

Genetic Variability, Diversity and Association of Quantitative Traits with Grain Yield in Bread Wheat (*Triticum Aestivum* L.)

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Abstract: Thirty genotypes of bread wheat (*Triticum aestivum* L.) evaluated for yield and other related characters. Six characters *i.e.* plant height, effective tillers per plant, grain yield per plant, spike length, grains per spike and 1000 grain weight exhibited high variability. The remaining traits shows moderate to low variability. Following the Mahalanobis D^2 analysis, all the thirty genotypes were grouped into six clusters. On the basis of the data on genetic divergence and mean performance of yield and other traits, diverse and superior genotypes namely, HUW 533, K 68, K 9465, K 65, K 816, HD 2891, HD 2643, HD 2687, HD 2824, PBW 343, HD 2733, Kalyansona and Sonalika. Were selected to involve in multiple crossing programme to recover transgressive segregants. Further, on the basis of cluster means, cluster VI has been identified for selecting parents for incorporating grain yield per plant, tillers per plant and plant height, cluster V for spike length, grains per spike and early maturity and cluster III for 1000 grain weight. On the basis of character associations, it is argued that selection of plants.

Key words: Wheat, cluster analysis, genetic divergence, morpho-physiological traits and variability.

INTRODUCTION

The germplasm, the reservoir of genetic diversity is often exploited to most of the changing needs for developing improved crop varieties. It is important that variability for economic traits must exist in the working germplasm for profitable exploitation following recombination breeding and selection. The Importance of genetic diversity for selecting plants for recombination breeding in an autogamous crop such as wheat to recover transgressive segregants has also been repeatedly emphasized (Murthy and Anand, 1966; Jatasara and Paroda, 1983). However the genetic diversity of selected parents is not always based on factors such as geographic diversity place of release of ploidy level. Hence, characterization of genotypes should be based on statistical procedure such as D^2 statistics and on hierarchical eclidean cluster analysis. These procedures characterize genetic divergence using the criterion of similarity or dissimilarity based on the aggregate effect of a number of agronomically important characters. In views of these facts, thirty wheat genotypes were evaluated in this study: i) to determine the magnitude of variability among the germplasm for yield and morpho-physiological traits. ii) To determine the grouping pattern of genotypes in different cluster. iii) To identify genetically diverse and agronomically desirable genotypes for exploitation in a breeding programme aimed at improving grain yield potential of wheat.

MATERIALS AND METHOD

The experimental material comprising of thirty genotypes of wheat were grown in Randomized Block

Design with two replications at the research farm of Department of Genetics and plant breeding, Allahabad Agricultural institute-Deemed University, Allahabad during *Rabi* season of 2007-08. Each plot consisted of five rows of 2.5 meter length spaced at 25cm plant and within a row at 5cm. All the recommended package of practices for wheat was followed to raise a healthy crop. Data were recorded on five randomly and competitive plants of each genotype from each replication for eight quantitative characters *viz.* days to 50% flowering, days to maturity, plant height (cm), number of tillers per plant, spike length (cm), number of grains per spike, 1000 grain weight (g) and grain yield per plant (g). The mean, range, phenotypic and genotypic coefficient of variation (PCV and GCV respectively). Correlation coefficient and genetic distance were calculated as per the standard statistical procedure. Mahalanobis D^2 statistic was conducted to estimate the intra and inter cluster distances and to group the genotypes into different clusters. The appropriate number of cluster to group thirty genotypes was determined following the sequential pseudo F-ratio test (Beale, 1969).

