

USE OF GENOMIC AND EST-DERIVED SSR MARKERS IN WHEAT PHILOGENETIC ANALYSIS

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Molecular markers are used for a wide range of purposes in crop genetics and breeding including genetic linkage and comparative mapping, positional cloning, genetic diversity assessment, phylogenetic analysis, genotypic profiling, detection of quantitative trait loci (QTLs) and marker-assisted selection (MAS). Genomic microsatellites (or Simple Sequence Repeats, gSSR) have attracted relatively more attention because of their abundance in plants genome, reproducibility, high level of polymorphism, and codominant inheritance. Recently, due to the availability of enormous data for expressed sequence tags (ESTs), more emphasis has been given to EST-derived SSRs, which belong to the transcribed regions of DNA and are expected to be more conserved and have a higher rate of transferability across species than genomic SSR markers. In the present study, 79 gSSR and 61 EST-SSR markers were used to investigate their transferability and level of DNA polymorphism in different ancestral tetraploid and diploid *Triticum* and *Aegilops* species more or less closely related to common wheat, and their applicability for phylogenetic analysis of wheat. The transfer rate was correlated with the genetic relatedness of the examined species. The average transfer rate of gSSR was different from the average transfer rate of EST-SSR markers. The range and the number of alleles per locus indicated that gSSRs are more polymorphic than EST-SSRs. Both phylogenetic trees based on gSSR and EST-SSR markers were in agreement with the phylogenetic relations based on cytogenetic and molecular analysis. The use of transferred polymorphic SSR markers for the characterization and evaluation of germplasm and for phylogenetic analysis of wheat are discussed.