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Short Communication

Genetic diversity pattern in wheat [*Triticum aestivum* (L.) em. Thell.]

M. C. Upreti, A. S. Jeena[1], S. K. Malik and T. B. Singh

Dept. of Genetics and Plant Breeding, G.B. Pant University of Agriculture & Technology, Pantnager 263 145

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The present study was aimed at evaluation of the genotypes and simultaneous clustering into diverse group in order to identify desirable parents for recombinant breeding to break the existing yield platue in wheat [*Triticum aestivum* (L.) em. Thell.]. The experiment was conducted at Crop Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar during *rabi* 2000-2001. Sixty elite breeding lines of wheat were evaluated for yield components in augmented design with three checks. Field layout consisted of six blocks with thirteen genotypes each and checks replicated in all the blocks. Each entry was sown in five rows of 5m length with a spacing of 23 cm × 10 cm. Days to heading and tillers per m^2 were recorded on plot basis, however, observations on other yield components *viz.*, plant height, grains per spike, test weight and biological yield along with seed yield were taken on a random sample of ten plants from each plot excluding the border rows. Harvest index was calculated as percentage of seed yield over biological yield. Data was subjected to analysis of variance for augmented design. Means for all characters were adjusted for block effect and used for genetic divergence analysis through hierarchical cluster analysis procedure [1]. A nonparametric measure of genetic distance between genotypes i.e. Euclidean distance, could be estimated from the mean of genotypes without replication. So that it can be applied to the adjusted mean obtained in the augmented design. In a broad sense all the methods of classifying genotypes into different groups were comparable but dendrogram clustering gave an additional advantage of identifying sub-cluster of the major groups at different phenon levels so that each small group can be more critically analysed [2]. The complete linkage based on Euclidean distances was utilized for sequential, agglomerative, hierarchic, non-overlapping clustering and dendrogram drawn through joining tree-clustering algorithm. Group constellation was done at 60%, 30% and 15% of the maximum distance recorded i.e. 60, 30 and 15 percent of the total dissimilarities observed among the genotypes studied. K-mean clustering was also worked out as described by [3]. The number of clusters was decided as observed at 30% dissimilarities in joining tree clustering. Statistical analysis was done using STATISTICA package [4] on computer.

Analysis of variance for checks revealed the significant differences among the checks for biological yield, harvest index and seed yield. Non-significant replication effect for all the traits revealed that the treatment means were indicative of genotypic values of the genotypes. The adjusted mean of the genotypes were tested using LSD against the superior check. On the *per se* performance, 26 genotypes were superior to the best check WH147 for days to heading in which 23 were significantly superior, reflecting earliness of the genotypes. The earliest three genotypes were WR849, WR841 and KLA9801. For plant height only 3 genotypes (PBNS4107, PBND4552 and RD615) exhibited significant superiority over the best check WH147, however, a total of 13 genotypes had dwarf stature then the check. Twenty-three genotypes expressed higher tillers/m^2 then the best check LOK1 but only two genotypes; PBNS4107 and WR833 surpassed the check significantly. Only VW 9641 genotype exhibited significant superiority over the best check WH147 for grains/spike while other 10 genotypes were at par with the check. A maximum of 31 genotypes had higher test weight than the best check HD2009. Among them only five genotypes *viz.*, UPD64, WR887, KYZ9721, UP2490 and UP2425, showed significant superiority. For harvest index, no genotype showed significant superiority. Three genotypes namely MP3077, K9906 and MP3075 exhibited significant superior performance for biological yield in which K9906 reflected significantly higher grain yield over the best check LOK1. For grain yield, however, six genotypes were higher yielder than check, but only one showed significant superiority over the best check LOK1.

