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Suman Devi

Department of Genetics & Plant
Breeding, CCS Haryana
Agricultural University, Hisar,
Haryana, India

Yogender Kumar

Department of Genetics & Plant
Breeding, CCS Haryana
Agricultural University, Hisar,
Haryana, India

Vikram Singh

Department of Genetics & Plant
Breeding, CCS Haryana
Agricultural University, Hisar,
Haryana, India

Rakesh Kumar

Department of Genetics & Plant
Breeding, CCS Haryana
Agricultural University, Hisar,
Haryana, India

Paras

Department of Genetics & Plant
Breeding, CCS Haryana
Agricultural University, Hisar,
Haryana, India

Corresponding Author:**Suman Devi**

Department of Genetics & Plant
Breeding, CCS Haryana
Agricultural University, Hisar,
Haryana, India

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Estimation of genetic divergence in barley (Two-rowed and six-rowed) under different growing conditions

Suman Devi, Yogender Kumar, Vikram Singh, Rakesh Kumar and Paras

Abstract

Genetic diversity among 50 barley genotypes was investigated using 18 different agro-morphological and seed vigour traits under timely and late growing conditions. The Euclidean cluster analysis assigned 50 barley genotypes into eight distinct clusters indicating presence of substantial genetic diversity in the evaluated breeding material. The average inter-cluster distance was found to be maximum between the cluster VIII and V (11.207) under timely and between cluster VI and IV (8.167) under late sown condition. The improvement in barley could be achieved through the use of genotypes assigned in clusters I and VII under timely sown, whereas the genotypes which contained in cluster II and VI might be considered as potential parents under late sown to obtain high heterotic response. Under timely sown condition, cluster I comprised of six genotypes, exhibited minimum number of days to heading and maturity, moderate plant height and number of tillers per meter and had highest cluster means for number of grains per spike, grain yield per plot and harvest index. Cluster IV comprised of seven genotypes, also had high cluster means for number of tillers per meter, number of grains per spike, grain yield per plot and harvest index. Similarly, under late sown condition, cluster II which comprised of two genotypes had low cluster mean for days to heading; moderate for plant height; high for number of tillers per meter, 1000 grain weight and biological yield per plot; and highest for grain yield per plot as well as harvest index. Cluster VI, contained five genotypes recorded for minimum number of days to heading; shortest plant height; high number of tillers per meter; highest 1000 grain weight along with high mean values for grain yield per plot and harvest index. Number of grains per spike, electrical conductivity and days to maturity under timely sown and days to heading, number of grains per spike and accelerated ageing (72 h) under late sown contributed maximum towards divergence. The contribution of various characters towards the expression of genetic divergence should be taken into consideration as a criterion for choosing parents for crossing programme for the improvement in such characters.

Keywords: Barley, seed vigour, cluster, genetic divergence

Introduction

Barley (*Hordeum vulgare* L.) is one of the oldest domesticated crops. It was domesticated about 10,000 years ago from its two rowed wild ancestor (*Hordeum vulgare* ssp. *spontaneum*) in the region of the Middle East known as the Fertile Crescent (Badr *et al.*, 2000) [4]. The cultivated barley (*Hordeum vulgare* ssp. *vulgare*) is a diploid with $2n=2x=14$ chromosomes. *Hordeum vulgare* is the only cultivated species which has two distinct phenotype form, viz., two-rowed and six rowed type based on ear morphology. These two have same chromosome number, intercross freely and produce fertile hybrids. It is frequently described as cosmopolitan crop which can be grown over diverse range of environments such as irrigated, rainfed, saline/alkaline soil, drought prone areas, marginal lands, diara lands, hill regions etc. Input requirements of the crop are very low while its adaptability is better under adverse environments in comparison to other cereals. Barley is mainly used for two purpose, feed for animals and malt for industrial uses. It has enormous potential as quality cereal especially for nutrition and medicinal point of view. Barley is one of the originator crops of old world agriculture and one of the first domesticated cereals. Barley rank fourth in world cereal production and used in order of importance; animal feed, brewing malt and human food. It became as a flourishing crop, because of its short life cycle and morphological, physiological, and genetic characteristics. Due to very low gluten, it is easily digestible as compared to wheat. Now Barley is key constituent for beer and wine industry. Barley contains eight essential amino acids. As compared to wheat, Barley foods are beneficial in various ways and

it also known as diuretics, emollient used in case of pancreas and other gastric problems. Most barley ingredients are whole grain, low fat and high in fiber, which make them model choices for individuals. The beta glucan or soluble fiber content of barley products provides low deposition of cholesterol property similar to oats. 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)^[19, 13].

