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PRINCIPAL COMPONENT AND FACTOR ANALYSIS IN SIX ROWED BARLEY (*HORDEUM VULGARE* L.) GENOTYPES

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SUMMARY

Efforts were made to study the pattern of diversity in 40 genotypes of six rowed barley (*Hordeum vulgare* L.) using the principal component method of factor analysis. First five principal components had eigen values more than one and have explained altogether 81.37 % of the total variation in 10 metric traits which were mainly associated with plant height, 1000-grain weight and biological yield; days to heading and maturity; harvest index and grain yield; spike length and number of grains per spike; and number of tillers per meter row. The remaining principal components made very little contribution towards total variation and thus could not be considered of much practical value to barley improvement. The genotypes BH 946, BH 15-02, BH 16-40, BH 16-44, BH 10-11, BH 15-06 and BH 15-07 were found to have high yield potential. The results of the present study provide evidence of diversity in barley and thus prove the adequacy of the principal component method in biological investigations.

Key words : Principal component analysis, factor analysis, barley, genotypes, variation

Barley (*Hordeum vulgare* L.) is primarily a cereal grain which belongs to the genus *Hordeum* in the Tribe *Triticeace* of grass family *Poaceae* which contains about 32 species, all with a basic chromosome number of x = 7. It is the fourth most important cereal crop after rice, wheat and maize. In India, the area under barley is around 0.69 million hectares with the production and productivity of 1.78 million tons and 2580 kg/ha, respectively. Haryana state achieved a productivity level of 3475 kg/ha on 40,000 hectares (Anonymous, 2017). It is grown for many purposes, but the majority of all barley is used for animal feed, human consumption, or malting. High protein barleys are generally valued for food and feeding, and starchy barley for malting. Barley is rather well-tolerant to drought, salinity and other dehydrative stresses (Kumar *et al.*, 2013).

Owing to lack of knowledge regarding relative importance and usefulness of variables, the investigator tried to include all possible variables which made the data matrix perceivably large, complicated, unmanageable and beyond comprehension. Therefore, the investigator required a technique for systematic reduction and summarization of data. Principal component analysis offers solution to this complex problem by transforming the original set of variables into a smaller set of linear combinations that account for most of the variability of the original set. It is basically a data reduction technique, where the total variation contained in a set of variables is considered. Factor analysis, also a data reduction technique, where no distributional assumption is required and interest centre on that part of variance which is shared by the common factors (Godshalk and Timothy, 1988). In view of the immense importance of principal component and factor analysis in plant breeding, these techniques were applied to 40 genotypes of six rowed barley.

MATERIALS AND METHODS

The experimental material consisted of 40 diverse genotypes of six rowed barley (Table 1), evaluated in randomized block design with three replications at Barley Research Area of the Department of Genetics & Plant Breeding, CCS Haryana Agricultural University, Hisar during *rabi* 2016-17. Each genotype was grown in six rows with a plot size of 5 x 1.38 m^2. Recommended package of practices

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TABLE 1
List of six rowed barley genotypes used in the study

S. No.	Genotypes	S. No.	Genotypes
1.	BH 10-11	21.	BH 393
2.	BH 12-46	22.	BH 16-06
3.	BH 13-22	23.	BH 16-07
4.	BH 14-01	24.	BH 16-10
5.	BH 14-13	25.	BH 16-11
6.	BH 14-42	26.	BH 16-13
7.	BH 15-02	27.	BH 16-17
8	BH 15-07	28.	BH 16-18
9.	BH 15-30	29.	BH 16-20
10.	BH 7-34	30.	BH 16-29
11.	BH 7-35	31.	BH 16-30
12.	BH 14-44	32.	BH 16-33
13.	BH 15-06	33.	BH 16-37
14.	BH 15-16	34.	BH 16-38
15.	BH 15-25	35.	BH 16-40
16.	BH 15-37	36.	BH 16-41
17.	BH 15-39	37.	BH 16-42
18.	BH 10-03	38.	BH 16-43
19.	BH 902	39.	BH 16-44
20.	BH 946	40.	BH 16-45

were followed to raise the good crop. The observations were recorded for 10 metric traits *viz*., days to heading, days to maturity, plant height (cm), spike length (cm), number of tillers per meter row, number of grains per spike, 1000-grain weight (g), harvest index (%), biological yield (kg/plot) and grain yield (kg/plot). Five randomly selected competitive plants in each replication were recorded for all the traits under study except of days to heading and maturity, biological yield and grain yield which were recorded on plot basis. Further, the value of harvest index was calculated as per the formula given by Donald and Humblin (1976).

