

Principal Component and Factor Analysis in Advance Barley Genotypes under Drought Condition

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ABSTRACT: The present study aimed to determine the genetic variability among barley (*Hordeum vulgare* L.) genotypes for 12 yield and its attributes using principal component method. The experimental material consisted of thirty barley genotypes grown under drought condition at Barley Research Area, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar during 2015-16 and 2016-17. The experiment was laid in randomized block design with three replications with a plot size of 2.3 m². Estimates of coefficients of variation (CV) were observed highest for initial vigour followed by number of grains per spike whereas days to heading and maturity exhibited the lowest coefficients of variation. First five principal components had eigen values more than one and altogether explained 73.05 % of the total variation in 12 traits which were mainly associated with 1000-grain weight, culm thickness and spike length; germination percent and initial vigour; days to heading and maturity, number of effective tillers per meter and grain yield; number of grains per spike; and internode length and plant height. The remaining principal components could not be considered of much useful for barley improvement because of very small contribution towards total variation. Among the material evaluated under drought, the genotypes viz., JB 481, Lakhan, 2nd GSBSN 28 and Azad were found to have high yield potential. The results of the current investigation exhibits evidence of having variability in studied barley genotypes and thus confirm the adequacy of the principal component method in genetic studies.

Keywords: Barley, drought, factor analysis, principal components, variation.

INTRODUCTION

Barley (*Hordeum vulgare* L.) is an annual cereal crop belongs to the *Poaceae* family. It has persisted as a major cereal crop during many centuries and in term of world cereal production; it is fourth important cereal crop after wheat, rice and maize. In India, barley occupied an area of 0.62 million hectare with production and national productivity of 1.69 million tonnes and 27.33 q/ha, respectively during the crop season 2022-23 (ICAR-IIWBR, 2023). Barley was cultivated on 15,300 hectares with a production level of 53,300 tons in Haryana which ranks second in average productivity (34.86 q/ha) after Punjab (36.54q/ha). It commonly used for making breads, soups, stews, and health products, though it is primarily grown as animal fodder and as a source of malt for alcoholic beverages, especially beer. Because of its hardiness, in many countries, it is considered the only possible rainfed cereal crop under low input and stressful environment. Drought is one of the most distressing abiotic stress globally that severely restrict normal plant growth and development thereby affecting final crop yield. Drought tolerance is perhaps the most complex genetic mechanism in crop plants to understand due to lack of adequate information (Ashraf, 2010). Further, drought

stress tolerance is also obstructed by low heritability and deficiency of successful selection approaches. Therefore, selection of barley genotypes should be adapted to drought stress. Besides drought tolerance, mechanism should be identified during the development of new genotypes to increase the yield potential. The best approach for crop productivity, yield improvement and stability under drought conditions is to develop drought tolerant crop varieties (Cattivelli *et al.*, 2008). The information about plant responses to drought are of great significance and also an essential part of crops breeding tolerant to drought stress. The reaction of plants to drought pressure depends on many factors viz., developmental stage, severity and duration of importance, and genotype. Therefore, sufficient genetic information concerning the genotypic variance and the magnitude of gene gain and heritability of yield characters under drought is essential in developing drought tolerant varieties. Numerous approaches are available to examine the genetic diversity. Principal component analysis (PCA) helps in recognizing the most relevant traits and represents them in more visualized dimensions through linear combinations of variables that accounts for most of the variation available in original set of variables. Hence, it is vital to know the mechanisms of drought tolerance in order to

obtain promising genotypes with enhanced response to this abiotic stress. The current study was aimed at the evaluation and screening of barley genotypes under drought condition intended to develop drought tolerant varieties.