Assessment of the extent of genetic variability within cultivated crop has important consequences in plant breeding and conservation of genetic resources. Genetic diversity among and within plant species is on the verge of being reduced now. In wild species genetic diversity may be lost because of severe decline in population size, whereas in cultivated crops genetic array may be lost because of the limited genetic base in various breeding programmes (Cao *et al.*, 1998)^[5]. Study the genetic diversity is the process that analyzes the variation among genotypes by a specific method or a combination of methods (Ibrahim *et al.*, 2011)^[11]. There are different criteria for the estimation of genetic diversity: pedigree records, morphological traits, biochemical markers and molecular markers. Based on morphological traits and pedigree information diversity in barley breeding programme was deliberated by Moralejo *et al.* (1994)^[15], Schut *et al.* (1997)^[20], Papa *et al.* (1998)^[17], Abebe *et al.* (2008)^[11] Chand *et al.* (2008)^[6]. They showed that Grain yield is an ultimate product of the action and interaction of number of components such as number of tillers, number of grains per spike, 1000-grain weight, plant height, harvest index and etc. D2 analysis is the most important statistical tool to identify diverse genotypes for hybridization programme in order to exploit the heterosis and to isolate desirable sergeants. Keeping the view of importance of barley crop in different purposes, the study was conducted to identify the best genotype for cultivation under normal and late sown conditions, by this way we can increase the production of barley crop in the particular area.

Materials and Methods

50 barley genotypes including 17 two-rowed and 33 six-rowed types were evaluated in randomized block design with three replications under two different environments i.e. timely and late sown under irrigated conditions during Rabi 2016-17. Each genotype was grown in three rows with a plot size of 3.0 x 0.69 m² and for good crop the recommended cultural practices were adopted. Five competitive random plants from the middle rows of the experimental plots were taken for recording the observations on plant height (cm), spike length (cm), number of tillers per meter row, number of grains per spike, 1000 grain weight (g). Characters like days to heading, days to maturity, biological yield and grain yield were observed on plot basis. Eight seed parameters viz; seedling length (cm), seed density (g/cc), standard germination (%), seedling dry weight (mg), vigour index I, vigour index II, electrical conductivity ($\mu\text{S}/\text{cm}/\text{seed}$) and accelerated ageing at 48 and 72 hours were also recorded to detect the vigour potential.

Genetic divergence among 50 genotypes was studied through Non-hierarchical Euclidean cluster analysis. Analysis of variance was executed to test the significance for each character as per the method given by Panse and Sukhatme (1967)^[16]. Estimates of divergence were analyzed by using Mahalanobis (1936)^[12] D2 statistics. The computation of D2 values and for deciding group constellations, as per method recommended by Rao (1952)^[18] was followed. The dendrogram was constructed as per Ward's minimum variance method.

Results and Discussion

The mean sums of squares due to genotypes for all the traits studied were highly significant thereby, revealing sufficient amount of genetic variation among the genotypes for all the characters studied. The Euclidean cluster analysis grouped the genotypes into eight distinct clusters under both the conditions. The distribution pattern of 50 genotypes in different clusters under timely sown condition is depicted in Table 1 & figure 1. Cluster pattern revealed that cluster II and VII were the largest one comprised of 14 and 10 genotypes respectively, followed by cluster III and IV with seven genotypes each, respectively while the cluster V was the smallest with one genotype. Table 2 & figure 2 revealed the membership profile of 50 genotypes under late sown condition. The cluster membership profile revealed that cluster IV had the largest number of genotypes (10) followed by cluster I (9) and III (7), while the cluster II was smallest with two genotypes only. For varietal improvement, the hybridization among genotypes falling in the most divergent clusters should be done.

