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Genetic diversity in barley (*Hordeum vulgare*) for traits associated with feed and forage purposes

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ABSTRACT

Barley (*Hordeum vulgare* L.) is an important coarse cereal cultivated in many parts of the world since ancient times and mostly used as cattle & poultry feed. However, in India due to climate change and frequent drought especially in drier areas barley offers a better alternative to extreme climate such as drought and winter. In the present study 220 cultivated barley accessions of indigenous and exotic origin were evaluated for different agro-morphological traits. The material was evaluated during the 2011-12 growing season at DWR, Karnal where observations were recorded on 13 agro-morphological traits. The results showed high variability among the accessions for grain per spike, green fodder yield, grain yield, grain yield of regenerated crop, biological yield and harvest index (HI). Based on K-mean clustering pattern, the genotypes were grouped into five clusters having significant inter-cluster distances. Shannon-Weaver's diversity index (H) and Simpson's index (1/D) was used to assess the phenotypic diversity of traits for each cluster genotypes and overall. Shannon's diversity index revealed large diversity for most traits. The average H for the whole population was 0.91 with the lowest 0.74 for HI, the highest (1.01) for days to heading. The simple correlation coefficients among traits were estimated, which showed significant positive relations between grain yield with plant height (r = 0.25**), green fodder yield (r = 0.15*), grain yield of regenerated crop (r = 0.13*) and HI (0.19**), while negative correlation with days to heading (r = –0.35**). Sources for individual traits in different genotypes of barley clusters were identified which can be used as donors in hybridization programme for dual purpose barley improvement programme.

Key words: Barley, Cluster analysis, Correlation, Genetic diversity, *Hordeum vulgare*, Phenotypic diversity, Shannon-Weaver diversity index

Barley (*Hordeum vulgare* L.) is one of the oldest and man's most dependable coarse cereal domesticated and cultivated since the beginning of civilization (Harlan 1968). It is grown over a wide range of environment because of its broad ecological adaptation, low input requirement and better adaptability to harsh conditions, i.e. drought, salinity, alkalinity and marginal lands. That is why it has been traditionally considered as poor man's crop throughout the world especially for people dependant on subsistence farming. In India, the area under this crop is concentrated in the states of Rajasthan, Uttar Pradesh, Punjab, Haryana, Madhya Pradesh, Bihar in plains and Himachal Pradesh, Uttarakhand and Jammu & Kashmir in the hills. The knowledge of genetic diversity and its distribution facilitate selection of the parents with diverse genetic background and thereby make crop improvement more efficient. A better utilization and exploitation of materials require details information on various traits, the level of association among traits and diversity estimates. The knowledge about variability in barley genotypes collected from different parts of the world for various agro-morphological traits, especially with the objectives of using parental lines for improvement of feed and forage purposes is necessary. Genetic diversity in the parent population is a prerequisite for effective selection of desirable recombinants in segregating breeding materials. Information on the nature and degree of divergence among the genotypes helps the plant breeders in choosing the suitable donor parents for initiating hybridization programme, as heterosis is believed to be correlated with genetic divergence among the parents (Ramanujam *et al*. 1974). Genetic diversity among the genotypes is not necessarily associated with geographic diversity or place of origin of the materials (Shekhawat *et al*. 2001, Singh *et al*. 2006). Multivariate analysis like cluster analysis and D^2 (Mahalanobis 1936) technique is considered a powerful tool in identifying the diverse genetic group and degree of divergence among the genotypes. The

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present study was mainly aimed to assess the extent and pattern of variation for various traits of the barley genotypes to be utilised in the hybridization programme for feed and forage purposes. The present investigation was undertaken for clustering of barley genotypes into different clusters based on genetic divergence, diversity index and the association among various traits and to identify suitable donors for use in the breeding programme.

MATERIALS AND METHODS

The study material comprised 220 barley genotypes having wide variation for various agro-morphological traits representing advanced breeding lines, released varieties, germplasm accessions of both indigenous and exotic sources including materials selected from international nurseries (ICARDA, Syria). The experiment was conducted at Directorate of Wheat Research (DWR), Karnal, India during 2011-12 crop season. The trial was arranged in 4 blocks, with 55 entries in each block. these accessions were sown each on 2 line of 2.5 m and spacing of 30 cm (in between rows) and 5 cm (within row) . The recommended agronomic package of practices (60 kg N: 40 kg P: 20 kg K /ha) was followed to raise a healthy crop. The germplasm was evaluated for 13 traits namely; plant height, numbers of seeds/spike, spike length(cm), leaf chlorophyll content, days to 75% heading, grain protein content, starch content, 1000-grain weight (g), green fodder yield (g/plot) , biological yield (g/plot) , grain yield (g/plot) , harvest index (HI) and grain yield (g/plot).