MATERIALS AND METHODS

Present investigation was carried out at the Barley Research Area of the Department of Genetics & Plant Breeding, CCS Haryana Agricultural University, Hisar 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. The experimental trial was conducted during *rabi* 2015-16 and 2016-17 under drought condition. A set of 30 advanced barley genotypes (Table 1) were used in the current study. The experimental material was planted in randomized block design (RBD) with three replications in 4 rows of 2.5 m length for each genotype, with spacing of 23 cm between rows. The observations on days to heading, days to maturity, plant height (cm), germination (%), initial vigour, 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. The recommended package of practices was applied to raise the crop. For data recording five randomly selected competitive plants in each replication were taken for all the traits under study except of days to heading and maturity, germination, initial vigour and grain yield which were recorded on plot basis.

All the recorded quantitative data pooled over two years (2015-16 and 2016-17) and was subjected to statistical analysis using statistical software SPSS (SPSS Statistics v. 20.0). The principal component analysis (PCA) was work out to reduce the number of variables into a few correlated components that can explain much of the variability of original set. It was carry out using the correlation matrix to define the pattern of variation in the experimental material based on the mean of metric traits and to identify traits that load the most in explaining the observed variability. In order to keep the number of principal components, Kaiser's (1958) suggestion to drop those components of correlation matrix with eigen roots less than one, was followed. Principal factor analysis was carried out using principal component method that does not require assumption of multivariate normal distribution of population (Jaiswal, 2000). The varimax method of orthogonal rotation was used to rotate the factor axes (Kaiser, 1958) which is the best method of which corresponded to spreading out of the squares of loading on each factor as much as possible. It made possible to obtain groups of large and negligible coefficients in different columns of the rotated factor loading.

RESULTS AND DISCUSSION

The estimates of genetic variability are provided in Table 2. In general, the results under investigation reflected a wide range of variability for all the variables. Estimates of coefficients of variation (CV)

were observed highest for initial vigour followed by number of grains per spike, number of effective tillers per plant, culm thickness and grain yield whereas days to heading as well maturity exhibited the low magnitude of coefficients of variation. Rest of the variables revealed moderate coefficient of variation, signifying hereby that selection based on these traits would support successful isolation of better plant types. Similar results for one or more traits have also been delineated by Kumar *et al.* (2018); Singh *et al.* (2015); Yadav *et al.* (2015).

Principal component analysis helps in recognizing most relevant traits and presents them in more interpretable and more visualized dimensions through linear combination of variables that account for most of the variation there in the original set of variables. This technique has been widely used in the studies relates to plant sciences for reduction of variables and grouping of genotypes. In the present study, principal components with eigen values more than one were selected for interpretation of results (Kaiser, 1958). The principal component analysis based on genetic distances of 12 studied morphological traits for 30 advance barley genotypes is depicted in Fig. 1. The results revealed hereby that first five principal components had eigen values more than one and altogether elucidate 73.05 % of cumulative variability (Table 3). Rest of the principal components accounted for a small amount of the total variation. This specifies that these components are not of much practical value to the barley improvement. The first principal component explained 25.842 % of the total variation. The second, third and fourth principal components exhibited 14.873, 12.237 and 11.630 % variation, respectively. The fifth principal component accounted for 8.465% of the total variability. The relative involvement of various characters to the total variability has also been described by Dyulgerova *et al.* (2016) in barley. Mekonnon *et al.* (2014) also reported the existence of high genetic variability among barley genotypes based on principal component analyses for various breeding approaches.

All the 12 variables showed high loading on different principal factors and none of them was left after rotation of the principal factor axes (Table 4). Moreover, it grouped the similar type of variables by loading them together on a common principal factor. The first principal factor was associated with 1000-grain weight, culm thickness and spike length. Germination (%) and initial vigour showed relation with second factor. The association of third principal factor was very high with days to heading and maturity, number of effective tillers per meter and grain yield per plot. Number of grains per spike was correlated with fourth factor. However, internode length and plant height exhibited high loading on fifth factor.

