Sandhya
Department of Genetics and
Plant Breeding, Narendra Deva
University of Agriculture and
Technology, Faizabad,
Uttar Pradesh, India

Aarti Sharma
Department of Genetics and
Plant Breeding, Narendra Deva
University of Agriculture and
Technology, Faizabad,
Uttar Pradesh, India

SR Vishwakarma
Department of Genetics and
Plant Breeding, Narendra Deva
University of Agriculture and
Technology, Faizabad,
Uttar Pradesh, India

Evaluating genetic divergence in barley (*Hordeum vulgare* L.) genotypes

Sandhya, Aarti Sharma and SR Vishwakarma

Abstract
A total of 114 barley genotypes were studied on 9 quantitative characters to assess the genetic diversity through Non-hierarchical Euclidean Cluster analysis. The result of pseudo F-test grouped the genotypes into 11 non-overlapping Clusters. The highest intra-Cluster distance was observed in case of Cluster VIII followed by Clusters II, while the maximum inter-Cluster distance was found between Cluster IV and Cluster XI. The genotypes having high mean performance for grain yield per plant and several other yield components were found to be concentrated in Cluster IX and XI. The results suggested that Cluster pairs exhibiting higher inter Cluster distances can be utilized in future breeding program to obtain transgressive segregants. The different Clusters showed considerable differences in intra-Cluster group means of 9 characters studied in the experiment.

Keywords: Barley, non-hierarchical euclidean cluster analysis, pseudo f-test

Introduction
Barley is one of the oldest crops cultivated by humans (Harlan 1968) [4]. Barley is grown in *Rabi* season in India and popularly called as poor's man crop. It is fourth most grown cereal after rice, wheat and maize. Being rich in digestible dry matter and protein make it an excellent animal fodder. It can be grown in marginal land with limited supply of farm inputs. Barley is found in two forms; hull-less, which is used in chapatti making and hulled type used in malting industries for preparation of beer, whisky and vinegar etc. Among its other uses, in form of pearl barley it serves as diet for sick people. Barley is not an important food crop, but it is in demand for brewing industries and hence making an important industrial crop. Barley productivity in India is far low than world productivity, indicating that a thorough research program is needed on this crop. In view that, presence of significant genetic diversity in any breeding material can be exploited to obtain heterosis, when used in hybridization program (Ramanujam et al. 1974) [9], a study was undertaken to evaluate the genetic variability in experimental material constituted of 114 barley genotypes including 3 checks (Azad, Lakhan and NDB 1173).

Material and Method
114 barley genotypes including three checks were sown in augmented block design. Experimental plot was divided into seven blocks of four meters in length, containing 16 entries along with three checks. Plant to plant spacing was kept 10 cm and 23 cm between the rows. Cultural practices were followed as recommended in the package of practice for barley to raise a healthy crop population. Data was collected on 9 quantitative traits to evaluate the genetic diversity present from the experimental material. Analysis of variance of Augmented Block Design was done according to Federer, 1996. Non-hierarchical Euclidean Cluster analysis (Beale, 1969; Spark, 1973) [3, 12] was used to group the 111 genotypes into different Clusters. These procedures were implemented to characterize genetic divergence using the criterion of similarity or dissimilarity based on the aggregate effect of 9 agronomic traits studied in the experiment.

Experimental results
Cluster analysis on 114 barley genotypes, performed according to Non-hierarchical Euclidean Cluster analysis, resulted into 11 non-overlapping Clusters. The Cluster means for 9 characters are presented in Table 3. Cluster VII emerged with highest number of entries with 27 entries followed by Cluster III having 16 genotypes, Cluster VIII had 15 genotypes, Cluster I, IV and

Correspondence
Aarti Sharma
Department of Genetics and
Plant Breeding, Narendra Deva
University of Agriculture and
Technology, Faizabad,
Uttar Pradesh, India

V had 10 genotypes each, Cluster VI had 8 genotypes, and Cluster X had 6 genotypes, Cluster IX had 5 genotypes, while Cluster II and XI had 2 genotypes respectively. The estimates of intra-and inter-Cluster distances for 11 Clusters are presented in Table 2.

