.306	0.772	0.450	0.961	0.131	<b>1.00</b>	-0.131	0.108
TGW	0.081	0.525	0.683	0.378	0.045	0.029	0.794	0.511	0.114	0.489	<b>1.00</b>	0.197
GYP	0.087	0.151	0.204	0.102	0.077	0.596	0.819	0.017	0.383	0.570	0.296	<b>1.00</b>

\*, \*\* Significant at 5 and 1 per cent, respectively; GP: Germination (%); IV: Initial vigour; DH: Days to heading; DM: Days to maturity; PH: Plant height; CT: Culm thickness; IL: Internode length; ETM: Number of effective tillers per meter; SL: Spike length; GPS: Number of grains per spike; TGW: 1000-grain weight; GYP: Grain yield per plot

## CONCLUSION

The current study concludes that a number of effective tillers might be considered a key component while selecting promising genotypes for drought tolerance, and the genotypes contained in cluster III might be considered desirable for the selection and isolation of genotypes which may be used as promising parents for hybridization aimed to developed drought tolerant barley varieties.

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### Conflict of Interest:

The authors declare no conflict of interest.

### Author Contributions

YK: Execution of field experiment, data recording and compilation, manuscript finalization, DP & HC: Manuscript writing, S & A: Statistical analysis.

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