The observations for plant height (cm), grains/spike and spike length (cm) were recorded on five representative plants. Data on whole plot basis was recorded for days to 75% heading. For recording green fodder yield each line of 1 meter length was given a cut at 60-65 days after sowing leaving 8-10 cm from the ground level and fresh weight was recorded. At harvest the biological yield (g per meter plot) of regenerated crop and grain yield from this regenerated crop was measured. The HI of regenerated crop was recorded to measure the potential and diversity for regeneration in barley as a dual purpose crop. Clustering analysis helps in grouping the materials in such a manner that similar types are grouped together, while dissimilar ones belong to different groups. Since clustering is the grouping of similar instances/objects, some sort of measure that can determine whether two objects are similar or dissimilar is required. There are two main types of measures used to estimate this relation: distance measures and similarity measures. Many clustering methods are used to determine the similarity or dissimilarity between any pair of objects (Farley and Raftery 1998 and Joshi and Kaur 2013).

The simplest and most commonly used algorithm, employing a squared error criterion is the K-means algorithm. This algorithm partitions the data into K clusters (C_1; C_2; : : : ; C_k), represented by their centers or means. The center of each cluster is calculated as the mean of all the instances belonging to that cluster. The algorithm starts with an initial set of cluster centers, chosen at random or according to some heuristic procedure. In each iteration, each genotype is assigned to its nearest cluster center according to the euclidean distance between the two. Then the cluster centers are re-calculated. The center of each cluster is calculated as the mean of all the instances belonging to that cluster:

$$\mu_k - \frac{1}{N_k}\sum_{a=1}^{N_k} x_c$$

where, N_k is the number of instances belonging to cluster k and μ_k is the mean of the cluster k. A number of convergence conditions are possible. For example, the search may stop when the partitioning error is not reduced by the relocation of the centers. This indicates that the present partition is locally optimal. K-means is based on the idea that a center point can represent a cluster. For K-means we use the notion of a centroid, which is the mean or median point of a group of points. A centroid almost never corresponds to an actual data point. The basics of K-means algorithm for finding K clusters are: 1. Select K points as the initial centroids. 2. Assign all points to the closest centroid. 3. Re-compute the centroid of each cluster. 4. Repeat steps 2 and 3 until the centroids don't change. Among various methods K-means method is preferred for large dataset because of its simplicity in interpretation (Dhillon and Modha 2001). The data were also analysed using Mahalanobis (1936) D^2 statistics to measure genetic divergence and 5 clusters were formed where there was significant distance between cluster using SAS statistical software version 9.3. The Pearson's correlation coefficient among these traits was also estimated to measure the association among various traits and their significance. In addition, Shannon-Weaver diversity index (H) and Simpson's index was used to assess the phenotypic diversity among the accessions for the 13 quantitative traits. The genotypes were grouped into five groups based on their means and standard deviations of each trait (Shakhatreh 2010). The five groups are: (1) Mean + 2 standard deviations. (2) Mean + 1 standard deviation. (3) Mean -1 to +1 standard deviation. (4) Mean - 1 standard deviation. (5) Mean - 2 standard deviations.

The above grouping is used for computing Shannon-Weaver's diversity index (*H*) and Simpson's index (1/*D*) to assess the phenotypic diversity for each of the 13 quantitative traits. Shannon's diversity index is computed as $H = -\sum_{i=1}^{5} p_i \ln(p_i)$, where p_i is is the relative frequency of genotypes belonging to *i*th group and ln is the natural logarithm (Magurran 1988) and Simpson's index is computed as $\frac{1}{D} = 1 \Big/ \sum_{i=1}^{5} \frac{n_i(n_i - 1)}{N(N - 1)}$, where n_i is is the frequency of genotypes belonging to ith group and *N* is the total number of observations for the trait under study (Magurran 1988). The data were also used to calculate simple correlation coefficient among traits (Snedecor and Cochran 1967) and its significance to measure the association among various traits.

