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Study of genetic diversity in bread wheat (*Triticum aestivum* L.em.Thell) under late sown irrigated conditions

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ABSTRACT: Wheat is one of the most important crop among the prime cereals at the global level. In the present investigation, 36 bread wheat (*Triticum aestivum* L.) genotypes were evaluated to estimate the extent of genetic diversity in late sown conditions in 2016-17 and 2017-18 at ICAR-IARI, New Delhi. Analysis of variance revealed that genotypes possess significant genetic variability among all traits. A significant positive correlation was observed among yield, grain weight per spike, grain number per spike, spike per meter square, harvest index and thousand grain weight in both the years whereas in 2017-18 biological yield also found positively significant correlated with yield. On contrary, days to 50% heading and grain filling duration revealed a negative correlation. Diversity analysis classified the evaluated wheat genotypes into four and eight distinct groups based on an index of similarity and dissimilarity of attributing traits in 2016-17 and 2017-18 respectively. A perusal of cluster means for all the traits for both the crop seasons revealed considerable difference all the characters between the clusters. Such differences in genetic component of traits can be applied as a new source of variation. The diverse parents indentified in this study could be used for creating desirable variability.

Key words: Bread wheat, cluster analysis, genetic diversity, late sown wheat

Wheat (*Triticum aestivum* L. em Thell) is a golden grained nutritious cereal crop, being grown during cool season in an estimated area of 220.19 million ha globally. It is an important component of staple food which fulfilled major portion of total calories and protein requirement. During 2018-19, wheat was grown in 29.55 million ha under diverse environment with a record production of 101.20 million tons and productivity level of 3424 kg/ha in the country. However, to sustain the food security for ever increasing population pressure there is necessity to further improve the productivity level of wheat.

Genetic diversity is of prime importance to the crop breeders in selection of genetically diverse parental lines for planned hybridization programme to create broad spectrum of variability in segregating generation. Evaluation of genetic diversity among the newly developed and released genotypes or adapted germplasm lines can provide predictive estimates of genetic variation among the segregating progeny for cultivar development Manjarrez- Sandoval *et al.* (1997). The Mahalanobis D² statistic gives information about the genetic divergence and provides the basis of selection of parental lines form breeding programme.

Correlation studies helps to quantify and evaluate the proportion of the phenotypic correlation associated with genetic backgrounds, to investigate whether the selection for a particular trait affects more traits, to examine indirect gains due to selection on correlated traits, and to dissect the complexity of the traits. Therefore, keeping in mind

the above facts, we investigated the extent of genetic variability present in a set of bread wheat genotypes for various traits and the phenotypic correlation coefficients between yield and component traits in late sown conditions.

MATERIALS AND METHODS

The experimental material consisted of 36 genotypes including released wheat varieties recommended for various production situations of different zones of the country and pre-released advance lines of bread wheat developed at Indian Agricultural Research Institute, New Delhi. The experiment was laid out in Randomized Block Design (RBD) replicated thrice under late sown irrigated conditions consecutively for two crop seasons i.e., 2016-17 and 2017-18. Each genotype was sown in a six-row plot having a gross area of 5 m x 1.20 m with a row spacing of 20 cm using self-propelled Norwegian Seed Drill in a well-prepared field. Recommended package of cultural and agronomic practices were followed to raise the healthy wheat crop. Observations in field were recorded from each experimental plot either on five randomly selected plants or on plot basis for 13 morpho-physiological characters viz., Plant height (PH), days to 50 % heading (HDNG), number of spike per square meter (SPMS), number of grains per spike (GNPS), grain weight per spike in grams (GWPS), spike length in cm (SL), days to maturity (DTM), grain filling period (GFD), grain yield per square meter in grams (GYPMS), biological yield per square meter in grams (BYPMS), harvest index (HI) and

1000-grain weight (TGW). The canopy temperature depression (CTD) was measured at anthesis stage using portable infrared thermometer Model AG-42 with a view of 2.5°. The data collected from field trials were subjected to statistical analysis. Analysis of variance was estimated following Panse and Sukhatame (1975). The genetic divergence amongst the genotypes was assessed inter se genetic distances using D^2 statistics of Mahalanobis (Generalized distance as recommended by Rao, 1952). The genotypes were grouped using Euclidean cluster analysis. Phenotypic correlation coefficients were calculated as per the Al-Jibouri *et al.*, (1958).