Intra- and inter- cluster distances:

The intra and inter cluster distances among 50 genotypes are presented in Table 3 and Table 4 for timely and late sown condition, respectively. The Mahalanobis' euclidean distances in timely and late sown barley genotypes are shown in figure 3 and figure 4. Highest intra-cluster distance was observed for cluster VIII (7.408) and cluster III (5.479) while it was lowest for cluster V (0.000). Under late sown condition, the highest intra-cluster distance was observed for cluster II (5.001) and cluster IV (4.988) while low for cluster III (4.348). When diversity was studied among the clusters based on the inter-cluster distances, it showed a range of 5.015 to 11.207 under timely sown and 5.231 to 8.167 under late sown condition. Under timely sown condition the inter-cluster distance was found to be highest between cluster VIII and V (11.207) followed by cluster V and III (9.689). The highest inter-cluster distance was observed between cluster VI and IV (8.167) along with cluster IV and II (8.045) under late sown condition. The higher inter cluster distance indicated the presence of more diversity among the genotypes in these clusters. Higher the value of inter-cluster distance between the clusters more likely they will produce better segregants on hybridization. Alam *et al.* 2007^[2] concluded that cluster with small statistical distances considered less diverse than those with larger distances. Shakhathreh *et al.* (2010)^[21], Ebrahim *et al.* (2015)^[9], Yadav *et al.* (2015)^[24], Yadav *et al.* (2018)^[25], also concluded with similar findings of diversity in barley.

Table 1: Cluster membership profile of different genotypes under timely sown condition

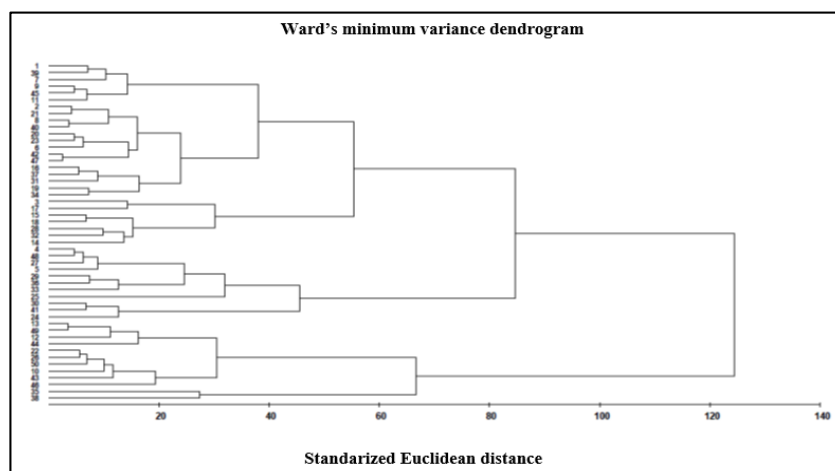
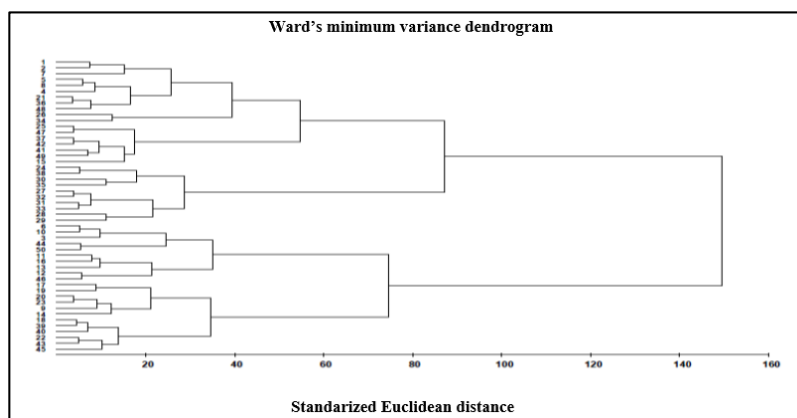
| Clusters | Genotypes | No. of genotypes |
|----------|---|------------------|
| I | IBYT-HI-19 (1), AZAD (39), IBYT-HI-15 (7), BH 959 (9), BH 14-42 (45), DWR 137 (11) | 6 |
| II | IBYT-HI-13 (2), 2 nd GSBSN-60 (2015) (21), IBYT-HI-20 (8), DWRB 143 (40), JB 481 (20), MGL-58 (23), IBYT-HI-23 (6), BH 13-22 (42), BH15-30 (47), BH 902 (34), HUB 242 (16), INBON 15-22 (37), IBON-HI-13 (2015-16) (31), K560 (19) | 14 |
| III | IBYT-HI-17 (3), 2 nd GSBSN-28 (2015) (17), UPB 1059 (15), 2 nd GSBYBT-23 (2015) (18), MGL-117 (28), IBON-HI-37 (2015-16) (32), RD2909 (14) | 7 |
| IV | IBYT-HI-16 (4), BH 946 (48), MGL-105 (27), IBYT-HI-18 (5), IBON-HI-1 (2015-16) (29), INBON-15-16 (36), IBON-HI-67 (2015-16) (33) | 7 |
| V | MGL-64 (25) | 1 |
| VI | IBON-HI-3 (2015-16) (30), BH 13-20 (41), MGL-62 (24) | 3 |
| VII | RD 2904 (13), BH 885 (49), MBGSN 145 (12), BH 14-25 (44), 2 nd GSBYBT-02 (2015) (22), DWRB 101 (26), DWRUB 52 (50), DWR 123 (10), BH 13-26 (43), BH 15-17 (46) | 10 |
| VIII | 2 nd GSBSN-15-8(35), 2 nd GSBSN-15-35 (38) | 2 |
| | Total | 50 |