Table 1 Mean, standard error, standard deviation, range and coefficient of variation of different traits

Traits	Mean ± SE	Standard deviation	Range		Coefficient of variation (CV %)
			Minimum	Maximum	
Plant height (cm)	106 ± 0.6	9.6	69	148	9.1
Grain/spike	55 ± 1.6	23.2	23	96	42.5
Spike length (cm)	9 ± 0.1	1.3	5	13	14.4
Chlorophyll content (%)	25 ± 0.5	7.3	12	67	28.7
Heading days (75%)	91 ± 0.4	5.9	74	107	6.4
Protein (%)	10 ± 0.1	1.3	8	16	12.5
Starch (%)	61 ± 0.1	1.1	58	67	1.9
Thousand grain weight (g)	42 ± 0.6	8.9	12	63	21.5
Green fodder yield (g/plot)	716 ± 22.8	337.8	100	1750	47.2
Biological yield (g/plot)	334 ± 9.4	139.5	50	850	41.8
Grain yield (cut) (g/plot)	69 ± 1.8	26.4	10	178	38.5
Harvest Index (HI)	0.22 ± 0.01	0.08	0.03	0.6	36.6
Grain yield (g/plot)	387 ± 8.1	119.4	79	701	30.8

RESULTS AND DISCUSSIONS

The mean, standard error, standard deviation, range (minimum, maximum) and coefficient of variation (CV) for all 13 agro-morphological traits which were recorded are summarized in Table 1. The basic statistics revealed high level of variability among the genotypes used in the study. The results indicated a high CV for most of the traits studied except starch content and days to heading where coefficient of variation were comparatively less.

The CV was high for green fodder yield followed by grains/spike, biological yield, grain yield from regenerated crop, HI, grain yield from uncut and chlorophyll content while CV was low for starch content and days to heading. The results showed that considerable diversity exist in the materials studied for using in dual purpose barley breeding. A wide range of values was observed for green fodder yield (100-1750 gm), biological yield (50-850 gm), grain yield from regenerated crop (10-178 gm), grain yield from uncut (79-701 gm) and chlorophyll content (12-67%). The phenotypic variation on various morphological traits on barley has also been reported by number of researchers (Yadav and Jag Shoran 1999, Manjunatha *et al*. 2007).

The data recorded on all these traits were subjected to a cluster analysis through K-means clustering method. Based on clustering pattern genotypes were grouped into five clusters where each genotype within a cluster centre was closest to the cluster mean. The genotypes belonging to different clusters are given in Table 2. The clustering pattern for different characters under study revealed considerable differences between the groups. The results showed that in case of green fodder yield, cluster-V have entries with highest forage yield followed by entries belonging in cluster-I. However, in case of biological yield highest performing