RESULTS AND DISCUSSION

The analysis of variance was carried out separately for each crop season and presented in Table 1. Significant genotypic differences were observed for all the traits under study in both the crop seasons suggesting presence of sufficient genetic variability among the genotypes chosen for the study.

Correlation coefficient analysis statistically measured the degree and direction of relationship between two traits. The knowledge of association among the various component traits with grain yield under terminal heat stressed environment is of prime importance for the plant breeders to make effective selection to improve the grain yield. The perusal of phenotypic correlation coefficients shown in the Table 2.

YPMS found highly significant positive correlation with GWPS (0.824**), GNPS (0.757**), SPMS (0.740**), HI (0.825**) and TGW (0.671**) during 2016-17 and amid 2017-18, YPMS found highly significant positive correlation with GWPS (0.666**), GNPS (0.350*), SPMS (0.821**), BYPMS (0.877**), HI (0.477**), TGW (0.338*). During 2016-17 HDNG showed significant positive correlation with DTM (0.539**), GWPS (0.376*), TGW (0.469**) and highly significant negative correlation with GFD (-0.643**). In the year 2017-18 HDNG showed significant correlation with DTM (0.657**). DTM showed highly significant correlation with GFD (0.573**) and SL (0.379*) during 2017-18. GFD found significantly positive correlated with PH (0.472**) and SL (0.406*) in the year 2017-18. PH showed positive significant correlation with BYPMS (0.389*) during 2017-18. GWPS showed highly significant positive correlation with GNPS (0.757**), HI (0.650**), TGW (0.913**) during 2016-17 and showed highly significant positive correlation with GNPS (0.694**), BYPMS (0.421*), HI (0.634**) amid 2017-18. GNPS found positively significantly correlated with SPMS (0.407*), HI (0.668**), TGW (0.429**) during 2016-17, and amid 2017-18 showed positive significant correlation with HI (0.662**), TGW (0.457**). During

2016-17, SPMS found significantly positively correlated with HI (0.637**) and during 2017-18 showed positive correlation with BYPMS (0.856**). In the year 2016-17, BYPMS showed significant positive correlation with TGW (0.342*) and significant negative correlation with HI (-0.329*). During 2017-18 BYPMS found significantly positively correlated with TGW (0.427**).

The comparative correlation coefficients for both crop seasons revealed that YPMSr under late sown conditions recorded highly significant positive correlation with GWPS, GNPS, SPMS, HI and TGW in both the crop seasons. Therefore, degree of relationship between these attributes and YPMS appeared to be more meaningful or stable. These findings are in conformity with the findings of earlier researchers. Hanchinal *et al.* (1994) reported that SPMS under very hot environment may serve as valuable selection criteria in wheat. Maintaining grain weight under heat stress during grain filling is a measure of heat tolerance (Tyagi *et al.*, 2003; Singha *et al.*, 2006). In this regard, Dias and Lidon (2009) proposed that high grain-filling rate and high potential grain weight can be useful selection criteria for improving heat tolerance. Choudhary *et al.* (1996) concluded that TGW and tillers number per plant were highly correlated with heat tolerance. Sheikh *et al.* (2001) reported strong correlation with harvest index under heat stress environment. Dhanda *et al.* (2004) also reported positive correlation with of grain yield with TGW under heat stress conditions. Kumar *et al.* (2017) reported that BYPMS and HI positively and significantly correlated with grain yield under terminal heat stress condition. For rest of traits, no consistency was observed during both the years and hence their relationship should not be considered as strong or stable.

The clustering pattern of different genotypes in various clusters, their inter and intra-cluster distances and the mean performance of various morpho-physiological traits are shown in Table 3 and Table 4 respectively. Cluster formation based on Euclidean analysis. The first cluster with 31 genotypes was largest cluster with intra cluster Euclidean distance of 2900.07. The maximum inter cluster distance was exhibited between cluster four and cluster six followed by cluster two and four. The minimum inter cluster distance was between clusters two and three followed by clusters one and two (Table 4).

