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Quantifying diversity through morphological and molecular markers in wheat genotypes

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ABSTRACT : Genetic diversity among 37 wheat genotypes belonging to *Triticum aestivum*, durum and dicoccum from DWR Karnal was studied using Mahalanobis D^2 analysis and random amplified polymorphic (RAPD) analysis. A total of 10 clusters were formed from morphological studies, with the major contribution from the characters like days to 50 per cent flowering and spike length. RAPD analysis with 10 primers, generated 56 amplification products of which 54 amplicons were polymorphic, however, the extent of polymorphism varied with each primer. The values of diversity coefficient ranged from 4.00 to 51. Cluster analysis showed considerable amount of diversity in the material used. The clustering pattern revealed that nine clusters formed from RAPD analysis showed that the genotypes which exhibited low diversity at phenotypic level, exhibited higher diversity at molecular level, *i.e.* D^2 analysis and DNA finger printing was not fully concurrent. The difference between morphological and molecular diversity showed that grouping of genotypes or diversity is independent of geographical location and ploidy level or even phenotypic markers.

Key Words : RAPD, Diversity, DNA finger printing

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Wheat is the world's second most important cereal crop. It is aptly described as the 'king of cereals' because of the acreage it occupies, high productivity and the prominent position it holds in the international food grain trade. Genetic diversity plays an important role in plant breeding either to exploit heterosis or to generate productive recombinants. The choice of parents is of paramount importance in breeding programme. Hence, the knowledge of genetic diversity and relatedness in the germplasm is a pre-requisite for crop improvement programmes.

Assessment of genetic diversity at the molecular level is more meaningful than at phenotypic level as the later involves data on morphological traits which are environmental dependent. Though, they significantly contribute towards phenotypic variation but cannot be accurately phenotyped. Hence, the study of polymorphism is best done at DNA level, the primary source of all biological information. At this level, even seemingly identical accessions could display enormous differences, if appropriate DNA profiling techniques are employed. Randomly amplified polymorphic DNA (RAPD) is one such method (Welsh and McClelland, 1990; Williams *et al.*, 1990) of identifying polymorphism that can be used to elicit information on genetic differences among individuals of a population, between lines or germplasm accessions or any breeding material. In the present study, 37 released and unique varieties were used for assessing the diversity at morphological and molecular level.

RESEARCH PROCEDURE

Morphological diversity:

The experiment was laid out in a Simple lattice design with two replications. Each genotype was grown in a plot of three meter rows of two meter length each with a spacing of 23 cm between rows at wheat Improvement Project, Main Agricultural Research station, Dharwad.The recommended package of practices was followed. The data on morphological characters were recorded on a five competitive plants in each plot.

DNA extraction:

The DNA was extracted from 5g of bulked sample of