Journal of Applied and Natural Science 8 (4): 2273-2277 (2016)

Genetic variability and divergence analysis for yield and yield contributing traits in released varieties of barley (*Hordeum vulgare* L.) under partially reclaimed saline sodic soil

Arun Kumar[3*], Baudh Bharti[4], Jaydev Kumar[2], P. N. Verma[2], J. P. Jaiswal[3], G. P. Singh[5] and S. R. Vishwakarma[1]

[1]Department of Genetics & Plant Breeding, Narendra Deva University of Agriculture & Technology, Faizabad-224229 (Uttar Pradesh), INDIA
[2]Department of Genetics & Plant Breeding, Chandra Shekhar Azad University of Agriculture & Technology, Kanpur-208002 (Uttar Pradesh), INDIA
[3]Department of Genetics & Plant Breeding, Govind Ballabh Pant University of Agriculture & Technology, Pantnagar-263145 (Uttarakhand), INDIA
[4]Department of Genetics & Plant Breeding, Maharana Pratap University of Agriculture & Technology, Udaipur-313001 (Rajasthan), INDIA
[5]ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001 (Haryana), INDIA
[*]Corresponding author. E-mail: arungangwar0581@gmail.com

Received: February 14, 2016; Revised received: September 8, 2016; Accepted: December 5, 2016

Abstract: Genetic variability is the back bone of crop improvement programme, effectiveness of selection depends upon nature and magnitude of genetic variability present in the genetic material. The aim of the present study was that to identify the potential genotypes performing well under partially reclaimed saline- sodic soil (pH 8.6-8.9, EC = 4-4.2 dSm^{-1}, ESP = > 15). Sixty four released varieties of barley collected from Directorate of Wheat Research, Karnal were grown during rabi season 2010-11, showing wide spectrum of variation for various characters. The characters studied were yield and yield contributing traits; namely plant height, days to maturity, fertile tillers / plant, length of main spike, grains per main spike, 1000-grains weight, grain yield per plant. The data on 7 characters was utilized for estimation of mean, range and least significant differences. The varieties RD-2552(8.52), HBL-276(8.35), RD-2592(8.17), PL-419(8.15), Kedar(8.11), PL-751(8.10), JB-58(8.06), K-508(7.96) produced higher grain yield per plant and showed high to very high mean performance for several other yield component also. These selected varieties can be used in breeding program and can be recommended direct cultivation under partially reclaimed saline-sodic soil.

Keywords: Barley (*Hordeum vulgare* L.), Genetic diversity, Quantitative characters

---

INTRODUCTION

Barley (Hordeum vulgare ssp. vulgare L.) is one of the major cereal grains, currently ranking fourth in world production behind maize, rice and wheat. In India, barley is generally cultivated in harsh environments like drought, cold, salinity/alkalinity and marginal lands. It is cultivated on about 0.695 mha area with production of 1.74 mt tonnes and productivity of 2508 kg/ha (Kumar et al., 2014). Barley is rather well-tolerant to drought, salinity and other dehydrative stresses. Germplasm serves as valuable natural reservoir in providing needed attributes, for developing successful varieties (Hawkes, 1981). The first archaeobotanical material of barley was two rowed barley which closely resemble with some races of wild barley, i.e., Hordeum spontaneum .This wild species crosses readily with cultivated barley and its progenitor species of H. vulgare L (H. Helback, 1966; R.J. Harlon, 1975). Proper management and channelization of genetic variability is the key factor in crop improvement. An efficient breeder always tries to get genetic transmissibility from parent to off-spring and for real genetic gain (I.J. Johnson and H.K. Hayes, 1955). Archaeologists also support the two-row species as progenitor of six-rowed barley (Hordeum vulgare L.). Hordeum vulgare is the only cultivated species which has two distinct phenotype form, viz., two-rowed and six rowed type based on ear morphology. Initially these two forms were classified as two separate but now these have been grouped into the single species H vulgare L. These two have same chromosome number, intercross freely and produce fertile hybrids (J.M. Poelman, 1987). There is a recognized need to reliably distinguish varieties of crop plants and establish their purity as a prerequisite for any breeding programme