The second environment of season 2017-18 classified 36 genotypes into eight clusters (Table 3). The sixth cluster with 10 genotypes was largest cluster with intra cluster Euclidean distance of 21442.09 followed by clusters third, second and eighth having six, five and four genotypes and intra cluster distances 9144.31; 8844.78 and 31357.17 respectively. The clusters four and seven had three genotypes each with intra cluster distances of 933.71 and 3106.34 respectively. Fifth cluster had two genotypes

Table 1: Analysis of Variance for different traits during Late Sown Rabi 2016-17 and 2017-18

| 2016-2017 | | | | | | | | | | | | | | |
|--|------|----------|----------|----------|----------|---------|---------|-----------|--------------|---------------|---------------|-----------|-----------|----------|
| SV | D.F. | HDNG | DTM | GFD | PH | SL | GWPS | GNPS | SPMS | YPMS | BYPMS | HI | TGW | CTD |
| REPLICATION GENOTYPE ERROR SE(d) C.D.(1%) C.V.(%) | 2 | 2.287 | 5.7315 | 2.1945 | 2.25 | 0.157 | 0.0005 | 0.926 | 17.361 | 4.3425 | 1.0001 | 0.0045 | 0.0245 | 0.007 |
| | 35 | 26.752** | 17.374** | 20.712** | 70.657** | 2.360** | 0.350** | 49.789** | 20,860.905** | 156,524.104** | 227,218.133** | 787.174** | 103.570** | 0.588** |
| | 70 | 0.782 | 1.055 | 0.909 | 1.574 | 0.015 | 0.002 | 0.259 | 47.19 | 440.171 | 90.714 | 1.864 | 0.973 | 0.031 |
| | | 0.722 | 0.839 | 0.778 | 1.024 | 0.1 | 0.032 | 0.416 | 5.609 | 17.13 | 7.777 | 1.115 | 0.805 | 0.143 |
| | | 1.443 | 1.676 | 1.556 | 2.047 | 0.2 | 0.063 | 0.831 | 11.211 | 34.239 | 15.543 | 2.228 | 1.61 | 0.286 |
| | | 1.09 | 0.894 | 2.815 | 1.395 | 1.34 | 2.423 | 1.175 | 1.48 | 2.794 | 0.611 | 2.782 | 2.683 | 9.594 |
| 2017-2018 | | | | | | | | | | | | | | |
| REPLICATION GENOTYPE ERROR SE(d) C.D.(1%) C.V.(%) | 2 | 3.3705 | 9.4535 | 5.25 | 0.7315 | 0.4105 | 0.0315 | 0.4535 | 142.676 | 16406.0095 | 1634.3425 | 29.934 | 8.8915 | 3.3705 |
| | 35 | 11.470** | 16.587** | 9.190** | 35.583** | 0.942** | 0.122** | 100.050** | 23,674.710** | 139,052.441** | 352,260.022** | 80.103** | 32.866** | 11.470** |
| | 70 | 0.342 | 0.435 | 0.193 | 0.817 | 0.014 | 0.009 | 0.854 | 96.057 | 3,808.26 | 383.171 | 10.612 | 3.784 | 0.342 |
| | | 0.477 | 0.538 | 0.359 | 0.738 | 0.097 | 0.077 | 0.754 | 8.002 | 50.387 | 15.983 | 2.66 | 1.588 | 0.477 |
| | | 0.954 | 1.076 | 0.717 | 1.475 | 0.194 | 0.154 | 1.508 | 15.995 | 100.71 | 31.945 | 5.316 | 3.175 | 0.954 |
| | | 0.729 | 0.597 | 1.445 | 1.248 | 1.241 | 5.194 | 1.869 | 1.662 | 5.747 | 1.017 | 5.837 | 5.264 | 0.729 |