Table 2 Clustering pattern of barley genotypes evaluated

Cluster no.	Number of genotypes	Genotypes
I	63	BCU1086, BCU1482, BCU1952, BCU2366, BCU4803, BCU549, BCU6031, BCU6810, BCU682,BCU6826, BCU6840, BCU6842, BCU6846, BCU6852, BCU6858, BCU6864,BCU6868, BCU6899, BCU6905, BCU6906, BCU6907, BCU6909, BCU6912, BCU6914,BCU6919, BCU6922, BCU6929, BCU6939, BCU6945, BCU6947,BCU6952, BCU6959, BCU6965, BCU698, BCU6984, BCU6985, BCU6989, BCU6999, BCU7005,BCU7008, BCU7009, BH902, BK315, DWR73, DWR83, EC667383, EC667385, EC667507, EC667508, EC667523, EC667530, EC667535, EC667536, EC667601, EC667611, EC671300, EC671314, EC671356, HUB205, Harmal, IBYT-HI1, MANLEY, NDB1173
II	28	BCU6702, BCU6704, BCU6729, BCU6733, BCU6742, BCU6748, BCU6749, BCU6750, BCU6751, BCU6752, BCU6780, BCU6813, BCU6833, BCU6841, BCU6873, BCU7030, BCU7033, BCU7046, BCU7179, BHS387, EC667489, EC667546, EC667550, EC667577, EC667603, EC671299, RD2052, RD2592
III	57	BCU139, BCU1511, BCU1549, BCU211, BCU2126, BCU456, BCU463, BCU4795, BCU516, BCU519, BCU530, BCU5911, BCU6038, BCU6722, BCU6738, BCU6753, BCU6757, BCU6761, BCU6764, BCU6766, BCU6770, BCU6778, BCU6782, BCU6792, BCU6801, BCU6818, BCU6821, BCU6827, BCU6834, BCU6847, BCU6857, BCU6861, BCU6913, BCU6948, BCU6996, BCU7003, BCU7007, BCU7027, BCU7028, BCU7040, BCU7041,BCU7045, BCU7076, BCU91, EC66750, EC667295, EC667381, EC667382, EC667498, EC667511, EC667512, EC667514, EC667515, EC667553, EC667593, EC667594, RD2715
IV	54	BCU105, BCU1813, BCU4756, BCU4769, BCU4770, BCU4793, BCU501, BCU6079, BCU6683, BCU6686, BCU6687, BCU6688, BCU6689, BCU6690, BCU6691, BCU6695, BCU6698, BCU6711, BCU6720, BCU6730, BCU6732, BCU6768, BCU6769, BCU6773, BCU6806, BCU7021, BCU7067, BCU7086, BCU7102, BCU7168, BCU7181, BCU7186, BCU7260, BCU7263, BCU8, BCU803, EC667150, EC667241, EC667499, EC667543, EC667548, EC667549, EC667572, EC667585, EC667586, EC667587, EC667589, EC667590,EC667602, EC667604, EC671322, RD2552, VJM601, VM150
V	18	BCU6900, BCU6901, BCU6926, BCU6927, BCU6943, BCU6961, BCU6969, BCU6971, BCU6974, BCU6975, BCU6979, EC667384, IBYTHI9, IEBON17, IEBON18, IEBON19, PL426, RD2035

Table 3 Mahalanobis inter cluster distances (D^2 statistics) between five clusters in barley

Cluster	2	3	4	5
1	16.7	9.7	45.3	16.3
2		7.1	12.2	61.3
3			15.4	45.7
4				109.9

genotypes belong to cluster-II, followed by cluster-I. In case of grain yield of regenerated crop after cut and uncut the superior genotypes are in cluster-II.

While cluster-IV has entries with poorest genotypes for most of the traits studied maximum number of genotypes were grouped in cluster I (63) followed by Cluster III (57), IV (54), II (28) and V (18). It was also observed that genotypes of both exotics and indigenous are distributed throughout all clusters. The analysis clearly indicates that an array of variability exists in the genetic materials used as feed and forage purpose crop. The similar studies on genetic diversity have been reported in barley (Vanhala *et al.* 2004, Shakhatreh *et al.* 2010).

To determine the inter-cluster distances the data were also analysed for calculation of D^2 statistics (Mahalanobis 1936) to measure genetic divergence among genotypes. Based on the relative magnitude of D^2 values, 220 genotypes were grouped into five clusters and the average inter cluster distances among 5 clusters are presented in Table 3. The maximum inter cluster distance was observed in between cluster IV and V (109.9) followed by cluster II and V (61.3), while lowest inter cluster distance was observed between cluster II and III (7.1). The genotypes from those clusters showing higher inter cluster difference, could be utilized in the hybridization programme as crossing between diverse parents is likely to produce wide genetic variability among the progenies of the segregating generations. The minimum inter cluster distance between clusters II and III reveals that the genotypes of these clusters were relatively closer. So the contrasting parents from clusters IV and V or II and V may be selected for different traits important as dual purpose barley and used in the crossing programme to widen the genetic base of the materials. The clustering pattern revealed that genotypes from both indigenous and exotic sources fell in the same cluster or different clusters suggesting that geographic diversity not necessarily reflect genetic diversity. Similar findings have also been reported by Shekhawat *et al.* 2001, Sandhyakishore *et al.* (2007) and Mittal *et al*. (2010). The grouping of genotypes from different sources into one cluster may be due to fact of free exchange of germplasm/breeding material between breeding programmes.

As there are genotypes superior for individual traits belongs to different clusters which indicates that none of the clusters contained genotypes with all the desirable characters. This implies that none of the clusters possessed a genotype which could be selected superior as such. However, the genotypes superior for specific characters from different clusters may be selected for utilization in recombination breeding programme. The superior genotypes for specific characters from different clusters are listed in Table 4. The genotypes belonging to the same cluster are considered similar with respect to aggregate effect of characters studied and the hybridization between them is not expected to provide superior segregants in the segregating generations. Therefore, potential parents for crossing programme should be selected from the diverse clusters which are characterized by large inter-cluster distances.