The clear cut grouping of similar types of variables by getting loaded on common principal factor elaborates the successful transformation of 12 interrelated variables into five independent factors explaining 73.05 % of the variability of the original set. Ebrahim *et al.* (2015) also studied 20 barley varieties for 10 traits and reported 84.22 % contribution of the total variation by

first three principal components having eigen value more than unity. In the findings of Abebe *et al.* (2010), the first three principal components with eigen values greater than one, explained about 73 % of the total variation among barley accessions for nine quantitative traits. Principal component analysis revealed 83.40 % contribution of the total variation in barley by five principal components having eigen values greater than one (Zaheer *et al.*, 2008).

Principal factor scores were estimated for all the genotypes using Anderson-Rubin method and were used to find out genotypes promising for different factors, *i.e.* for all characters cumulatively ascribed to that factor. A high value of score of a particular genotype in a particular factor indicates high value for those variables in that genotype, which that factor is representing. Thus, the genotypes LAKHAN, KB 1326, JB 485, 2nd GSBSN 28 and KB 1317 which were having high score in PF 1 denote that they are having high 1000-grain weight, culm thickness and spike length. Similarly, genotypes 2nd GSBSN 60, 2nd GSBYT 23, AZAD and 2nd GSBYT 02 had high score in PF 2, therefore, exhibited high initial vigour and germination percent. The correlation of early maturing genotypes *viz.*, RD 2624, 2nd GSBSN 94, RD 2660, LAKHAN and JB 483 with PF 3, suggest that early heading and maturing genotypes with higher number of tillers per plant may result in higher grain yield. In addition, genotypes JB 485, NDB 3, JB 481 and PL 751 had high score in PF 4, therefore, have number of

grains per spike. Likewise, genotypes 2nd GSBSN 60 and KB 1302 for PF 5 were found to have high score, hence, performed good for the characters to which the factor associated. Study has also been conducted on barley for various quantitative traits based on principal component and factor analyses by Khajavi *et al.* (2014). The results of the current study can be used as a stepping stone for developing well defined approach based on evaluation and characterization of genetic variation in barley and can be used in breeding programme aimed to develop drought tolerant genotypes.

Table 1: List of barley genotypes used in the study.

Sr. No.	Genotypes	Sr. No.	Genotypes
1.	PL 751	16	KB 1302
2.	PL 890	17	KB 1401
3.	NDB 1	18	2 nd GSBSN 28
4.	NDB 2	19	2 nd GSBSN 60
5.	NDB 3	20	2 nd GSBSN 66
6.	BL 1122	21	2 nd GSBSN 93
7.	BL 1163	22	2 nd GSBSN 94
8.	JB 481	23	2 nd GSBYT 02
9.	JB 482	24	2 nd GSBYT 23
10.	JB 483	25	AZAD
11.	JB 484	26	RD 2660
12.	JB 485	27	RD 2624
13.	KB 1055	28	K 560
14.	KB 1326	29	K 603
15.	KB 1317	30	LAKHAN

Table 2: Descriptive statistics in barley.

Traits	Mean± S.E. (m)	Range	Minimum	Maximum	SD	CV (%)
Germination (%)	78.53±0.86	18.2	70.8	89.0	4.72	6.01
Initial Vigour	2.69±0.12	2.66	1.17	3.83	0.68	25.15
Days to heading	85.90±0.47	12	81	93	2.55	2.97
Days to maturity	129.07±0.61	13	121	134	3.35	2.60
Plant height (cm)	71.83±0.89	20	62	82	4.86	6.77
Culm thickness (mm)	1.57±0.03	0.75	1.30	2.05	0.18	11.42
Internode length (cm)	10.83±0.15	3.0	9.0	12.0	0.82	7.55
Number of effective tillers per meter	82.70±1.77	36	64	100	9.72	11.75
Spike length (cm)	6.68±0.07	1.6	6.0	7.6	0.41	6.13
Number of grains per spike	56.24±1.38	47.6	25.7	73.3	7.58	13.48
1000 grain weight (g)	43.94±0.50	14.9	35.8	50.7	2.75	6.26
Grain yield per plot (g)	636.57±12.78	286	520	806	70.02	11.00