Values in parenthesis indicates serial number of genotypes

Table 2: Cluster membership profile of different genotypes under late sown condition

| Clusters | Genotypes | No. of genotypes |
|----------|---|------------------|
| I | IBYT-HI-19 (1), IBYT-HI-13 (2), IBYT-HI-15 (7), IBYT-HI-18 (5), IBYT-HI-20 (8), IBYT-HI-16 (4), 2 nd GSBSN-60 (2015) (21), INBON-15-16 (36), BH 946 (48) | 9 |
| II | DWRB 101 (26), BH 902 (34) | 2 |
| III | MGL-64 (25), BH 15-30 (47), INBON-15-22 (37), BH-13-22 (42), BH-13-20 (41), BH 885 (49), UPB1059 (15) | 7 |
| IV | MGL-62 (24), 2 nd GSBSN-15-35 (38), IBON-HI-3 (2015-16) (30), 2 nd GSBSN -15-8 (35), MGL- 105 (27), IBON-HI-37 (32), IBON-HI-13 (31), IBON-HI-67 (33), MGL-117 (28), IBON-HI-1 (29) | 10 |
| V | IBYT-HI-23 (6), DWR 123 (10), IBYT-HI-17 (3), BH 14-25 (44), DWRUB 52 (50) | 5 |
| VI | DWR 137 (11), HUB 242 (16), RD 2904 (13), MBGSN 145 (12), BH 15-17 (46) | 5 |
| VII | 2 nd GSBSN -28 (2015) (17), K 560 (19), JB 481 (20), MGL-58 (23), BH 959 (9), RD 2909 (14) | 6 |
| VIII | 2 nd GSBYBT-23 (18), AZAD (39), DWRB 143 (40), 2 nd GSBYBT-02 (22), BH 13-26 (43), BH 14-42 (45) | 6 |
| | Total | 50 |

Values in parenthesis indicates serial number of genotypes

**Fig 1:** Dendrogram showing the clustering pattern of timely sown barley genotype**Fig 2:** Dendrogram showing the clustering pattern of late sown barley genotype