*, ** Significant at 5% and Significant at 1% levels, respectively

Table 2: Pearson's correlation coefficients among 13 characters during late sown 2016-2017 (lower diagonal) and 2017-2018 (upper diagonal)

| 2017-18 | | | | | | | | | | | | | | | | |
|---------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|--|--|--|
| | HDNG | DTM | GFD | PH | SL | GWPS | GNPS | SPMS | YPMS | BYPMS | HI | TGW | CTD | | | |
| HDNG | - | 0.657** | -0.207NS | -0.144NS | 0.022NS | 0.308NS | 0.324NS | -0.238NS | -0.013NS | -0.120NS | 0.246NS | -0.066NS | 0.278NS | | | |
| DTM | 0.539** | - | 0.573** | 0.278NS | 0.379* | 0.217NS | 0.247NS | -0.017NS | 0.114NS | 0.089NS | 0.121NS | -0.049NS | 0.278NS | | | |
| GFD | -0.643** | 0.281NS | - | 0.472** | 0.406* | -0.043NS | -0.030NS | 0.265NS | 0.190NS | 0.248NS | -0.058NS | 0.020NS | 0.134NS | | | |
| PH | -0.089NS | -0.056NS | 0.090NS | - | 0.333* | 0.310NS | 0.253NS | 0.183NS | 0.324NS | 0.389* | -0.060NS | 0.056NS | 0.061NS | | | |
| SL | 0.141NS | 0.261NS | 0.055NS | 0.146NS | - | 0.005NS | 0.184NS | -0.232NS | -0.178NS | -0.161NS | -0.090NS | -0.208NS | 0.192NS | | | |
| GWPS | 0.376* | 0.092NS | -0.298NS | 0.264NS | 0.218NS | - | 0.694** | 0.128NS | 0.666** | 0.421* | 0.634** | 0.314NS | 0.125NS | | | |
| GNPS | 0.135NS | -0.113NS | -0.219NS | 0.066NS | 0.000NS | 0.757** | - | -0.056NS | 0.350* | 0.048NS | 0.662** | 0.457** | 0.238NS | | | |
| SPMS | 0.039NS | -0.020NS | -0.061NS | -0.133NS | 0.119NS | 0.247NS | 0.407* | - | 0.821** | 0.856** | 0.138NS | 0.204NS | 0.031NS | | | |
| YPMS | 0.235NS | 0.009NS | -0.224NS | 0.160NS | 0.223NS | 0.824** | 0.757** | 0.740** | - | 0.877** | 0.477** | 0.338* | 0.081NS | | | |
| BYPMS | 0.155NS | 0.094NS | -0.110NS | 0.255NS | 0.161NS | 0.285NS | 0.116NS | 0.090NS | 0.217NS | - | 0.002NS | 0.427** | -0.002NS | | | |
| HI | 0.158NS | -0.009NS | -0.142NS | -0.033NS | 0.185NS | 0.650** | 0.668** | 0.637** | 0.825** | -0.329* | - | -0.081NS | 0.180NS | | | |
| TGW | 0.469** | 0.237NS | -0.281NS | 0.310NS | 0.302NS | 0.913** | 0.429** | 0.101NS | 0.671** | 0.342* | 0.480** | - | -0.149NS | | | |
| CTD | 0.297NS | 0.164NS | -0.205NS | -0.139NS | -0.012NS | 0.263NS | 0.214NS | 0.198NS | 0.273NS | 0.070NS | 0.219NS | 0.232NS | - | | | |

with intra cluster distance of 471.45 (Table 4). The maximum inter cluster distance was exhibited between cluster two and cluster seven followed by cluster seven and eight. The minimum inter cluster distance was between clusters two and three followed by clusters one and two (Table 4).

The distribution pattern of the genotypes in both the years was different suggesting thereby that change of growing environments in both the years effectively changed the phenotypic performance of genotypes which led to difference in clustering pattern. Comparative magnitude of inter and intra cluster distances under both the years suggested that inter cluster distance values were more than the intra cluster distance values. Thus, the genotypes included within a cluster tended to have lower degree of divergence among themselves as compared to genotypes present in different clusters. Therefore, the genotypes belonging to different clusters separated by high statistical distances will be genetically more divergent. These genetically more divergent genotypes have the potential utility to be used in future recombination programme for getting a wide spectrum of variation among the sergeants.