[1]Present address: Regional Rice Research Station, Sher-e-Kashmir University of Agricultural Sciences and Technology (Kashmir), Khudwani 192 102 Anantnag (J&K)

The adjusted means of the genotypes were subjected to hierarchical cluster analysis. Euclidean distances were calculated as a measure of dissimilarities among the genotypes and dendrogram was drawn using complete linkage (Fig. 1). In dendrogram euclidean distances were given as percentage of the maximum distance i.e. percentage dissimilarities. Truncation at 60% dissimilarity level created three genetic diverse groups with 43, 9 and 11 genotypes each. Cluster I divided into two sub-clusters *viz.*, I A and I B at 30% level of dissimilarity with 20 and 23 genotypes, respectively. Similarly at 15% level both cluster II and III got divided into two sub-clusters each. Sub-cluster II A and II B comprised seven and two genotypes, respectively while sub-cluster III A and III B consisted nine and two genotypes, respectively. One more division at this level (15% dissimilarity) occurred in the sub-clusters of cluster I, which partitioned sub-cluster I A and I B into two and three sub-sub-clusters, respectively. At this level cluster I A_1 accommodated 15 genotypes and I A_2 five genotypes. The genotypes of I B distributed into clusters I B_1 (9 genotypes), I B_2 (2 genotypes) and I B_3 (12 genotypes).

Four clusters were observed at 30% level of dissimilarities and this number was given for group constellation through K-mean clustering. This algorithm provides exactly same number of clusters as desired with the view that distribution of genotypes will give best solution to maximise inter cluster distance and minimise intra cluster distance. Clustering pattern resulted from this algorithm was almost same as obtained in hierarchical clustering. The significance of group constellation is also evident from the ANOVA for clusters and cluster means for different traits. High and highly significant differences among the clusters were recorded for all the characters except grains per spike. The analysis created four clusters with 25, 11, 20 and 7 genotypes respectively. A comparison was made between clustering pattern arose from both the analysis. It was revealed that distribution of the genotypes through hierarchical cluster analysis (at 30% level of dissimilarity) corresponds to the observed clusters in K-mean clustering to the extent of 93.7% i.e. 59 genotypes out of 63 remained in the same cluster. The discrepancy for the rest of the genotypes could be attributed to the differences in the method of group constellation. Inter cluster distances indicated that cluster IV stands at maximum distance from cluster II (648.53) followed by cluster III with II (461.69) and cluster IV with I (363.87). It could be expected here that hybridization between genotypes of cluster IV with II and I and cluster III with II will results in high heterotic F_1's and better recombinants in segregating generations. Cluster I could serve as donor for earliness and high harvest

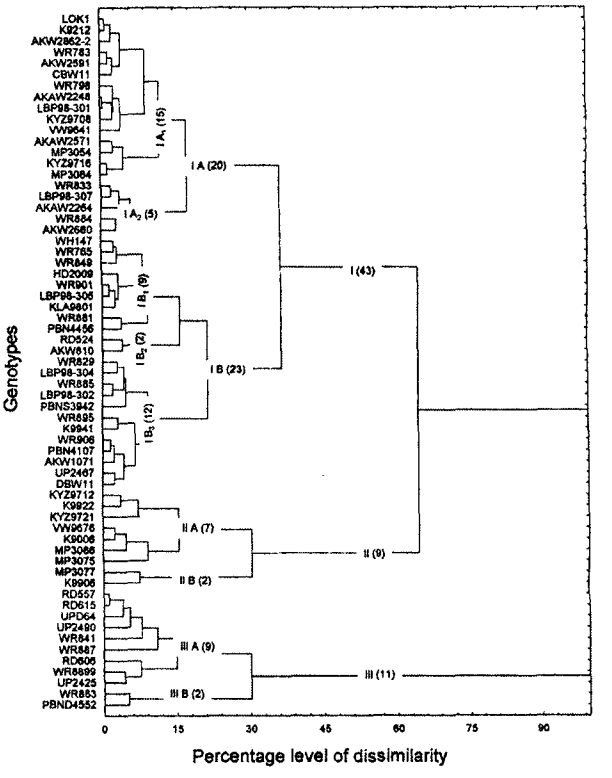

Fig. 1. Dendrogram of wheat genotypes based on Euclidean distance (complete linkage)

index and cluster III for grains per spike only, Cluster II exhibited high test weight and dwarf ness. Best parents for high biological as well as seed yield and tillers per m^2 could be obtained from cluster IV.

The present study indicated the usefulness of hierarchical classification of the genotypes. This method is equally good to D^2 analysis [2], especially when a large collection of genotypes have to be classified [5]. The results of cluster analysis can contribute directly to development of classification schemes and also to identification of diverse parents for hybridization.

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