(Russel *et al*., 1997; Matus *et al*., 2002). Assessment of the extent of genetic variability within cultivated crop has important consequences in plant breeding and conservation of genetic resources (Petersen *et al*., 1994). The systematic evaluation of the molecular diversity encompassed in barley genetic resources is a prerequisite for its efficient exploitation in breeding as well as for development of the strategies for optimal conservation of genetic diversity (Malysheva *et al*., 2006). Different studies have shown that barley surpassed other cereal crops in the content of B-glucon, total dietary and soluble fibre, beneficial in treating hyper cholesteralemia (Anderson *et al*., 1990). Keeping the view of importance of barley crop in different purposes, the study was conducted to identify the best genotype for cultivation under partially reclaimed saline- sodic soil, by this way we can increase the production of barley crop in particular area.

MATERIALS AND METHODS

The experimental materials for investigation was comprised of 64 released varieties of barley collected from Directorate of Wheat Research, Karnal were grown under partially reclaimed saline- sodic soil (pH 8.6-8.9, EC = 4-4.2 dSm^{-1}, ESP = > 15). The said 64 varieties were evaluated in a Simple Lattice Design with two replications. Each plot consists of three rows, each of three meter long with spacing of 23 cm. The plants within a row were spaced approximately 10 cm apart. The eight contiguous plots collectively constituted one tier. Thus there were eight tiers each of eight plots in a replication. The varieties were allocated randomly in each replication. The recommended cultural practices were adopted to grow a good crop. Data were recorded on five randomly selected competitive plants from each plot on 7 quantitative characters namely, plant height (cm), days to maturity, number of fertile tillers^{-1}, length of main spike (cm), grains per main spike, 1000-grain weight (g), grain yield plant^{-1} (g). Data recorded on the above characters were subjected to Non-hierarchical Euclidean cluster analysis (Beal, 1969 and Sparke, 1973).

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences among varieties for all the traits studied, indicating the presence of sufficient diversity in the material under study. This suggested that adequate scope is available for use in a program aimed at enhancing genetic yield potential of barley under saline sodic soil condition. Significant differences among varieties for grain yield and related traits in different sets of material were also reported earlier by (Chaitali and Mishra *et al.,* 2007; Pal *et al.,* 2009) which revealed that selection was effective for a population with broad genetic variability.

Statistical analysis: The results of the analysis of variance for Simple Lattice Design (Cochran and Cox 1957) in respect of 7 characters are presented in (Table 1). The variation due to replication was highly significant for plant height, days to maturity, fertile tillers per plant, and length of main spike, grains per main spike, 1000-grain weight and grain yield per plant. The variation due to treatment were found to be highly significant for plant height, days to maturity, length of main spike, grains per main spike, and significant for grain yield per plant, but non-significant for remaining two characters viz. fertile tillers per plant, 1000-grain weight.

Genetic divergence analysis for seven characters in the varieties of barley: The Non-hierarchical Euclidean cluster analysis (Beale, 1969; Spark, 1973) was employed to study the genetic divergence existing among 64 released varieties of barley on the basis of 7 quantitative characters. The varieties were accepted to be grouped in to 8 non-overlapping clusters. Cluster VIII emerged with highest number of entries as it was constituted by 12 entries followed by cluster II having 11 varieties. Cluster III had 10 varieties, and Cluster V and I possessed 7 varieties each. Cluster IV and VII possessed 6 varieties each. Cluster VI possessed 5 varieties. The estimates of intra-and inter-cluster distances for 8 clusters are presented in (Table 3). The highest intra-cluster distance was observed in case of cluster I (8.124), followed by cluster III (7.316). The lowest intra-cluster value was noted for cluster IV (5.320), followed by cluster VIII (5.700). The maximum inter-cluster distance was observed between cluster I and VI (33.142) followed by cluster I and V (28.858). The minimum inter-cluster distance was observed between cluster IV and V (8.675) fallowed by cluster V and VI (9.627). The cluster means for 7 characters are present-

Table 1. Analysis of variance of Simple Lattice Design for 7 characters in released varieties of barley.