Out of 36 genotypes, set of some genotypes came together in both the years for example DW1629 and HD3184 occupied cluster I in both the seasons. Three genotypes HD3086, DW1627 and DW1632 occupied cluster I and cluster II in 2016-17 and 2017-18 respectively. Six genotypes viz., DW1635, HD3090, HD3262, HD3252, HD2932 and HD3059 came under cluster I and cluster III in 2016-17 and 2017-18 respectively. DW1636 and

DW1638 occupied cluster I and cluster IV in the year 2016-17 and 2017-18 respectively. DW1630 and DW1645 came under cluster I and cluster V in 2016-17 and 2017-18 respectively. Nine genotypes viz., HD3171, HD2864, HD3255, DW1633, DW1634, HD3265, DW1642, DW1643 and DW1644 occupied cluster I and cluster VI in the year 2016-17 and 2017-18 respectively. Three genotypes viz., DW1639, DW1640 and HD 3318 came under cluster I and cluster VII in 2016-17 and 2017-18 respectively. Four genotypes HD3266, DW1615, HDCSW18 and DW1631 occupied cluster I and cluster VIII in the year 2016-17 and 2017-18 respectively.

Considering the immediate parentage of these genotypes revealed that none of these genotypes possess the same parentage indicating that different parents are involved in their parentage. However, similarity in parentage at grand parental level cannot be ruled out. Similarly, we do not have any idea whether parental lines involved in these parents are genetically divergent or not. This type of clustering pattern suggested that these genotypes are having more or higher degree of similarity among themselves however they are genetically diverse as compared to other genotypes under study. Murty and Arunchalam (1966) were of the opinion that many genotypes originating from or developed at one research organisation were found to be scattered over different clusters could be due to factors like heterogeneity, genetic architecture of the populations, past history of selection, developmental traits and degree of general combining ability. In present case such genotypes having DW number and some with HD numbers were developed at

Table 3: Clustering pattern of 36 genotypes based on D² Statistic during late sown 2016-17 and 2017-18

| Crop season 2016-17 | | |
|---------------------|-------------|---|
| Cluster # | Genotypes # | Genotypes in cluster |
| I | 31 | DW1639, DW1640, HD3318, HD3265, DW1642, DW1643, DW1644, DW1645, HD3059, HD3266, DW1615, HDCSW18, DW1631, DW1632, HD3255, DW1633, DW1634, DW1635, HD3090, HD3262, DW1636, DW1638, HD3171, HD2864, HD3086, DW1627, DW1629, HD3184, HD3252, DW1630, HD2932 |
| II | 1 | DW1616 |
| III | 1 | DW1628 |
| IV | 1 | WR544 |
| V | 1 | HD3249 |
| VI | 1 | DW1637 |
| Crop season 2017-18 | | |
| I | 3 | DW1628, DW1629, HD3184 |
| II | 5 | HD3086, HD3249, DW1627, DW1632, WR544 |
| III | 6 | DW1635, HD3090, HD3262, HD3252, HD2932, HD3059 |
| IV | 3 | DW1636, DW1637, DW1638 |
| V | 2 | DW1630, DW1645 |
| VI | 10 | HD3171, DW1616, HD2864, HD3255, DW1633, DW1634, HD3265, DW1642, DW1643, DW1644, |
| VII | 3 | DW1639, DW1640, HD3318 |
| VIII | 4 | HD3266, DW1615, HDCSW18, DW1631 |

Table 4: Mahalanobis Euclidean intra (diagonal) and inter cluster distance during late sown 2016-17 and 2017-18

| Crop Season 2016-17 | | | | | | | | |
|---------------------|---------|---------|----------|----------|----------|----------|------------|----------|
| Cluster | I | II | III | IV | V | VI | | |
| I | 2900.07 | 6197.76 | 6248.97 | 9028.16 | 7509.17 | 13565.06 | | |
| II | | 0 | 6002.01 | 23588.19 | 2276.41 | 7839.91 | | |
| III | | | 0 | 16658.51 | 12550.41 | 10719.8 | | |
| IV | | | | 0 | 23716.47 | 31609.21 | | |
| V | | | | | 0 | 10468.05 | | |
| VI | | | | | 0 | | | |
| Crop Season 2017-18 | | | | | | | | |
| Cluster | I | II | III | IV | V | VI | VII | VIII |
| I | 139.7 | 435550 | 30958.25 | 76030.22 | 16295.82 | 94121.37 | 353728.8 | 434923.9 |
| II | | 8844.78 | 435562.1 | 837985.4 | 527939.1 | 170208.7 | 1550986.00 | 72600.61 |
| III | | | 9144.31 | 80833.23 | 27645.9 | 81407.53 | 369938 | 363420 |
| IV | | | | 933.71 | 43341.14 | 282732 | 111283.20 | 762611.8 |
| V | | | | | 471.45 | 124199.1 | 282570 | 500807.8 |
| VI | | | | | | 21442.09 | 739638.30 | 157513.5 |
| VII | | | | | | | 3106.34 | 1435484 |
| VIII | | | | | | | | 31357.17 |