The highest intra-Cluster distance was observed in case of Cluster VIII (10.265), followed by Cluster II (9.840). The lowest intra-Cluster value was noted for Cluster IX (5.981). The maximum inter-Cluster distance was observed between Cluster IV and XI (66.573), followed by Cluster V and XI (58.118).The minimum inter-Cluster distance was observed between Cluster IV and V (11.408). The highest Cluster mean for days to 50% flowering was recorded for Cluster XI (87), followed by Cluster X (86). The lowest Cluster mean for days to 50% flowering was found in case of Cluster III (80), while remaining Cluster had moderate means for days to 50% flowering. The genotype of Cluster II was responsible for highest Cluster mean for days to maturity (128 days), followed by entries of Cluster XI (128 days). The genotypes with early maturity were concentrated in Cluster III (119 days), followed by Cluster IV (122 days). The highest Cluster mean for plant height was recorded in case of Cluster XI (86.82 cm) followed by Cluster IX (86.46 cm). The lowest Cluster mean for plant height was found in case of Cluster IV

(50.81 cm), while remaining Clusters had moderate means for plant height. The genotypes occurring in Cluster II (9.22 cm), followed by Cluster XI (8.88 cm) higher Cluster mean for spike length. The lowest mean for spike length was exhibited by Cluster V (4.97 cm). The genotypes of Cluster IX (43.952 g) were responsible for highest Cluster mean for 1000-grain weight, followed by the genotypes Cluster VIII (40.886 g). Cluster X resulted in lowest Cluster mean for 1000-grain weight (29.786 g).

Cluster IX (26.838 g), followed by Cluster XI (26.571 g) showed highest Cluster mean for biological yield per plant. Thus, the genotypes with higher biomass production ability appeared to be present in the two Clusters mentioned above. The lowest mean for biological yield per plant was recorded for Cluster V (17.087 g). The highest Cluster mean for grain yield per plant was observed in case of Cluster IX (10.829 g) which indicated that lines having higher grain yield were concentrated in this Cluster. The genotypes with very low grain yield were found to be grouped in Cluster IV (4.944 g). The highest Cluster mean for harvest-index was observed in case of Cluster IX (41.726%), followed by Cluster VII (40.910%). The lowest mean for harvest-index was exhibited by Cluster II (29.619%), while remaining seven Clusters were characterized by moderate means for harvest-inde.

Table 1: Clustering pattern of 114 barley genotypes on the basis of non-hierarchical Euclidean Cluster analysis for nine characters in genotypes of barley (*Hordeum vulgare* L.)

Cluster number	No. of genotypes	Genotypes
I	11	EIBGN 1, EIBGN 2, EIBGN 6, EIBGN 18, EIBGN 7, EC 667356, EIBGN 34, EIBGN 45, EC 667365, EC 667580, EC 667462
II	2	EIBGN 74, EC 667498
III	16	EIBGN 5, EIBGN 8, EC 667511, EIBGN 16, EC 667429, EIBGN 48, EIBGN 100, EC 667520, EIBGN 49, EIBGN 50, LAKHAN, NDB 1173, AZAD, EC 667458, EC 667514, EC 667512
IV	11	EIBGN 55, EIBGN 69, EIBGN 54, EIBGN 56, EIBGN 72, EIBGN 57, EIBGN 63, EIBGN 68, EIBGN 64, EIBGN 73, EIBGN 3
V	10	EIBGN 9, EIBGN 10, EIBGN 61, EC 667442, EIBGN 4, EIBGN 11, EC 667541, EIBGN 78, EIBGN 66, EIBGN 67
VI	8	EIBGN 12, EC 667509, EC 667502, EC 667496, EC 667535, EIBGN 52, EIBGN 59, EIBGN 14
VII	27	EIBGN 13, EIBGN 62, EIBGN 37, EC 667430, EIBGN 47, IBONHI 4, EIBGN 42, EC 667540, PL 851, EIBGN 20, EIBGN 41, EIBGN 31 EIBGN 24, EIBGN 26, EIBGN 25, EIBGN 28, EIBGN 39, EIBGN 40, EIBGN 43, EIBGN 27, EIBGN 35, EIBGN 29, EC 667454, EIBGN 22, EC 667499, EC 667501, EC 667500
VIII	15	EIBGN 21, EIBGN 46, EIBGN 17, EIBGN 33, EC 667504, EC 667355, EC 667410, EC 667422, EC 667377, EC 667384, EC 667374, EIBGN 51, EC 667351, EC 667350, EC 667370
IX	5	EC 667353, EC 667428, EC 667360, EC 667404, EC 667407,
X	6	EIBGN 36, EC 667482, EIBGN 44, EC 667526, EC 667477, IBONHI 908
XI	2	IBONHI 43, EMBSN 90345

Table 2: Intra-and inter-Cluster distances for 11 Clusters of barley (*Hordeum vulgare* L.)