S. No.	Characters	Source of variation		
		Replication	**Treatments**	**Error**
	Degree of freedom (d. f.)	1	63	63
1	Plant height (cm)	214.78**	113.01**	2.46
2	Days to maturity	76.57**	6.09**	0.74
3	No. of fertile tillers per plant	13.78**	0.52	0.93
4	Length of main spike (cm)	15.46**	0.80**	0.30
5	No. of grains per main spike	250.32**	10.75**	5.00
6	1000-grain weight (g)	298.62**	6.02	4.70
7	Grain yield per plant (g)	21.73**	0.99*	0.64

*Significant at 5 % probability level; ** Significant at 1 % probability level.

Table 2. Clustering patterns of 64 released varieties of barley on the basis of Non-hierarchical Euclidean cluster analysis.

Cluster No.	No. of Varieties	Varieties
I	7	Clipper,JB-58,BH-75,DWRUB-52,Sonu,PL-426,Ratna
II	11	Jyoti,K-603,Manjula,DWR-73,Lakhan,NB-1,BG-101,PL-56,RD-2552,BHS-380,DWR-28
III	10	K-141,HBL-316,Karan-16,K-560,BH-169,DL-88,BHS-46,PL-751,PL-419,RD-2660
IV	6	Amber,RD-2503,RD-2668,BH-902,RD-2508,RD-2715
V	7	RD-31,BCU-73,Gitanjali,RD-2624,Alfa-93,PL-172,NB-2
VI	5	RS-6,NDB-1173,Bilara-2,UPB-1008,Jagrity
VII	6	RDB-1,RD-2592,Kedar,Azad,VLB-1,NB-3
VIII	12	Vijay,BHS-352,K-508,Dolma,VLB-56,RD-2035,HBL-276,K-409,K-551,Himani,BH-393,RD 2052

Table 3. Estimates of average intra-and inter-cluster distances for the 8 clusters of released varieties of barley.

Cluster no.	I	II	III	IV	V	VI	VII	VIII
I	8.124	10.079	13.200	27.752	28.858	33.142	21.310	12.550
II		5.833	11.144	18.661	20.995	24.948	17.991	11.228
III			7.316	17.769	17.769	17.197	16.321	11.389
IV				5.320	8.675	10.179	10.648	11.587
V					5.892	9.627	11.815	11.458
VI						5.963	10.805	16.038
VII							5.785	9.767
VIII								5.700

Table 4. Cluster means for different characters of released varieties of barley.

Cluster number	Plant height (cm)	Days to maturity	No. of fertile tillers/ plant	Length of main spike (cm)	No. of grains per main spike	1000-grain weight (g)	Grain yield/ plant (g)
I	59.198	115.427	4.283	7.118*	31.062*	35.693*	6.120*
II	58.400*	112.995*	4.225	7.456	32.723	37.083	6.632
III	62.587	115.905	3.646*	7.862	33.173	38.126	6.544
IV	78.346**	114.085	4.587	8.200	35.508	39.439	7.381
V	69.882	115.925	4.713	8.313	34.104	40.499**	7.979**
VI	70.821	116.693**	4.194	8.637**	37.841**	39.373	7.717
VII	69.116	116.412	5.003**	8.427	36.121	37.486	6.828
VIII	68.741	115.800	4.632	7.804	32.223	37.258	7.129