RESULTS AND DISCUSSION

The results of the present study showed moderate to high variability for all the eight characters under study. Considerable genetic divergence was also present among the genotypes. This suggested that adequate scope is available for selection of superior and diverse genotypes for use in a programmed aimed at enhancing genetic yield potential of wheat. The data present in table 1 showed

wide range for all the eight characters, but the estimates of PCV and GCV were high only for numbers of plant height (cm), number of tillers per plant, spike length (cm), number of grains per spike, 1000 grain weight (g) and grain yield per plant (g), whereas other characters showed relatively low variability. However, there is still ample scope for selection of superior genotypes for these traits. Based on Mahalanobis' D^2 analysis, thirty genotypes were grouped into six clusters with variables number of genotypes (Table 2) suggesting considerable amount of genetic diversity in the material. The cluster I was the largest having 8 genotypes indicating overall genetic similarity among them, cluster III and IV had 6 genotypes, whereas cluster II, VI and V had 5, 4 and 1 genotypes. The pattern of distribution of genotypes in different cluster exhibited that geographical diversity was not related to genetic diversity as genotypes of same geographical region were grouped into different clusters and vice-versa. The data of inter cluster distances (Table 3) and the mean performance of the cluster (Table 4) were used to select genetically diverse and agronomically superior genotypes from among the 30 genotypes studied. The members of cluster III and VI exhibited the maximum divergence followed in descending order by the members of cluster IV & VI, II & V, III & V and I & VI, respectively. The average intra cluster distance between the members of cluster VI (295.33) was the maximum followed in descending order by cluster III (227.29) and cluster II (197.29). So on, suggesting that genotypes in cluster VI were relatively more diverse than the genotypes in the above selected clusters as also reported by Redhu *et al.* (1995). The highest mean value for number of effective tillers per plant was recorded by cluster VI (9.15) followed by cluster I (8.60). Cluster V had the genotypes with the highest mean spike length (10.52) followed by cluster II (10.34) and cluster VI (9.95). Highest mean value for 1000 grain weight was recorded for cluster III (42.23) followed by cluster VI (41.31), cluster I (40.12) and V (37.84). In terms of seed yield per plant, cluster VI was the best having highest mean value (12.84) followed by cluster I (11.81) and cluster III (11.05). Cluster means suggested that contribution of plant height was the maximum towards genetic divergence followed by days to flowering, grains per spike, 1000 grain weight and days to maturity. Thus, on the basis of good performance for seed yield and its components, clusters *viz.*, III, V, VI and I can be categorized as the best clusters. These results were in complete agreement with that of Singh, (1992) 1000 grain weight, Bhawsar, (1993) for plant height and Sharma *et al.*, (1998) for grains per spike. As the D^2 values represent the index of genetic diversity among the clusters, it would be most appropriate to make cross between genotypes belonging to cluster separated by high estimates of statistical distances. In view of this, the most divergent cluster i.e. clusters V and VI separated by a D^2 value. Based on cluster means, the cluster have been identified for selecting parents for future hybridization programme

Table 1: Estimation of mean, range, co-efficient of variation (PCV and GCV) for eight characters and correlation coefficient of grain yield with seven other characters.

| Characters | Mean | Range | | PCV | GCV | Correlation with grain yield |
|-----------------------|--------|--------|--------|-------|-------|------------------------------|
| | | Max. | Min. | | | |
| Days to 50% flowering | 74.78 | 84.006 | 3.50 | 7.45 | 7.38 | 0.24 |
| Days to maturity | 114.43 | 121.50 | 110.00 | 2.87 | 2.70 | 0.32 |
| Plant Height | | | | | | |
| -In cm | 101.16 | 135.27 | 76.75 | 14.85 | 14.78 | 0.48 |
| Effective tillers | | | | | | |
| -per plant | 8.17 | 13.00 | 5.90 | 20.64 | 19.03 | 0.54 |
| Spike length | 9.63 | 12.14 | 6.53 | 13.20 | 11.93 | 0.29 |
| Number of seeds | | | | | | |
| -per spike | 42.11 | 33.40 | 51.70 | 10.73 | 10.45 | 0.65 |
| 1000 seed weight | | | | | | |
| -weight | 39.22 | 48.17 | 33.54 | 10.73 | 10.40 | 0.32 |
| Seed yield per plant | 11.25 | 16.70 | 9.10 | 18.30 | 16.75 | |