In the present investigation, correlation matrix was used to extract the principal components by using SPSS Statistics 17.0. The number of principal components to be retained, Kaiser's (1958) suggestion of dropping those principal components of correlation matrix with eigen roots less than one was followed. Principal factor analysis was carried out using principal component method, which does not require assumption of multivariate normal distribution of population (Jaiswal, 2000). As the initial factor loading was not clearly interpretable, the factor axes were rotated using varimax method of orthogonal rotation (Kaiser, 1958) which is the most popular 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

Principal component analysis helps in identifying most relevant characters and presents them in more interpretable and more visualized dimensions through linear combination of variables that account for most of the variation present in original set of variables. In the present study, principal components with eigen values greater than one were selected for interpretation (Kaiser, 1958). The first five principal components had eigen values more than one and all together explained 81.37 % of cumulative variability (Table 2). Each of the remaining principal components accounted for a little amount of the total variation. This indicated that these components are not of much practical value to the barley improvement. However, for more detailed study of the data, these components may provide good information. The first principal component explained 22.91 % of the total variation. The second, third, fourth and fifth principal components exhibited 20.77, 13.76, 12.20 and 11.73 % variation, respectively. The relative contribution of various traits to the total variability has also been reported by Zakova and Benkova (2006); Manjunatha *et al.* (2007) and Dyulgerova *et al*. (2016) in barley. Mekonnon *et al.* (2014) also showed the presence of high genetic divergence among barley genotypes based on principal component analyses for breeding strategies.

TABLE 2
Total variance explained by different principal components

Principal Components	Eigen values	Per cent variability	Cumulative % variability
1	2.291	22.907	22.907
2	2.077	20.771	43.679
3	1.376	13.760	57.438
4	1.220	12.204	69.642
5	1.173	11.726	81.368
6	0.661	6.614	87.983
7	0.596	5.962	93.945
8	0.392	3.920	97.865
9	0.208	2.078	99.942
10	0.006	0.058	100.000

Initially, the principal factor analysis was carried out without any rotation (Table 3) which revealed that three variables, *viz*., 1000-grain weight, grain and biological yield had high loading on first factor, while days to heading and maturity were found to have high loading on second factor. Similarly, number of grains per spike on third; and number of tillers per meter row on fourth have high loading. None

of the variables was found to be highly loaded on fifth factor. Factor loading of different variables indicated that three out of 10 variables were left without high loading on any of the principal factors. The failure of principal factor analysis without rotation to draw sensible conclusions incited to go for analysis with rotation. All the 10 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 plant height, 1000-grain weight and biological yield. Days to heading and maturity showed relation with second factor. The association of third principal factor was very high with harvest index and grain yield. Spike length and number of grains per spike were correlated with fourth factor. However, number of tillers per meter row 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 10 interrelated variables into five independent factors explaining 81.37 % of the variability of the original set. Ebrahim *et al*. (2015) also studied genetic diversity among 20 barley varieties for 10 traits and reported 84.22 % contribution of the total variation by first three principal components having eigen value greater than one. In the findings of Abebe *et al*. (2010), the first three principal components (PCs), with eigen values greater than unity, explained about 73 % of the total variation among barley accessions for the nine quantitative traits. According to the work of Zaheer *et al*. (2008), the variation studied through principal component analysis revealed that five principal components having eigen values greater than unity

TABLE 3
Factor loading of different characters with respect to different principal factors (unrotated)

Characters/ Principal factors	PF 1	PF 2	PF 3	PF 4	PF 5
1000-grain weight (g)	0.779*	0.087	-0.091	-0.102	0.127
Grain yield (Kg/plot)	0.667*	-0.472	0.238	0.409	0.151
Biological yield (kg/plot)	0.636*	0.208	0.533	0.033	-0.398
Plant height (cm)	0.576	0.567	0.082	-0.142	0.359
Days to maturity	0.269	0.723*	-0.347	0.251	0.202
Days to heading	-0.346	0.613*	-0.311	0.471	-0.007
No. of grains per spike	-0.462	0.085	0.633*	-0.075	0.309
Spike length (cm)	-0.296	0.305	0.540	0.227	0.480
No. of tillers per meter row	-0.059	0.034	0.210	0.717*	-0.458
Harvest index (%)	0.092	-0.694	-0.257	0.407	0.519
Explained variability	2.291	2.077	1.376	1.220	1.173
Proportion of total (%)	22.907	20.771	13.760	12.204	11.726

PF: Principal Factor.