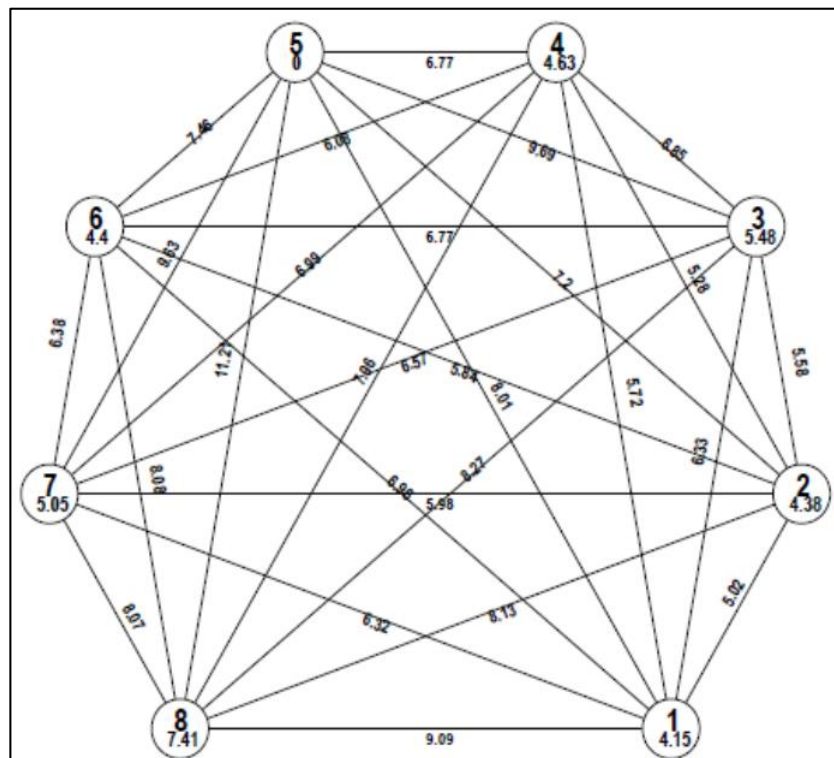


Fig 3: Mahalanobis Euclidean distances in timely sown barley

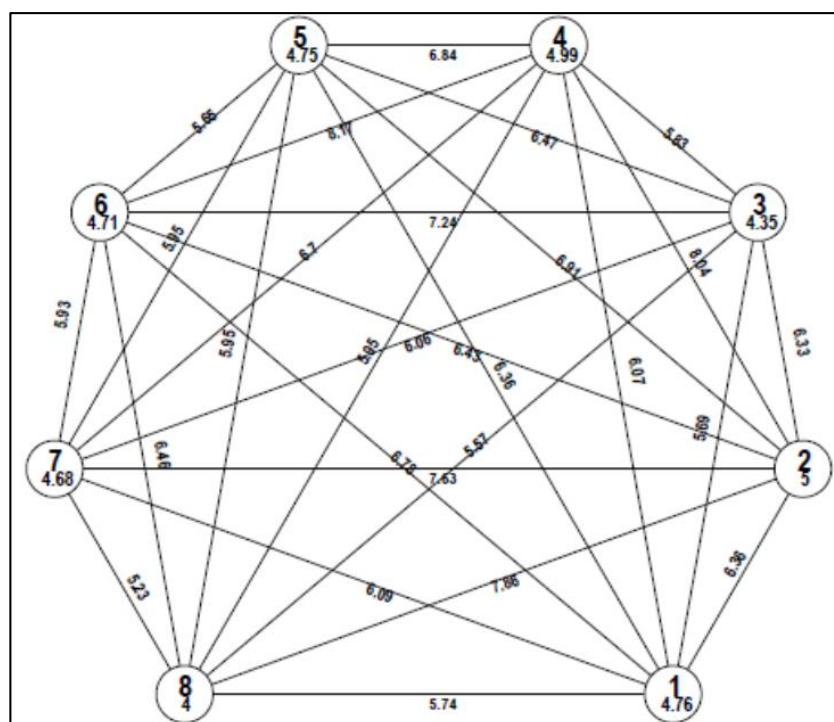


Fig 4: Mahalanobis Euclidean distances in late sown barley

Table 3: Estimates of intra-and inter-cluster distances in barley under timely sown condition

| Clusters | I | II | III | IV | V | VI | VII | VIII |
|----------|-------|-------|-------|-------|-------|-------|-------|--------|
| I | 4.154 | 5.015 | 6.328 | 5.722 | 8.011 | 6.964 | 6.317 | 9.091 |
| II | | 4.375 | 5.581 | 5.278 | 7.196 | 5.836 | 5.983 | 8.126 |
| III | | | 5.479 | 6.849 | 9.689 | 6.771 | 6.574 | 8.271 |
| IV | | | | 4.634 | 6.766 | 6.085 | 6.989 | 7.964 |
| V | | | | | 0.000 | 7.460 | 9.632 | 11.207 |
| VI | | | | | | 4.400 | 6.376 | 8.084 |
| VII | | | | | | | 5.054 | 8.074 |
| VIII | | | | | | | | 7.408 |

Diagonal: Intra-cluster distances Off-diagonal: Inter-cluster distances

Table 4: Estimates of intra-and inter-cluster distances in barley under late sown condition

| Clusters | I | II | III | IV | V | VI | VII | VIII |
|----------|-------|-------|-------|-------|-------|-------|-------|-------|
| I | 4.759 | 6.356 | 5.694 | 6.072 | 6.362 | 6.781 | 6.088 | 5.739 |
| II | | 5.001 | 6.333 | 8.045 | 6.909 | 6.430 | 7.627 | 7.862 |
| III | | | 4.348 | 5.829 | 6.467 | 7.236 | 6.056 | 5.574 |
| IV | | | | 4.988 | 6.843 | 8.167 | 6.704 | 5.952 |
| V | | | | | 4.749 | 5.647 | 5.945 | 5.948 |
| VI | | | | | | 4.707 | 5.931 | 6.463 |
| VII | | | | | | | 4.682 | 5.231 |
| VIII | | | | | | | | 4.005 |

Diagonal: Intra-cluster distances Off-diagonal: Inter-cluster distances

Mean performance of different clusters

The cluster means for grain yield and its component traits revealed considerable differences among all the clusters for most of the characters studied (Table 5 & 6). It was evident that cluster III and VII had low mean values for days to heading, days to maturity and plant height among the clusters under timely sown condition likewise under late sown condition, cluster VI had low mean values for days to heading and plant height and cluster V had lowest mean value for days to maturity. Therefore, the genotypes from these clusters can be preferred to develop early and short statured varieties.