Table 2: Distributing pattern of thirty genotypes of wheat into six clusters based on D^2 statistics

| Cluster number | Number of genotypes | Genotypes included |
|----------------|---------------------|--|
| I | 8 | KALYANSONA, UP-2594, RAJ-6560, RAJ-1555, SONALICA, HD-1981, K-9162, K-9533 |
| II | 5 | RAJ-1972, K-9006, HUW-55, K-9106, K-9107 |
| III | 6 | HD-2891, HD-2643, HD-2687, HD-2824, PBW-343, HD-2733 |
| IV | 6 | HD-2009, HUW-468, K-9351, PBW-524, HUW-510, PBW-373 |
| V | 1 | K-816 |
| VI | 4 | HUW-533, K-68, K-9465, K-65 |

Table 3: Average intra and inter cluster D^2 values among 6 clusters for 30 Genotypes.

| Cluster number, | I | II | III | IV | V | VI |
|-----------------|-------|-------|-------|-------|-------|-------|
| I | 15.35 | 18.92 | 20.30 | 18.92 | 27.15 | 33.74 |
| II | | 14.06 | 26.12 | 25.89 | 37.70 | 25.48 |
| III | | | 15.07 | 29.17 | 33.80 | 41.46 |
| IV | | | | 12.51 | 21.42 | 39.25 |
| V | | | | | 0.00 | 54.35 |
| VI | | | | | | 17.18 |

Table 4: Mean values of clusters and contribution of different characters towards genetic divergence in 30 wheat genotypes.

| Cluster/ No./ Character | I | II | III | IV | V | VI |
|-------------------------|--------|---------|--------|--------|--------|--------|
| 1Days to 50% flowering | 73.56 | 77.10 | 81.91 | 69.00 | 63.50 | 75.12 |
| 2Days to maturity | 114.06 | 114.20 | 118.83 | 111.08 | 113.50 | 114.12 |
| Plant Height | | | | | | |
| -In cm | 96.91 | 111.324 | 92.45 | 90.74 | 76.75 | 131.76 |
| Effective tillers | | | | | | |
| -per plant | 8.59 | 7.38 | 7.40 | 8.55 | 7.10 | 9.15 |
| Spike length | 9.26 | 10.33 | 9.55 | 9.26 | 10.52 | 9.95 |
| Number of seeds | | | | | | |
| -per spike | 44.21 | 42.18 | 43.60 | 38.81 | 48.60 | 38.92 |
| 1000 seed weight | 40.14 | 35.43 | 42.22 | 36.94 | 37.84 | 41.30 |
| Seed yield per plant | 11.88 | 10.33 | 11.05 | 10.66 | 9.10 | 12.84 |

Promising genotypes selected from diverse cluster:

| Cluster | Desirable characters and mean values in parentheses. |
|---------|---|
| VI | Grain yield per plant (12.84), tillers per plant (9.15) and plant height (131.76). |
| V | Spike length (10.52), grains per spike (48.60) and days to 50% flowering. |
| III | Test weight(42.27) |
| I | Grains per spike (44.22), grain yield per plant (11.88) and tillers per plant (8.59). |

and accordingly, cluster IV has been identified for selecting parents for incorporating early maturity and tillers per plant. Cluster V for early maturity, spike length and number of grains per spike. Cluster VI for tiller per plant, 1000 grain weight and grain yield per plant and it is also reported as Bergale *et al.*, (2001). The genotypes superior in the above cluster may be involve in a multiple

crossing programme to recover transgressive segregants with high genetic yield potential. It is observed that days to maturity, plant height, grains per spike and effective tillers per plants are showing positive significant relationship with grain yield. So it is further suggested that grain/ spike and tillers per plant may be used a criteria for single plant selection in the early segregating generation derived from the multiple crosses among the selected genotypes. So, hybridization between genotypes of divergent cluster will lead to accumulation of favourable genes in a single variety and also suggested to create variability for developing the varieties involving a large number of different lines instead of closely instead of closely related ones.

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