SD: Standard Deviation; CV: Coefficient of variation

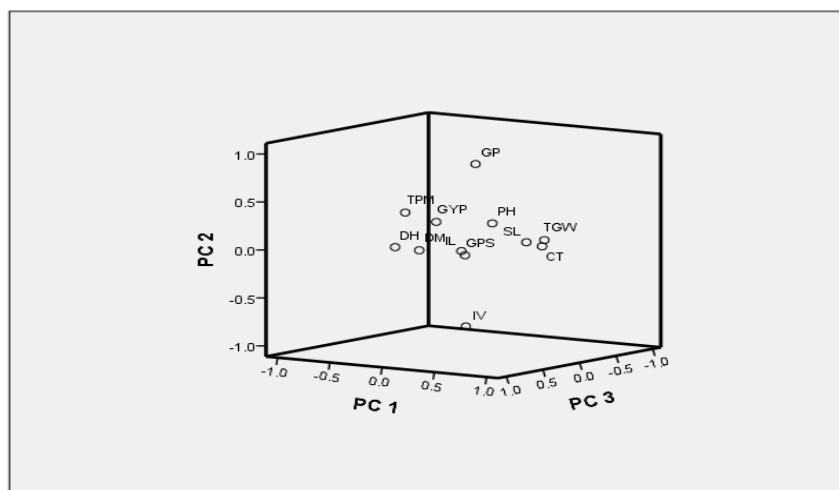
Table 3: Principal component analysis of studied phenotypic traits.

Principal Components	Eigen values	Per cent variability	Cumulative % variability
1	3.10	25.84	25.84
2	1.78	14.87	40.72
3	1.47	12.24	52.95
4	1.40	11.63	64.58
5	1.02	8.46	73.05
6	0.89	7.40	80.44
7	0.65	5.43	85.87
8	0.60	4.99	90.87
9	0.43	3.58	94.44
10	0.35	2.91	97.35
11	0.17	1.42	98.77
12	0.15	1.23	100.00

Table 4: Factor loadings of different traits with respect to different PCs in barley.

Traits	PC 1	PC 2	PC 3	PC 4	PC 5
Germination (%)	0.200	0.885	0.120	-0.091	-0.007
Initial Vigour	-0.065	-0.870	-0.126	-0.041	0.043
Days to heading	-0.068	0.095	0.837	0.005	-0.043
Days to maturity	0.173	0.088	0.850	-0.171	-0.187
Plant height (cm)	0.381	0.289	0.149	0.512	0.544
Culm thickness (mm)	0.760	0.067	0.009	0.007	-0.179
Internode length (cm)	-0.133	-0.096	-0.162	-0.186	0.861
Number of effective tillers per meter	-0.284	0.369	0.389	0.350	0.150
Spike length (cm)	0.644	0.105	0.059	0.541	-0.283
Number of grains per spike	-0.072	-0.129	-0.125	0.820	-0.144
1000 grain weight (g)	0.797	0.140	0.032	-0.115	0.294
Grain yield per plot (g)	0.082	0.322	0.488	0.367	0.248

PC: Principal Component



GP: Germination (%); IV: Initial vigour; DH: Days to heading; DM: Days to maturity; PH: Plant height; CT: Culm thickness; IL: Internode length; TPM: Number of effective tillers per meter; SL: Spike length; GPS: Number of grains per spike; TGW: 1000-grain weight; GYP: Grain yield per plot

Fig. 1. Principal component analysis based on genetic distance measured for 30 barley genotypes using 12 morphological traits.

CONCLUSIONS

Among the experimental material evaluated under drought, the genotypes namely JB 481, Lakhan, 2nd GSBSN 28 and Azad exhibited high yield potential, thus can be used breeding programme aimed to develop drought tolerant genotypes. Further, the results of the current investigation revealed evidence of having variability in studied barley genotypes and thus confirm the adequacy of the principal component method in genetic studies.

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Conflict of Interest. None.

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