Number of tillers per meter and 1000 grain weight were found highest for cluster VII under timely sown condition while under late sown condition, number of tillers per meter for cluster V and 1000 grain weight in cluster VI were found highest. Number of grains per spike was the characteristic feature of cluster I under both the environments. Cluster V under timely and cluster I under late sown condition accounted highest biological yield per plot. Grain yield and harvest index were noted highest for cluster I and cluster II under timely and late sown condition, respectively.

Cluster VII and VIII performed best for seedling length under both conditions. Cluster V possessed highest mean value for germination per cent followed by cluster II under timely sown condition whereas under late sown condition it was highest in cluster VIII and VII. Cluster III and VIII were responsible for highest vigour index-I under timely and late sown conditions, respectively. Vigour index-II was maximum in cluster VII under timely and Cluster VI under late sown. Cluster VIII was

recorded lowest for electrical conductivity under timely likewise cluster I under late sown. Cluster V exhibited highest mean value for accelerated ageing (48 h, 72 h) under timely and in case of late sown cluster I possessed highest mean value for accelerated ageing (48 h) and cluster II for accelerated ageing (72 h).

The eight clusters showed considerable difference in mean values for the characters under study. Under timely sown condition, cluster I comprised of six genotypes, exhibited minimum number of days to heading and maturity, moderate plant height and number of tillers per meter and had highest cluster means for number of grains per spike, grain yield per plot and harvest index. Cluster IV comprised of seven genotypes, also had high cluster means for number of tillers per meter, number of grains per spike, grain yield per plot and harvest index. Similarly, under late sown condition, cluster II which comprised of two genotypes had low cluster mean for days to heading; moderate for plant height; high for number of tillers per meter, 1000 grain weight and biological yield per plot; and highest for grain yield per plot as well as harvest index. Cluster VI, contained five genotypes recorded for minimum number of days to heading; shortest plant height; high number of tillers per meter; highest 1000 grain weight along with high mean values for grain yield per plot and harvest index. Similar studies had also been done by earlier workers namely, Ali *et al.* (2007)^[3], Mishra *et al.* (2008)^[14], Singh *et al.* (2013)^[23], Sharma *et al.* (2014)^[22], Dyulgerova *et al.* (2016)^[8] and Hailu *et al.* (2016)^[10].

Table 5: Mean performance of different clusters for yield and its contributing traits under timely sown condition

| Clusters | DH | DM | PH | SpL | T/M | G/S | 1000 GW | BY/P | GY/P | HI |
|----------|-------|--------|-------|-------|--------|-------|---------|---------|--------|-------|
| I | 82.61 | 126.89 | 91.89 | 7.68 | 100.89 | 62.28 | 42.56 | 2327.78 | 780.56 | 33.94 |
| II | 83.50 | 124.43 | 94.12 | 7.93 | 105.07 | 58.12 | 38.92 | 2130.95 | 547.74 | 25.89 |
| III | 81.71 | 122.00 | 88.91 | 8.11 | 105.05 | 56.43 | 38.29 | 1695.24 | 485.09 | 28.47 |
| IV | 90.05 | 129.67 | 98.71 | 7.23 | 107.95 | 60.76 | 35.45 | 2173.81 | 582.52 | 27.11 |
| V | 94.67 | 130.33 | 93.33 | 8.41 | 98.67 | 58.67 | 27.03 | 2700.00 | 523.33 | 19.46 |
| VI | 90.67 | 127.89 | 95.22 | 10.53 | 125.33 | 28.33 | 40.44 | 1944.45 | 446.67 | 22.99 |
| VII | 80.93 | 123.70 | 86.87 | 7.79 | 135.17 | 24.60 | 46.88 | 2220.00 | 580.67 | 26.49 |
| VIII | 83.50 | 124.67 | 95.67 | 9.05 | 106.67 | 42.83 | 37.10 | 1550.00 | 360.83 | 23.49 |