TABLE 4
Factor loading of different characters with respect to different principal factors (Varimax rotation)

Characters/ Principal factors	PF 1	PF 2	PF 3	PF 4	PF 5
Plant height (cm)	0.839*	0.222	-0.107	0.134	-0.163
1000-grain weight (g)	0.733*	-0.074	0.143	-0.291	-0.040
Biological yield (kg/plot)	0.612*	-0.303	-0.294	-0.019	0.581
Days to heading	-0.167	0.860*	-0.137	0.086	0.144
Days to maturity	0.478	0.763*	-0.068	-0.066	-0.031
Harvest index (%)	-0.147	-0.069	0.974*	-0.060	-0.107
Grain yield (Kg/plot)	0.424	-0.341	0.667*	-0.067	0.410
Spike length (cm)	0.055	0.185	0.042	0.844*	0.052
No. of grains per spike	-0.168	-0.151	-0.130	0.807*	-0.052
No. of tillers per meter row	-0.201	0.196	0.046	0.016	0.832*
Explained variability	2.143	1.684	1.557	1.488	1.265
Proportion of total (%)	21.434	16.841	15.567	14.877	12.649

PF : Principal Factor.

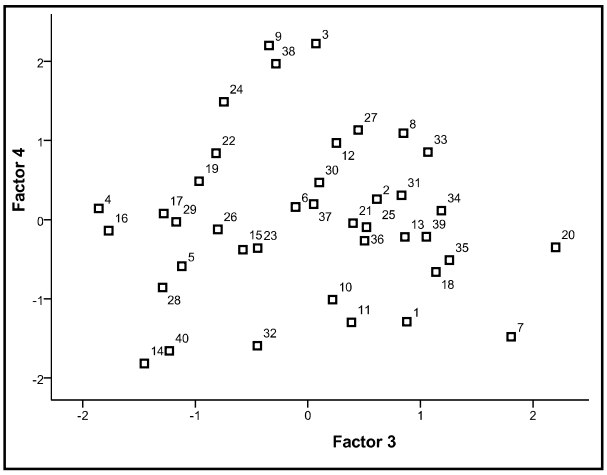

Fig. 1. Location of genotypes based on PF Score w. r. t. factors 3 & 4

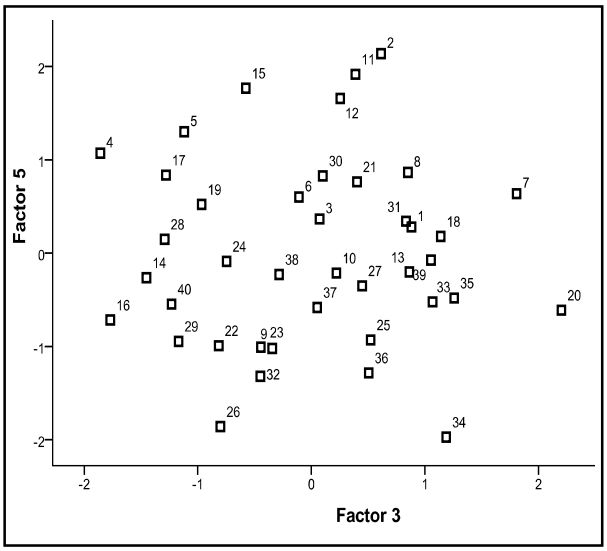

Fig. 2. Location of genotypes based on PF Score w. r. t. factors 3 & 5

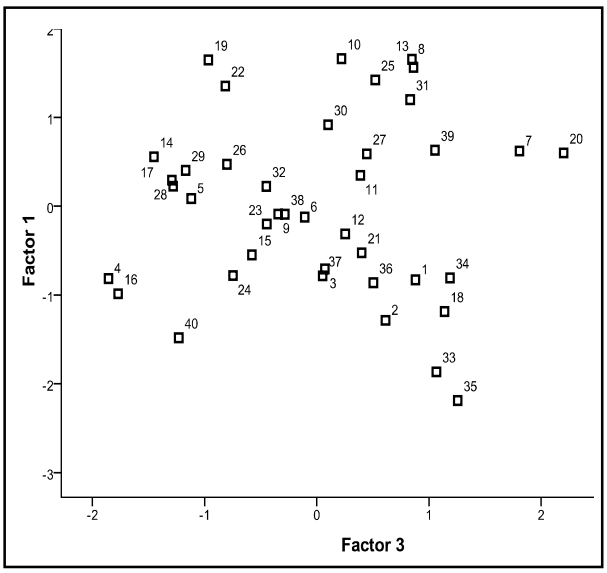

Fig. 3. Location of genotypes based on PF Score w. r. t. factors 3 & 1

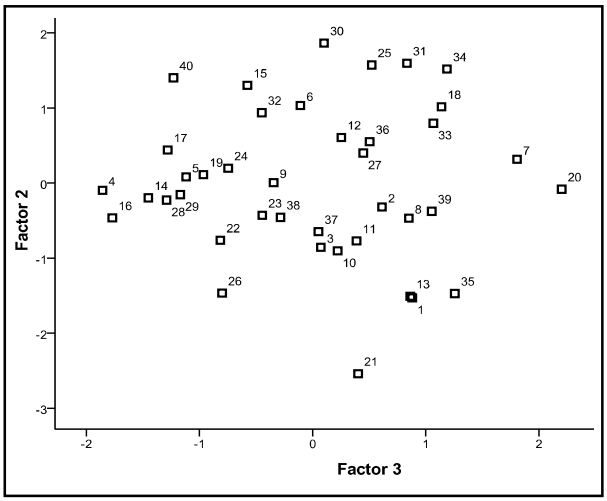

Fig. 4. Location of genotypes based on PF Score w. r. t. factors 3 & 2

contributed 83.40 % of the total variation.

Principal factor scores were calculated for all the genotypes for all the five factors using Anderson-Rubin method and were utilized to find out genotypes superior 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 denotes high value for those variables in that genotype, which that factor is representing. Thus, the genotypes BH 946, BH 15-02, BH 16-40, BH 16-44, BH 10-11, BH 15-06 and BH 15-07 which were having high score in PF 3 denotes