Table 5: Cluster mean for 13 characters in bread wheat genotypes during late sown season 2016-17 and 2017-18

| Traits | Crop Season 2016-17 | | | | | | Crop Season 2017-18 | | | | | | | |
|--------|---------------------|--------|--------|--------|--------|--------|---------------------|--------|---------|---------|-------|--------|--------|---------|
| | I | II | III | IV | V | VI | I | II | III | IV | V | VI | VII | VIII |
| HDNG | 81.44 | 82.5 | 81.5 | 72.5 | 79.5 | 78.5 | 81.67 | 81.6 | 79.33 | 79.67 | 80 | 78.8 | 81 | 81.25 |
| DTM | 114.74 | 121 | 116 | 112 | 113.5 | 115 | 110 | 113.8 | 109.67 | 110 | 110.5 | 109 | 111.67 | 111 |
| GFD | 33.31 | 38.5 | 34.5 | 39.5 | 34 | 36.5 | 28.67 | 32.4 | 30.83 | 30.67 | 30.5 | 30.3 | 30.67 | 30 |
| PH | 89.87 | 91.17 | 92.82 | 90.38 | 90.83 | 88.25 | 74 | 75.8 | 74.33 | 72 | 74 | 73.9 | 69 | 74.25 |
| SL | 9.12 | 9.75 | 8.51 | 7.8 | 10.25 | 10.12 | 9.4 | 9.52 | 9.43 | 8.97 | 9.55 | 9.43 | 8.8 | 9.6 |
| GWPS | 1.61 | 1.8 | 1.42 | 0.87 | 1.81 | 1.78 | 1.95 | 2.12 | 1.87 | 1.71 | 1.59 | 1.88 | 1.6 | 2.17 |
| GNPS | 43.55 | 42.5 | 41.2 | 39.5 | 41.1 | 45 | 51.67 | 52 | 49.17 | 49 | 49 | 46.8 | 48.67 | 57.25 |
| SPMS | 471.69 | 335.5 | 445 | 428 | 353.5 | 527.5 | 527.67 | 643.8 | 616.33 | 563.67 | 628 | 647.9 | 504 | 705 |
| YPMS | 769.1 | 605.46 | 631.87 | 370.22 | 639.49 | 936.84 | 1026.33 | 1365.2 | 1148.17 | 963.67 | 995 | 1216.3 | 806.33 | 1522.25 |
| BYPMS | 1571.4 | 1947 | 1252 | 1001 | 2201 | 1000 | 1991 | 2542 | 1925.33 | 1725.67 | 1920 | 2174.9 | 1440 | 2372.5 |
| HI | 49.21 | 31.1 | 50.47 | 36.99 | 29.05 | 93.68 | 51.53 | 53.7 | 59.68 | 55.84 | 51.83 | 55.99 | 55.99 | 64.23 |
| TGW | 36.81 | 42.46 | 34.47 | 21.9 | 44.01 | 39.47 | 37.79 | 40.83 | 38.04 | 34.83 | 32.55 | 40.46 | 32.98 | 37.91 |
| CTD | 1.87 | 2.25 | 1.1 | 1.05 | 1.35 | 1.95 | 2.97 | 1.92 | 1.85 | 2.07 | 2.15 | 2.17 | 1.97 | 2.55 |

IARI New Delhi. These genotypes found to be scattered over different clusters. Such type of clustering pattern of the genotypes suggested that lack of relationship between pedigree of different genotypes and genetic divergence between them. Many earlier researchers like Gartan and Mittal (2003), Sharma and Suri (2005), Dobariya *et al.* (2006), Kumar *et al.* (2017) and Eyebernova *et al.* (2018) also reported lack of relationship between geographic distribution/pedigree and genetic divergence.