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI
Cluster I	9.545	21.468	12.013	16.368	14.608	16.873	14.350	15.427	27.310	15.965	45.282
Cluster II		9.840	27.983	22.853	22.000	21.639	26.862	33.031	50.403	21.340	37.774
Cluster III			7.412	11.925	14.693	16.069	19.352	19.174	38.225	25.697	55.384
Cluster IV				6.937	11.408	14.827	21.148	24.771	50.306	34.358	66.573
Cluster V					7.637	11.472	11.828	21.489	42.819	23.750	58.118
Cluster VI						6.323	12.734	16.121	32.791	19.345	37.465
Cluster VII							6.092	13.872	27.252	15.173	47.308
Cluster VIII								10.265	15.375	16.990	38.657
Cluster IX									5.981	19.151	31.821
Cluster X										6.566	21.004
Cluster XI											8.798

Table 3: Clusters means for nine characters in genotypes of barley (*Hordeum vulgare* L.)

	Days to 50% flowering	Flag leaf area (cm2)	Plant height (cm)	Days to maturity	Spike length (cm)	Biological yield/ plant (g)	Grain yield/ plant (g)	Test weight (g)	Harvest index (%)
Cluster I	82.575	2.794	64.879	124.190	6.151	21.988	7.234	35.619	32.983
Cluster II	86.381	5.243	61.795	128.857	9.220	18.738	5.429	34.119	29.619
Cluster III	80.131	4.743	61.916	119.920	5.884	19.613	6.408	34.640	32.679
Cluster IV	81.926	4.980	50.813	122.524	5.981	16.753	4.944	40.346	30.804
Cluster V	85.169	4.367	55.619	124.797	4.975	17.087	5.641	34.043	33.443
Cluster VI	84.089	9.782	60.220	125.815	5.536	17.988	6.512	35.369	36.327
Cluster VII	85.529	3.919	58.362	126.861	5.008	19.411	7.947	33.113	40.910
Cluster VIII	83.248	6.033	68.024	124.257	5.599	22.060	8.895	40.886	40.732
Cluster IX	84.514	6.353	86.469	126.124	5.373	26.838	10.829	43.952	41.726
Cluster X	86.714	5.600	75.406	127.190	6.887	23.849	8.873	29.786	36.786
Cluster XI	87.381	14.713	86.829	128.524	8.886	26.571	9.595	30.952	35.952

Discussion

The estimates of average intra and inter Cluster distances for nine characters, presented in Table 2, revealed that the genotypes present in a Cluster have little genetic divergence from each other with respect to aggregate effect of nine characters under study, while much more genetic diversity was observed between the indigenous lines belonging to different Clusters. In order to increase the possibility of isolating good segregates in the segregating generations it would be logical to attempt crosses between the diverse exotic lines belonging to Clusters referred by large inter-Cluster distances in the present investigation.

The highest intra-Cluster distance was observed in case of Cluster VIII followed by Cluster-II and the highest inter Cluster distance was observed between Cluster IV and XI followed by V and III may also be fruitful for obtaining desirable recombinants in segregating generations. The lowest inter-Cluster distance values observed between Cluster-IV and V followed by Cluster- V and VI, indicated that the members of these Cluster pairs were genetically close to each other. Eleven direct clusters obtained through cluster analysis suggested presence of high degree of genetic diversity in the material evaluated. Earlier workers have also reported substantial genetic divergence in the barley materials (Sharma *et al.,* 2005; Singh *et al.,* 2006; Alam *et al.,* 2006, Ali *et al.,* 2007; Mishra *et al*., 2007) [11, 1, 7].