** Highest Mean Value; * Lowest Mean Value

ed in (Table 4). The highest cluster mean for plant height was recorded in case of cluster IV (78.34 cm) followed by cluster VI (70.82cm). The lowest cluster mean for plant height was found in case of cluster II (58.40 cm), followed by cluster I (59.19 cm), while remaining clusters had moderate means for plant height. The varieties of cluster VI was responsible for highest cluster mean for days to maturity (116.69 days), followed by entries of cluster VII (116.41 days). The varieties with early maturity were concentrated in cluster VII (112.99 days), followed by cluster I (114.08days).The highest and lowest cluster means for fertile tillers per plant were observed for cluster VII (5.00) and cluster III (3.64), respectively. The second highest and second lowest means for fertile tillers per plant were recorded for cluster V (4.71) and VI (4.19), respectively. The varieties occurring in cluster VI (8.63 cm), followed by cluster VII (8.42) higher cluster mean for length of main spike. The lowest mean for length of main spike was exhibited by cluster I (7.11 cm), followed by cluster II (7.45 cm).The highest cluster mean for grains per spike was recorded for cluster VI (37.84), followed by cluster VII (36.12). Cluster I (31.06), followed by cluster VIII (32.22) exhibited lowest cluster mean for this trait. The remaining clusters were characterized by moderate means for grains per spike. The varieties of cluster V (40.49g) were responsible for highest cluster mean for 1000-grain weight, followed by the varieties cluster IV (39.43g). Cluster I resulted in lowest cluster mean for 1000-grain weight (35.69g), followed by the varieties of cluster II (37.08g). The highest cluster mean for grain yield per plant was observed in case of cluster V (7.97g) which indicated that lines having higher grain yield were concentrated in this cluster. The cluster means for grain yield were also of higher order in case of cluster VI (7.71g). The varieties with very low grain yield were found to be grouped in cluster I (6.12g) followed by cluster III (6.54g). Cluster analysis through a dendrogram showed a high adjustment with a genetic dissimilarity matrix verified by the high (r= 0.88) and significant ($p \leq 0.001$) cophenetic correlation coefficient, be-

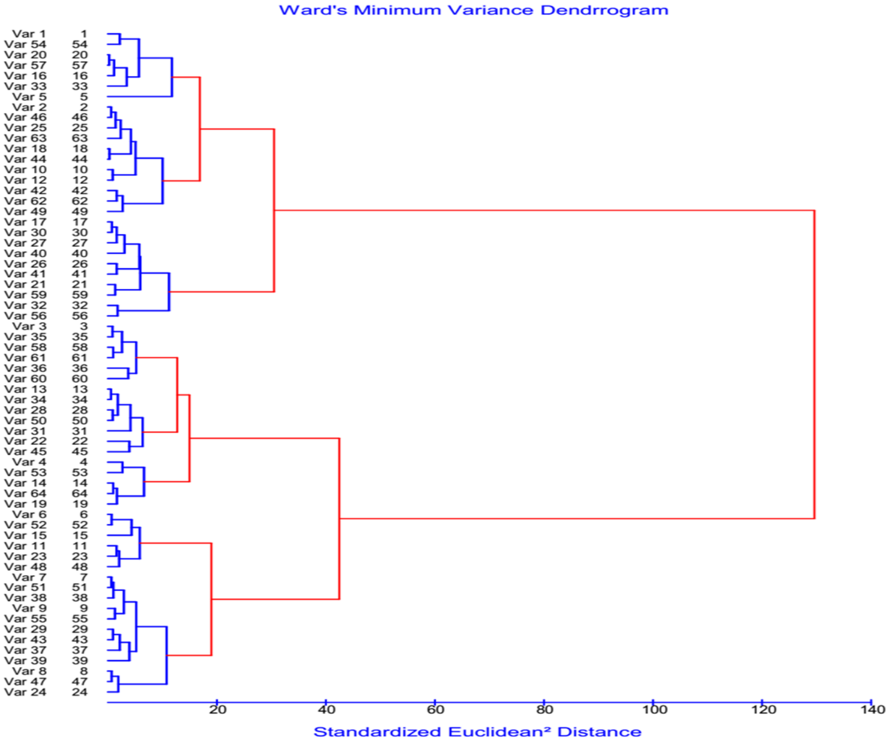

Fig. 1. *Clustering for sixty four released varieties of barley for seven characters.*