In terms of green fodder yield, biological yield and grain yield cluster IV is poorest among all clusters, however, there are a few genotypes, such as BCU 6711, EC 667241, BCU 6806, BCU 6686, BCU 6683 and BCU 6732 in this cluster which have comparable green fodder yield, biological yield, grain yield and high thousand grain weight and may be used in crossing programme. The Shannon-Weaver diversity index (H) and Simpson's index estimated according to the method suggested by Shakhatreh *et al.* (2010) are given in Table 5. The results indicated high genetic diversity for most traits for Shannon-Weaver diversity index (H) and Simpson's index. The average H for the whole population was 0.91 with a minimum of 0.74 for HI to highest for heading days (1.01). Among clusters, the Shannon's diversity index (H) was higher for grains/spike, spike length, starch content and green fodder yield in cluster I while for chlorophyll content and biological yield in cluster III; for plant height, thousand grain weight, HI and grain yield in cluster IV and for heading days and protein content in cluster V. The overall average Simpson's index was 1.91 with minimum values of 1.54 for HI and maximum 2.49 for grains per spike.

Table 4 List of superior genotypes selected from different clusters

Cluster No.	Genotypes	Superior for character(s)
I	BCU6864, BCU6909, BCU6868, DWR83, BCU1086, BCU2366, BCU6912, BCU6985	High green fodder yield
II	BCU6752, BHS387, EC667489, EC667546, RD2052, RD2592, BCU6873, RD2052, RD2592, BHS387	High biological yield and grain yield of regenerated crop
III	BCU139, BCU456, BCU530	Better harvest index of regenerated crop
IV	BCU8, BCU6686, BCU6690, BCU6691	High thousand grain weight
V	BCU6900, BCU6927, BCU6971, EC667384, IEBON19, RD2035, PL426	High green fodder yield

Table 5 Shannon-Weaver's diversity index (H) for different traits in different clusters and whole population

Parameters	Shannon Diversity Index (H)						Reciprocal of Simpson's Index (1/D)					
	Cluster -I	Cluster -II	Cluster -III	Cluster -IV	Cluster -V	Overall	Cluster -I	Cluster -II	Cluster -III	Cluster -IV	Cluster -V	Overall
Plant height	0.88	0.83	0.87	0.92	0.76	0.88	1.75	1.76	1.72	1.99	1.66	1.77
Grain per spike	1.02	0.62	0.90	0.74	0.58	1.00	2.69	1.57	2.17	1.71	1.48	2.49
Spike length	1.05	0.56	0.94	0.87	0.87	0.93	2.12	1.36	1.87	1.71	2.13	1.83
Chlorophyll content	0.73	0.88	0.95	0.85	0.87	0.86	1.61	1.90	2.07	1.89	2.13	1.83
Heading days (75%)	0.93	0.88	0.91	1.02	1.06	1.01	1.98	1.90	2.08	2.23	3.12	2.21
Protein content (%)	0.94	0.90	0.86	0.81	1.04	0.84	2.12	2.02	1.84	1.70	2.94	1.79
Starch content (%)	0.96	0.91	0.80	0.77	0.93	0.91	1.95	1.92	1.59	1.68	2.39	1.80
Thousand grain weight (g)	0.86	0.74	0.88	0.99	0.85	0.93	1.75	1.61	1.91	2.23	1.89	1.89
Green fodder yield (g/plot)	1.04	0.94	0.95	0.83	0.85	0.95	2.48	2.35	2.33	1.75	1.89	2.06
Biological yield (g/plot)	0.95	0.83	1.08	0.85	1.06	0.87	2.11	1.76	2.57	1.77	2.51	1.81
Grain yield of regenerated crop (g/plot)	0.90	0.90	0.88	0.80	0.85	0.90	1.98	1.91	1.79	1.75	1.89	1.89
Harvest Index	0.52	0.86	0.83	0.96	0.43	0.74	1.31	1.88	1.65	2.13	1.28	1.54
Grain yield (g/plot)	0.87	0.85	0.90	0.95	0.76	0.98	1.86	2.02	1.92	2.00	1.66	1.98
Average SDI	0.90	0.82	0.90	0.87	0.84	0.91	1.98	1.84	1.96	1.89	2.07	1.91
Max SDI	1.05	0.94	1.08	1.02	1.06	1.01	2.69	2.35	2.57	2.23	3.12	2.49
Min SDI	0.52	0.56	0.80	0.74	0.43	0.74	1.31	1.36	1.59	1.68	1.28	1.54

Shannon-Weaver's diversity index is widely used in studies of germplasm collections (Jaradat 1991, Bechere 1996, Ayana and Bekele 1998).

