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# GENETIC DIVERGENCE IN BARLEY

**Mritunjay Singh, S.R. Vishwakarma and Amrendra Pratap Singh**

*Dept. of Genetics and Plant Breeding, N.D. Univ. of Agric. and Tech. Kumarganj, Faizabad-224 229 (U.P.)*

*E-mail: singhmritunjay706@gmail.com*

## ABSTRACT

**The experiment was conducted with 108 elite Barley genotypes for study the diversity among the genotypes, which were grouped into 11 clusters revealing the presence of considerable amount of genetic diversity in the materials. Cluster V had the maximum number of 22 genotypes followed by cluster-X, cluster-IX and cluster III which have 16,14,11 genotypes, respectively. The highest intra-cluster value was found for cluster-XI (109.85), followed by cluster-IX (97.19). The maximum inter-cluster distance was recorded between cluster-VI and VIII (1939.04) followed by cluster-V and VIII (1843.79). Which indicate that the genotypes included these clusters will give high heterotic response and thus better segregants.**

***Key words :*** *Barley, $D^2$ statistic, Genetic Divergence, Intra and Inter Cluster distance.*

Barley (*Hordeum vulgare*; 2*n* = 14, Poaceae family) is an important rabi cereal and ranked fourth after wheat, rice and maize. Barley a high energy, nutritionally and environmentally safe crop, has potential to produce satisfactory yield under problematic soils qualitatively and quantitatively both. It is hardy crop able to produce reliable harvest in area with poor rainfall and poor soils. Barley being very versatile, it is used in major staple food for millions of people in developing countries. It is a key animals feed in dry areas and principal ingredient in beer, many beverages and health tonics. Barley is better option for poor farmer to cope with the climate change, land degradation and desertification. Barley florish well under less resources of irrigation and fertilizers. Thus, this crop has great elasticity of adaptation under various stress situation. The production of Barley has been on a decline due to non availability of early maturity, high yielding, input-responsive varieties, resistant/tolerant to various biotic and abiotic stresses and their suitability in prevailing crop rotation. The choice of potential genetically diverse parents for use in hybridization programme is based on the hypothesis that crosses involving divergent parents offer greater possibility of obtaining desirable segregents in the segregating generation. The clustering of parents based on genetic diversity is a pre-requisite for a successful hybrid breeding program. The use of diverse parents gives better opportunities to a breeder for selection and development of superior varieties.

## MATERIALS AND METHODS

The 105 varieties /strains of barley including elite lines and land races with three popular varieties check viz., NDB-1173, AZAD and RD-2552, were evaluated. These germplasm lines were procured from Coordinated unit of Barley Department of Genetics and Plant Breeding, N.D. University of Agriculture and Technology, Kumarganj, Faizabad. The experimental material was evaluated at Genetics and Plant Breeding Research Farm of Narendra Deva University of Agriculture and Technology, Narendra Nagar Kumarganj, Faizabad (U.P.) in Augmented Block Design during Rabi, 2009-10. The experimental field was divided into 5 blocks of equal size. Twenty four entries including checks were accommodated in each block. Each plot consisted of a single row of 4m length the inter and intra –row spacing was 25 cm and 10 cm, respectively. To avoid the border effect the experimental plot was surrounded on all side by non experimental rows. Recommended cultural practices were followed to raise a good crop.

## RESULTS AND DISCUSSION

The Non-hierarchical Euclidean cluster analysis was employed to study the genetic divergence existing among 108 barley germplasm collections on the basis of 10 quantitative characters. The pseudo F-test revealed that 11 cluster arrangement was most appropriate for grouping the 108 genotypes. Therefore,

**Table-1:** Clustering pattern of 105 barley genotypes on the basis of Non-hierarchical Euclidean cluster analysis of ten characters.