| Clusters | SL | SD | GP | SDW | VI | VII | EC | AA48 | AA72 |
|----------|-------|------|-------|--------|---------|----------|-------|-------|-------|
| I | 36.24 | 1.05 | 98.94 | 169.72 | 3582.20 | 16771.55 | 0.321 | 85.56 | 78.00 |
| II | 36.39 | 1.07 | 99.29 | 164.91 | 3609.47 | 16347.24 | 0.326 | 84.14 | 74.14 |
| III | 39.01 | 1.51 | 98.91 | 174.53 | 3809.41 | 17256.79 | 0.366 | 85.05 | 76.00 |
| IV | 35.91 | 1.33 | 98.91 | 152.14 | 3543.66 | 15025.49 | 0.279 | 75.43 | 63.43 |
| V | 30.83 | 0.64 | 99.33 | 129.80 | 3062.67 | 12563.43 | 0.330 | 91.33 | 84.00 |
| VI | 35.17 | 1.60 | 99.11 | 168.33 | 3484.01 | 16680.13 | 0.303 | 83.33 | 75.33 |
| VII | 36.51 | 1.31 | 98.87 | 190.39 | 3590.11 | 18721.37 | 0.326 | 76.40 | 63.80 |
| VIII | 38.33 | 1.18 | 97.17 | 185.27 | 3686.75 | 17866.46 | 0.220 | 49.00 | 40.00 |

Table 6: Mean performance of different clusters for yield and its contributing traits under late sown condition

| Clusters | DH | DM | PH | SpL | T/M | G/S | 1000 GW | BY/P | GY/P | HI |
|----------|-------|--------|-------|------|--------|-------|---------|---------|--------|-------|
| I | 81.59 | 114.07 | 92.15 | 7.33 | 85.93 | 68.00 | 31.40 | 1953.70 | 436.48 | 22.31 |
| II | 78.67 | 115.50 | 86.50 | 7.67 | 115.33 | 48.17 | 38.80 | 1850.00 | 535.00 | 29.04 |
| III | 83.09 | 115.52 | 82.81 | 8.20 | 80.48 | 55.38 | 29.49 | 1366.67 | 292.14 | 21.58 |
| IV | 89.17 | 117.90 | 96.27 | 9.07 | 101.20 | 60.33 | 27.79 | 1803.33 | 289.83 | 16.44 |
| V | 77.47 | 112.00 | 86.93 | 7.64 | 121.33 | 29.27 | 36.60 | 1800.00 | 399.33 | 22.86 |
| VI | 74.73 | 114.07 | 77.20 | 7.27 | 110.40 | 41.47 | 42.43 | 1706.67 | 469.67 | 27.07 |
| VII | 77.17 | 113.83 | 89.06 | 8.08 | 70.11 | 63.00 | 36.61 | 1527.78 | 350.00 | 22.63 |
| VIII | 81.39 | 114.39 | 81.83 | 8.04 | 87.22 | 53.06 | 29.71 | 1305.56 | 336.11 | 25.10 |

| Clusters | SL | SD | GP | SDW | VI | VII | EC | AA48 | AA72 |
|----------|-------|------|-------|--------|---------|----------|-------|-------|-------|
| I | 30.34 | 1.12 | 96.70 | 131.76 | 2920.10 | 12671.63 | 0.396 | 91.04 | 72.07 |
| II | 25.13 | 1.09 | 90.50 | 129.62 | 2273.12 | 11708.38 | 0.453 | 82.33 | 74.67 |
| III | 29.37 | 1.26 | 94.76 | 116.57 | 2781.29 | 10999.73 | 0.454 | 78.19 | 60.29 |
| IV | 33.43 | 1.21 | 97.03 | 127.87 | 3243.89 | 12383.56 | 0.418 | 83.27 | 55.13 |

| | | | | | | | | | |
|------|-------|------|-------|--------|---------|----------|-------|-------|-------|
| V | 33.18 | 1.30 | 95.93 | 156.93 | 3175.11 | 15152.32 | 0.429 | 72.00 | 48.73 |
| VI | 31.74 | 1.09 | 95.07 | 176.92 | 2999.09 | 16898.23 | 0.499 | 84.80 | 69.07 |
| VII | 33.51 | 1.43 | 97.06 | 160.82 | 3251.61 | 15609.94 | 0.496 | 84.67 | 66.89 |
| VIII | 36.50 | 1.18 | 98.56 | 137.21 | 3594.30 | 13518.02 | 0.443 | 86.67 | 68.00 |