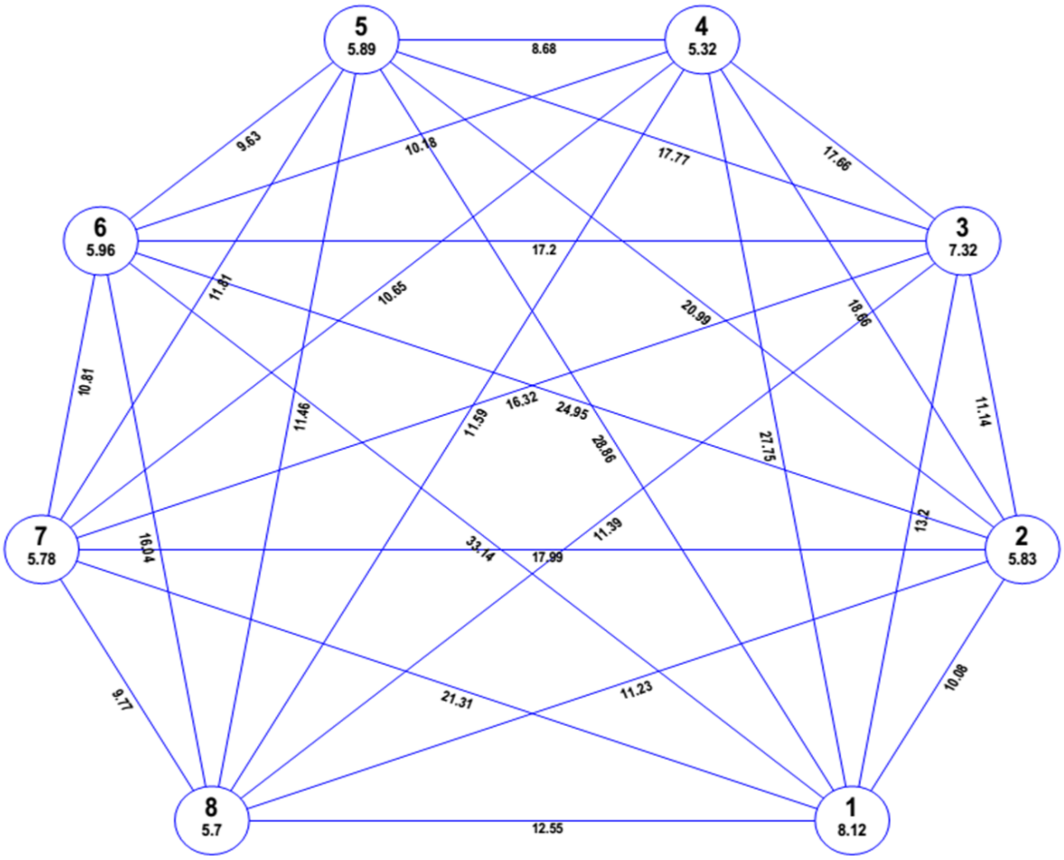

Fig. 2. *Intra and Inter-cluster distance (D) for sixty four released varieties of barley for seven characters.*

ing higher than the value (0.70) proposed by Rohlf (2000). Based on the genetic distance among the accessions of different clusters, the contrasting parents might be selected and used in a hybridization programme for a greater variability concerning the malting quality, as recommended by Sarkar *et al.* (2008). Cultivars may have a common place of development, but breeders may have used different selection criteria using diverse germplasm derived originally from widely separated geographical regions. This may be the reason of no relationship between genetic diversity and place of origin of the genotypes could be ascertained. Manjunatha *et al.* (2007) studied barley landraces from Uttarakhand Himalaya of India for different morphological traits as well as on yield components.

Conclusion

The highest intra-cluster distance was observed in case of cluster I followed by cluster III and the highest inter -cluster distance was observed between cluster I and VI followed by cluster I and V may also be fruitful for obtaining desirable recombinants in segregating generations. The lowest inter-cluster distance values observed between clusters-IV and V followed by cluster-V and VI, indicated that the members of these cluster pairs were genetically close to each other. The study showed wide variation from one cluster to another in respect of cluster means for 7 characters, which indicated that varieties having distinctly different mean performance for various characters were reported into different clusters. In breeding program the crossing between the entries belonging to cluster pairs having large inter-cluster distances and possessing high cluster means for one or other characters to be improved may be recommended for isolating desirable recombinants in the segregating generation in barley. The varieties RD-2552(8.52), HBL-276(8.35), RD-2592(8.17), PL-419(8.15), Kedar (8.11), PL-751(8.10), JB-58(8.06), and K-508 (7.96) produced higher grain yield per plant under partially reclaimed saline- sodic soil (pH 8.6-8.9, EC = 4-4.2 dSm^{-1}, ESP = > 15). These selected varieties can be recommended direct cultivation under partially reclaimed saline- sodic soil. Based on distance between genotypes of different clusters, contrasting parents may be selected and used in the hybridization programme for generation of wider variability. The present investigation provides useful information about the genetic diversity in the in Indian varieties as some of these varieties could be used in the future breeding programme.