that they are having high yield potential and harvest index. Similarly, genotypes BH 13-22, BH 15-30 and BH 16-43 had high score in PF 4, therefore, were better for spike length and number of grains per spike. Likewise, genotypes BH 12-46, BH 7-35 and BH 14-44 for PF 5; and BH 7-34, BH 15-07, BH 902 and BH 15-02 for PF 1 were found to have high score, hence, performed good for the characters to which the factor associated. The correlation of early maturing genotypes *viz*., BH 393, BH 10-11 and BH 15-06 with PF 2, suggest that early heading and maturing genotypes may result in higher grain yield. Studies on genetic diversity has also been conducted on barley for various quantitative traits based on principal component and factor analyses by Khajavi *et al*. (2014)

Further, all the genotypes were plotted on graph utilizing their scores based on two factors simultaneously. The genotypes which found place towards the better end of both the factors were found to be superior for those two factors and hence superior for all the characters, which are defined by these two factors. Thus, the genotype BH 15-07 was found better for PF 3 and PF 4 (Fig. 1), BH 12-46 and BH 7-35 for PF 3 and PF 5 (Fig. 2), BH 15-02, BH 15-07, BH 15-

06, BH 946 and BH 16-44 for PF 3 and PF 1 (Fig. 3); and BH 10-11, BH 15-06 and BH 393 exhibited superiority for PF 3 and PF 2 (Fig. 4), meaning hereby that these genotypes are better for characters for which principal factors ascribed. The results of the present study can be used as a stepping stone for evolving well defined approach based on evaluation and characterization of genetic variation in barley and can be utilized in various breeding programme to suit their specific objective.

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