Cluster VII contained highest number of genotypes i.e. 27, it revealed second lowest Cluster mean for flag leaf area and second highest mean for harvest index also showed moderate means for remaining characters. Cluster III containing 16 genotypes exhibited lowest Cluster mean performance for harvest index and moderate Cluster mean for remaining characters. Cluster-VIII, containing 15 genotypes, exhibited highest Cluster mean for harvest index and test weight. While it showed lowest Cluster mean for spike length and showed moderate mean performance for remaining characters. Cluster-I comprising 11 genotypes was characterized by lowest Cluster means for flag leaf area and moderate Cluster means for remaining characters. The Cluster-IV containing 11 genotypes produced third highest Cluster means for 1000-grain weight besides possessing lowest mean for plant height. Remaining characters showed average means performance. Cluster-V, containing 11 genotypes emerged with second lowest Cluster means for plant height. Remaining characters showed average means performance. The Cluster-VI, containing 8 genotypes had second highest Clusters mean for flag leaf area. Cluster-X comprised of 6 germplasm lines, showed second highest Cluster means for days to 50% flowering and lowest Cluster means for test weight and third lowest for days to maturity, spike length and grain yield per

plant. Remaining characters possessed moderate means for rest of the characters. Cluster IX comprised of 5 genotypes showed highest Cluster mean for plant height, 1000-grain weight, grains yield per plant and biological yield per plant. Remaining characters possessed moderate means for rest of the characters. Cluster-II comprised 2 genotypes, showed highest Cluster means for spike length and second highest Cluster means for days to 50% flowering. Cluster-XI comprised 2 genotypes, showed highest Cluster means for days to 50% flowering, plant height and flag leaf area and second highest Cluster means for spike length and grain yield per plant. The above discussion clearly shows wide variation from one Cluster to another in respect of Cluster means for 9 characters, which indicated that genotypes having distinctly different mean performance for various characters were reported into different Clusters. Presence of substantial genetic diversity among the germplasm lines screened in the present study indicated that these materials may serve as good source for selecting the diverse parents for hybridization programme aimed at isolating desirable segregates for grain yield as well as the important characters. But the presence of genetic diversity in the genotypes does not imply that these genotypes will show geographic diversity (Shekhawat et al. 2001, Singh et al. 2006) [10, 11].

References

1. Alam AKMM, Begum M, Chaudhury MJA, Naher N, Gomes R. D^2 analysis in early maturity hull-less barley. International Journal of Sustainable Crop Production. 2007; 2(1):15-17.
2. Ali, Hasmat, Singh SK, Mishra CN, Daya Ram, Bharadwaj DN, Singh HL. Divergence analysis of exotic strains in barley (*Hordeum vulgare* L.). Asian journal of Bio Science. 2007; 2(1/2):66-68.
3. Beale EML. Euclidean Cluster analysis. A paper contributed to 37th session of International Statistical Institute, 1969.
4. Harlan JR. On the origin of barley. US Dept Agriculture Handbook. 1968; 338:9-31.
5. Federer WT. Augmented designs, "Hawain Planters", Record. 1956; 14:208-742.
6. Mahalanobis PC. On generalized distance in statistics. Proc. Natl. Inst. Sci. 1936; 2:49-55.
7. Mishra CN, Singh SK, Singh PC, Bhardwaj DN, Singh HL. Genetic variability in barley. International Journal of Plant Science, Muzaffarnagar. 2007; 3(2):220-221.
8. Harlan JR. On the origin of barley. US Dept Agriculture Handbook. 1968; 338:9-3.

9. Ramanujam S, Tiwari AS, Mehta RB. Genetic divergence and hybrid performance in mungbean. Theoretical and Applied Genetics. 1974; 45:211-4.
10. Shekhawat US, Prakash V, Singhania DL. Genetic divergence in barley (*Hordeum vulgare* L.). Indian Journal of Agricultural Research. 2001; 35:121-3.
11. Singh RV, Khedar OP, Prakash V, Singh NP. Genetic divergence in barley (*Hordeum vulgare* L.). Research on Crops. 2006; 7:165-6.
12. Spark DN. Euclidean cluster analysis. Algorithm. As. 58. Appl. Stats. 1973; 22:126-130.
13. Surma M, Adamski T, Bichonski A, Bilinski Z, Bystry Z, Jarosz P, *et al.* Genetic divergence of spring barley breeding lines. Biuletyn Instytutu Hodowli and Aklimatyzacji Roslin. 2005; 236(1):137-146.