Contribution of different traits towards divergence

The contribution of various characters towards genetic divergence is depicted in Table 7 and Table 8 for timely and late sown conditions, respectively. Under timely sown condition, out of 18 traits studied, contribution of number of grains per spike among morphological traits towards divergence was maximum (33.47) followed by days to maturity (12.16), days to heading (10.20) and 1000 grain weight (10.04) whereas the remaining traits like biological yield per plot, harvest index, grain yield per plot, spike length, plant height and number of tillers per meter contributed very little to divergence. Among seed vigour traits, electrical conductivity (15.10) contributed maximum towards divergence followed by accelerated ageing (48h, 72 h) (5.47, 5.63) and seed density (2.20) whereas the remaining traits such as seedling dry weight, vigour index-I and seedling length accorded very less to divergence. Among morphological characters studied under late sown condition, contribution of number of days to heading (34.53) and

number of grains per spike (34.45) towards divergence was maximum while rest of the morphological traits like 1000 grain weight (5.47), grain yield (1.71) and biological yield (1.14) imparted very little to diversity. Maximum contribution among seed vigour traits was recorded for accelerated ageing (72 h) (11.43) towards divergence thereafter electrical conductivity (3.76), accelerated ageing (48 h) (2.78) and seedling length (2.69) while the little contribution of rest of the traits was observed towards divergence.

Number of grains per spike, electrical conductivity and days to maturity under timely sown and days to heading, number of grains per spike and accelerated ageing (72 h) under late sown imparted maximum towards divergence. Alam *et al.* (2007)^[2] also reported similar results for number of grains per spike. The contribution of various characters towards the expression of genetic divergence should be taken into account as a criterion for selecting the parents in crossing programme for the enhancement of such characters.

Table 7: Contribution of different characters towards divergence in timely sown condition

| Sr. No. | Source | Times ranked 1 st | Contribution towards divergence (%) |
|---------|--|------------------------------|-------------------------------------|
| 1 | Number of days to heading | 125 | 10.20 |
| 2 | Number of days to maturity | 149 | 12.16 |
| 3 | Plant height (cm) | 2 | 0.16 |
| 4 | Spike length (cm) | 5 | 0.41 |
| 5 | No. of tillers/meter | 0 | 0.00 |
| 6 | No. of grains/spike | 410 | 33.47 |
| 7 | 1000 grain weight (g) | 123 | 10.04 |
| 8 | Grain yield/plot (g) | 6 | 0.49 |
| 9 | Biological yield/plot (g) | 38 | 3.10 |
| 10 | Harvest index (%) | 8 | 0.65 |
| 11 | Seedling length (cm) | 1 | 0.08 |
| 12 | Seed density (g/cc) | 27 | 2.20 |
| 13 | Germination (%) | 0 | 0.00 |
| 14 | Seedling dry weight (mg) | 7 | 0.57 |
| 15 | Vigour index- I | 3 | 0.24 |
| 16 | Vigour index- II | 0 | 0.00 |
| 17 | Electrical Conductivity (μ S/cm/seed) | 185 | 15.10 |
| 18 | Accelerated ageing (48 h) | 67 | 5.47 |
| 19 | Accelerated ageing (72 h) | 69 | 5.63 |

Table 8: Contribution of different characters towards divergence in late sown condition

| Sr. No. | Source | Times ranked 1 st | Contribution towards divergence (%) |
|---------|--|------------------------------|-------------------------------------|
| 1 | Number of days to heading | 423 | 34.53 |
| 2 | Number of days to maturity | 4 | 0.33 |
| 3 | Plant height (cm) | 2 | 0.16 |
| 4 | Spike length (cm) | 2 | 0.16 |
| 5 | No. of tillers/meter | 0 | 0.00 |
| 6 | No. of grains/spike | 422 | 34.45 |
| 7 | 1000 grain weight (g) | 67 | 5.47 |
| 8 | Grain yield/plot (g) | 21 | 1.71 |
| 9 | Biological yield/plot (g) | 14 | 1.14 |
| 10 | Harvest index (%) | 0 | 0.00 |
| 11 | Seedling length(cm) | 33 | 2.69 |
| 12 | Seed density(g/cc) | 1 | 0.08 |
| 13 | Germination (%) | 2 | 0.16 |
| 14 | Seedling dry weight(mg) | 11 | 0.90 |
| 15 | Vigour index I | 2 | 0.16 |
| 16 | Vigour index II | 1 | 0.08 |
| 17 | Electrical Conductivity (μ S/cm/seed) | 46 | 3.76 |
| 18 | Accelerated ageing (48 h) | 34 | 2.78 |
| 19 | Accelerated ageing (72 h) | 140 | 11.43 |

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