ACKNOWLEDGEMENTS

This research work was supported by Directorate of Wheat Research Karnal. The authors thank to Project Director, Directorate of Wheat Research Karnal, for provide experimental material, valuable help and support.

REFERENCES

Anderson, J.W., Deakine, D.A., Floore, T.L. Smith, B.M. and White, S.E. (1990). Dietary fibre and coronary heart disease. *Critical Reviews in Food Science and Nutrition,* 29: 95-147

Beal, E.M.L. (1969). Euclidean cluster analysis. A paper contributed to 37th session of the International Statistical Institute.

Chaitali, S. and Bini, T. (2007). Variability, character association and component analysis in wheat (*T. aestivum* L.). *Crop Research*, Hisar), 34 (1-3): 166-170

Cochran, W.G. and Cox. G.M. (1957). Experimental designs. Bombay, Asia.

Harlon, R.J. (1975). Crops and Man, Madison, Wis : American Society of Agronomy and Crop Sciences, Society of America, pp. 295.

Hawkes, J.G. (1981). Germplasm collection, preservation and use. In: Plant Breeding II ed., K.J. Frey-lowa State Univ. Press, lowa, pp.57-84

Helback, H. (1966). Commentary on the Polygenesis of *Triticum* and *Hordeum*. *Econ. Bot.,* 20: 350-360

Johnson, I.J. and Hayes, H.K. (1955). The value in hybrid combination of inbred lines of corn selected from single crosses by the pedigree method of breeding. *J. Amer. Soci. Agron*., 39: 479-485

Kumar, V., Khippal, A., Singh, J., Selvakumar, R., Malik, R., Kumar, D., Kharub, A.S., Verma, R.P.S. and Sharma, I. (2014). Barley research in India: retrospect and prospects. *Journal of Wheat Research* 6(1): 1–20

Malysheva-Otto L.V., Ganal M.W. and Roder M.S. (2006) Analysis of molecular diversity, population structure and linkage disequilibrium in a worldwide survey of cultivated barley germplasm (Hordeum vulgare L). *BMC Genet*. 7, 6

Manjunatha, T., Bisht, I.S., Bhat, K.V. and Singh, B.P. (2007). Genetic diversity in barley (Hordeum vulgare L. ssp vulgare) landraces from Uttaranchal Himalaya of India. *Genetic Resources and Crop Evolution*, 54: 55–65

Matus I.A. and Hayes P.M. (2002). Genetic diversity in three groups of barley germplasm assessed by simple sequence repeats. *Genome*, 45: 1095–1106

Mishra, C.N., Singh, S.K., Singh P.C., Bhardwaj, D.N. and Singh, H.L. (2007). Genetic variability in barley. *International Journal of Plant Science*, 3(2): 220-221

Pal, D., Kumar, S. and Rana, J.C. (2009). Collection and characterization of wheat germplasm from North-West Himalaya. *Journal of Plant Genetic Resources*, 20(2): 170-173

Petersen, L., Ostergard, H. and Giese, H. (1994). Genetic diversity among wild and cultivated barley as revealed by RFLP. *Theor. Appl. Genet.* 89: 676–681

Poelman, J.M. (1987). Breeding Field Crops. 378-420. AVI Pub. Co. Inc. Westport, Connecticut.

Rohlf, F.J. (2000) NTSYS-pc: Numerical Taxonomy and Multivariate Analysis System, version 2.1, New York.

Russel J., Fuller, J., Young, G., Thomas, B., Taramino, G., Macaulay, M., Waugh, R. and Powell, (1997). Discriminating between barley genotypes using microsatellite markers. *Genome*, 40: 442–450

Sarkar, B., Verma, R.P.S. and Mishra, B. (2008). Genetic diversity for malting quality in barley (Hordeum vulgare L.), *Indian J. Agric. Sci*., 68: 163–170

Sparke, D.N. (1973). Euclidean cluster analysis. Algorithm As.58. *Applied Statistics*, 22: 126-136