



RESEARCH PAPER

# Assessing genetic diversity in bread wheat using inter simple sequence repeat (ISSR) markers

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A major effort of a plant breeder is the constant improvement of the best available genotypes for further enhancement in their yield potential either directly or through improvement of various factors which contribute indirectly to high yield. Genetic diversity of wheat cultivars is very important in reducing genetic vulnerability during plant breeding efforts. In order to estimate the genetic diversity, molecular markers provide excellent tools. The aim of this study was to molecularly characterize the fifty wheat accessions to assess phylogenetic relationship and mutual genetic distances through the use of 10 ISSR markers and 50 accessions of wheat. The dendrogram separated genotypes into two clusters I and II comprising of 49 and 1 accessions, respectively. The allelic polymorphism information content (PIC) value ranged from 0.147 to 0.467 with an average of 0.287. The similarity co-efficient ranged from .41 to .89. Significant correlation of microsatellite genetic distance was tested by mantel test ( $r=0.77557$ ). Results shows that high level of polymorphism among the wheat accessions. Cluster analysis suggested that ISSR markers were efficient tools for estimating intra-specific genetic diversity in wheat and this molecular marker could differentiate the accessions obtained from different locations. ISSRs have been successfully used to estimate the extent of genetic diversity at inter- and intra-specific level in a wide range of crops. The genetic relationships estimated by the polymorphism of ISSR markers revealed greater level of genetic variability in wheat accessions of wide adaptability and applicability.

**Key words** : Bread wheat, Genetic diversity, ISSR markers, Wheat accessions

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