| Cluster No. | No. of genotypes | Genotypes |
|---|---|---|
| I | 9 | IBON-HI-19,IBON-MRA-52, NDB-1484, NDB-1491, IBON-HI-24, ISEBON-128, NDB-1497, IBON-HI-14, IBON-HI-5 |
| II | 4 | IBSC-GP-25, IBON-MRA-67, IBON-MRA-101, IBON-MRA-69 |
| III | 11 | IBON-HI-125, NDB-1496, IBONHI-156, IBYT-LRA-C-5, NDB-1478, IBON-HI-26, ISEBON-34, IBCB-S-116, ISEBON-24, HBSN-92, IBON-HI-97 |
| IV | 5 | IBONHI-128, IBONHI-159, NDB-1492, IBYT-LRA-C-2, INBON-46 |
| V | 22 | IBON-HI-93, ISEBON-72, IBON-HI-117, IBCB-S-41, INBON-24, IBON-HI-107, IBON-LRA-C-10, INBON-29, IBON-HI-98, IBON-HI-112, IBYT-MRA-16, IBON-HI-124, IBCB-S-45, IBYT-LRA-C-25, IBYT-LRA-C-8, IBYT-LRA-M-9, IBON-HI-107, IBYT-MRA-6, IBYT-LRA-C-18, INBON-71, IBYT-LRA-C-3, IBYT-MRA-24 |
| VI | 5 | INBON-101, IBCB-S-2, IBCB-S-39, IBSTR-GP-26, IBYT-MRA-20 |
| VII | 11 | IBON-HI-21, NDB-1173, HBSN-100, NDB-1498, NDB-1173, IBON-HI-52, IBON-HI-31, NDB-1488, IBON-HI-15, RD-2552, IBON-HI-27 |
| VIII | 4 | IBYT-MRA-22, NDB-1490, ISEBON-43, INBON-118 |
| IX | 14 | IBON-HI-32, IBCB-S-128, IBYT-LRA-M-7, ISEBON-11, HSBN-9657, HSBN-43, IBON-HI-33 IBON-HI-76, NDB-1482, ISEBON-45, IBON-HI-161, INBON-108, IBCB-S-101, IBCB-S-114 |
| X | 16 | IBYT-LRA-M-20, INBON-106, ISEBON-35, NDB-1493, NDB-1497, NDB-1485, NDB-1489, Azad, NDB-1494, HSBN-9650, ISBON-11, ISEBON-37, INBON-1116, IBCB-S-25, ASBN-9715 INBON-131 |
| XI | 7 | IBCB-S-2, IBCB-S-31, IBCB-S-78, HSBN-41, IBLS-GP-13, IBON-MRA-56, IBYT-LRA-C-16 |

**Table-2:** Estimates of average intra-and inter-cluster distances for the 11 clusters in exotic and indigenous lines of barley.

| Cluster no. | I | II | III | IV | V | VI | VII | VIII | IX | X | XI |
|---|---|---|---|---|---|---|---|---|---|---|---|
| I | 88.890 | 168.348 | 159.504 | 372.982 | 489.010 | 819.347 | 477.611 | 932.522 | 364.205 | 444.648 | 419.764 |
| II | | 67.585 | 245.343 | 327.221 | 411.634 | 558.730 | 701.852 | 1044.510 | 414.101 | 451.739 | 249.267 |
| III | | | 86.631 | 179.919 | 362.121 | 584.067 | 437.256 | 786.733 | 246.905 | 435.781 | 320.225 |
| IV | | | | 57.462 | 228.989 | 291.991 | 752.006 | 992.414 | 349.522 | 578.46 | 255.381 |
| V | | | | | 83.266 | 194.988 | 1353.790 | 1843.798 | 842.514 | 1156.068 | 614.684 |
| VI | | | | | | 81.914 | 1648.803 | 1939.046 | 963.497 | 1300.282 | 578.112 |
| VII | | | | | | | 71.062 | 191.630 | 200.623 | 220.509 | 572.533 |
| VIII | | | | | | | | 28.459 | 277.894 | 246.615 | 618.887 |
| IX | | | | | | | | | 97.190 | 165.109 | 232.838 |
| X | | | | | | | | | | 96.704 | 280.38 |
| XI | | | | | | | | | | | 109.855 |