To understand the nature of correlation between traits data were analysed to determine the Pearson simple correlation coefficients among these traits (Table 6). The study revealed significant positive correlation between grain yield and plant height (r=0.25**), green fodder yield (r=0.15*), grain yield of regenerated crop (r=0.13*) and harvest index (r=0.19**), while negative correlation with heading days (r=-0.35**). On the other hand biological yield showed significant positive correlation with grain yield of regenerated crop (r=0.69**), heading days (r=0.28**) and protein content (r=0.20**) but negative correlation with harvest index of regenerated crop (r=-0.54**). This indicates that selection of genotypes with high biomass will identify the genotype with high fodder yield, better regeneration and high grain yield from regenerated crop. This will help in selecting genotypes suitable for using as a dual purpose crop. The correlation studies among various traits were reported by number of workers (Briggs 1978, Spunar 1991, Hayter and Riggs 1973, Henry 1989, Verma *et al.* 2008 and Sarkar *et al.* 2008)

As most of the traits studied showed either positive or

Table 6 Correlation coefficient and their significance among various traits

	Grain /spike	Spike Length	Chloro phyll	HD	GFY	BY	GY (cut)	HI	GY	Protein (%)	Starch (%)	TGW
PH	0.12	0.14*	0.09	–0.18**	0.28**	0.05	0.08	–0.04	0.25**	0.05	0.09	0.26**
Grains/spike		–0.04	0.08	–0.10	0.28**	–0.06	–0.17**	–0.06	–0.05	–0.41**	–0.19**	–0.49**
Spike length			0.08	0.06	0.06	0.06	–0.02	–0.15*	0.02	0.23**	0.07	–0.06
Chlorophyll content			–0.13*	0.26**	0.10	0.001	–0.16**	0.07	0.27**	0.001	–0.11	
HD (75%)					–0.26**	0.28**	0.08	–0.30**	–0.35**	0.16**	–0.21**	–0.28**
GFY (g/plot)						0.04	–0.02	–0.06	0.15*	–0.001	0.04	–0.14*
BY (g/plot)							0.69**	–0.54**	0.01	0.20**	–0.04	–0.07
GY (cut) (g/plot)								0.08	0.13*	0.05	0.13*	0.11
HI									0.19**	–0.23**	0.18**	0.20**
GY (g/plot)										–0.12	0.23**	0.22**
Protein (%)											–0.27**	0.16*
Starch (%)												0.19**

PH, plant height; HD, heading days; GFY, green fodder yield; BY, biological yield; GY(cut), grain yield; GY, grain yield; HI, harvest index; TGW, thousand grain weight; N, 220.

negative correlation with each other, it becomes difficult to combine all the desirable traits in one single genotype by selecting only for a single trait in the breeding materials. The optimum level for important traits needs to be combined while making some compromises. This could be achieved by using a selection index that is flexible enough to allow balancing moderate defects in one trait with obvious gain in others. Such an approach of using multiple trait selection index uses the concept of "intuitive index selection" described by Simmonds (1981). The present study showed that, sufficient variability exists in the material for most of the traits for using as a dual purpose crop. Any variety to be recommended for commercial cultivation as dual purpose barley must have high level of grain yield along with resistance to prevalent biotic and abiotic stresses and better regeneration capacity after cutting for green fodder. The identification of suitable donors for different traits will help in the development of better dual purpose variety. Cluster analysis clearly helped in differentiating genotypes into major groups for various traits useful for breeding barley for use as both feed and forage purposes. Based on distance between genotypes of different clusters, contrasting parents were identified and may be used in the hybridization programme to generate wider variability for selection in the breeding programme. Designing a crossing programme by identifying genotypes of interest from different clusters will make the breeding process more directional and effective. The present investigation provided useful information about the level genetic diversity and correlation among traits in relation to dual purpose barley.

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