The perusal of cluster mean performance during crop season 2016-17 (Table 4) revealed that HDNG was higher (82 days) for first, second and third cluster followed by clusters fifth and sixth (79-80 days) and was minimum for third cluster with 73 days. DTM was maximum for second cluster (121days) followed by third (116 days), sixth and first (115 days), fifth (114 days) and minimum for fourth

cluster (112days). GFD was maximum for fourth cluster (40 days) followed by second cluster (39 days), sixth cluster (37 days) and about 34 days in rest of the clusters. Maximum SL was observed fifth and sixth cluster (10 cm +) and minimum in fourth cluster (7.8 cm) and almost similar trend was observed for GWPS with maximum weight was observed fifth (1.81g) and sixth clusters (1.78g) and minimum in fourth cluster (0.87g). GNPS was maximum in sixth cluster (45) followed by first cluster (44) and minimum in fourth cluster (40). Spikes per meter square (SPMS) was maximum in sixth cluster (523) followed by first cluster (472) and minimum in second cluster. However, the YPMS was closely following the trend of GNPS with maximum in sixth cluster (936.84) followed by first cluster (769.1) and minimum in fourth cluster (370.22). The BYPMS was maximum for cluster five (2201g) followed by cluster two

(1947g) and minimum for fourth cluster (1001g). The HI for this environment exhibited by cluster six and three reaching to 50% and minimum for cluster five (29.05%) followed by cluster two (31.1%) but surprisingly the TGW was maximum for the clusters having minimum HI i.e. Cluster five (44.01g) followed by cluster two (42.46g) and these clusters also expressed higher CTD as well with 1.95 °C and 2.25 °C respectively.

The perusal of cluster mean performance during crop season 2016 -17 (Table 4) revealed that days to heading (HDNG) ranged from 79 -82 days with minimum in sixth cluster and maximum in first, second and eighth clusters while rest of the clusters were having 80-81 days. Days to maturity was maximum for second cluster (114 days) followed by seventh (112 days), eighth (111 days) with modal value of 110 days for rest of clusters. Grain filling duration was maximum for second cluster (32.4 days) and minimum in first cluster (29 days) and about 30 days in rest of the clusters. Plant height ranged from 69 cm in cluster seventh to 75.8 cm in second cluster while in rest of the cluster the height was about 75 cm. The spike length was ranging from 8.8 cm to 9.5 cm with insignificant variation among the clusters. Grain weight per spike with maximum weight was observed third and sixth clusters (2.17g and 2.12 respectively) and minimum in fifth and seventh cluster (1.60g). Grain number per spike was maximum in eighth cluster (57) followed by first and second clusters (~52) and minimum in sixth cluster (47) while rest of groups had about 49 grains per spike. Spikes per meter square (SPMS) was maximum in eighth cluster (705) followed by sixth cluster (648) and minimum in seventh cluster (504). The YPMS was maximum in eighth cluster (1522.25g) followed by second cluster (1365.2g) and minimum in fifth cluster (226.83g) followed by second cluster (343g). The BYPMS was maximum in sixth cluster (1477.67g) followed by fourth cluster (1290g) and minimum in seventh cluster (806.33g) followed by fourth cluster (995g). The Harvest index for this environment was maximum 53% in cluster eighth followed by second, third and fourth (>50% each) and about 50 % in first, sixth and seventh and minimum for fifth cluster (46.93%). The TGW was maximum (~41 g) in second and sixth clusters followed by first and third cluster (~38g) and cluster four (~35g) while rest of the clusters were having (33g). Slight variation among clusters for CTD was observed within the range of 2-3 °C.

A perusal of cluster means for 13 traits for both the crop seasons revealed considerable difference for all the characters between the clusters. The results of cluster mean for both crop seasons suggested that selection of parental line for recombination breeding should be performed based on individual trait or a combination of traits as well as inter cluster differences to get the high level of genetic variability for the further improvement.

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