**Table-3:** Cluster means for different characters in exotic and indigenous lines of barley.

| Cluster number | Days to 50% flowering | Plant height (cm) | Effective tiller per plant | Days to maturity | Ear length (cm) | Grains per spike | 1000-grain weight (g) | Biological yield/plant (g) | Grain yield plant/(g) | Harvest index (%) |
|---|---|---|---|---|---|---|---|---|---|---|
| I | 84.34 | 76.43* | 4.57 | 128.47 | 7.36 | 51.68 | 36.43 | 20.47 | 7.44 | 36.32 |
| II | 95.60 | 79.45 | 3.86* | 129.48 | 8.20 | 54.16 | 37.27 | 17.95 | 6.36 | 36.08 |
| III | 85.11 | 82.24 | 6.48 | 129.40 | 6.96 | 41.06 | 36.51 | 23.85 | 8.08 | 33.83 |
| IV | 88.33 | 92.88 | 6.48 | 130.46 | 7.40 | 31.12 | 35.36 | 20.93 | 7.00 | 33.04 |
| V | 90.03 | 81.45 | 5.29 | 130.88 | 6.10 | 28.07 | 35.41 | 17.31* | 5.24* | 30.38* |
| VI | 99.80** | 86.12 | 5.94 | 135.66** | 5.92* | 25.55* | 35.63 | 18.24 | 5.53 | 30.56 |
| VII | 81.79* | 87.82 | 6.32 | 127.18* | 7.95 | 54.09 | 37.13 | 30.03 | 11.78 | 39.28** |
| VIII | 87.60 | 97.89** | 6.82** | 130.06 | 9.05** | 55.93 | 37.74 | 33.24** | 12.99** | 39.21 |
| IX | 88.26 | 90.03 | 6.17 | 130.71 | 8.00 | 50.13 | 36.68 | 28.82 | 9.91 | 34.62 |
| X | 88.27 | 93.53 | 5.11 | 129.82 | 8.92 | 59.88** | 37.16 | 24.60 | 9.52 | 38.59 |
| XI | 96.60 | 92.41 | 5.10 | 133.30 | 7.86 | 50.22 | 36.78 | 22.46 | 7.86 | 35.27 |

** Highest Mean Value.

the 108 genotypes were accepted to be grouped in to 11 non-overlapping clusters. The distribution of 108 barley lines in seven clusters is presented in Table-1. Cluster V emerged with highest number of entries as it was constituted by 22 entries followed by cluster X having 16 genotypes. Cluster IX had 14 genotypes. Cluster III and VII possessed 11 genotypes each. While Cluster I containing 9 genotypes and Cluster XI had 7 genotypes. Cluster IV and VI possessed 5 genotypes each, while cluster II and VIII had 4 number of entries.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 XI (109.85), followed by cluster IX (97.19). The lowest intra-cluster value was noted for cluster VIII (28.45), followed by cluster IV (57.46). The maximum inter-cluster distance was observed between cluster VI and VIII (1939.04), fallowed by cluster V and VIII (1843.79). The minimum inter-cluster distance was observed between cluster I and III (159.50) fallowed by cluster IX and X (165.10). The cluster means for 10 characters are presented in Table-3. The highest cluster mean for days to 50% flowering was recorded for cluster VI (99.80), followed by cluster XI (96.60). The lowest cluster mean for days to 50% flowering was found in case of cluster I (84.34), followed by cluster III (85.11) while remaining cluster had moderate means for days to 50% flowering. The highest cluster mean for plant height was recorded in case of cluster VIII (97.89 cm) followed by cluster X (93.53cm). The lowest cluster mean for plant height was found in case of cluster I (76.43 cm), followed by cluster II (79.45 cm), while remaining clusters had moderate means for plant height. The highest and lowest cluster means for tillers per plant were observed for cluster VIII (6.82) and cluster IV (3.86), respectively. The second highest and second lowest means for tillers per plant were recorded for cluster III and IV (6.48) and cluster I (4.57), respectively. The genotype of cluster VI was responsible for highest cluster mean for days to maturity (135.66 days), followed by entries of cluster XI (133.30 days). The genotypes with early maturity were concentrated in cluster VII (127.18 days), followed by cluster I (128.47days).The genotypes occurring in cluster VIII (9.05cm), followed by cluster X (8.92) higher cluster mean for ear length. The lowest mean for ear length was exhibited by cluster VI (5.92 cm), followed by cluster V (6.10 cm).The highest cluster mean for grains per spike was recorded for cluster X (59.88), followed by cluster VIII (55.93). Cluster VI (25.55), followed by cluster V (28.07) exhibited lowest cluster mean for this trait. The remaining seven clusters were characterized by moderate means for grains per spike. The genotypes of cluster VIII (37.74g) were responsible for highest cluster mean for 1000-grain weight, followed by the genotypes cluster II (37.27g). Cluster IV resulted in lowest cluster mean for 1000-grain weight (35.36g), followed by the genotypes of cluster V (35.41g). Cluster VIII (33.24g), followed by cluster VII (30.03g) 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 (17.31g).The highest cluster mean for grain yield per plant was observed in case of cluster VIII (12.99g) 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 VII (11.78g). The genotypes with very low grain yield were found to be grouped in cluster V (5.24g) followed by cluster VI (5.53g). The highest cluster mean for harvest-index was observed in case of cluster VII (39.28%), followed by cluster VIII (39.21%). The lowest mean for harvest-index was exhibited by cluster V (30.38%), followed by cluster VI (30.56%). Remaining seven clusters were characterized by moderate means for harvest-index.

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