Abstract

Discoveries of miniature inverted-repeat transposable elements (MITEs) reaching high copy numbers in eukaryotic genomes have become increasingly prevalent in genome studies. Consequently, an understanding of the underlying mechanisms of their transposition as well as the characterization of existing and novel MITEs has become highly sought after in these studies. Experimentally, an IPCR-based system using an asexual population of *Saccharomyces cerevisiae* was developed to detect the copy number of the T7-neo MITE in the yeast genome and allow for subsequent investigations into MITE amplification. However, this system resulted in minimal detection of the T7-neo MITE present in the genome. Additionally, using bioinformatics programs MITE Digger and Mite Analysis Kit (MAK), MITE families were classified and characterized in the recently sequenced genome of *Solanum lycopersicum*. A total of 37 MITE families were classified, showing characteristics of DNA transposon superfamilies including *Tc1/mariner*-, *CACTA*--, *PIF/Harbinger*-, *hAT*- and one *Transib*-like element. Divergence of the MITE families was calculated based on a consensus sequence and those least diverged were
analyzed for evidence of transcription. BLASTn searches of NCBI EST databases were conducted and four of these families showed evidence of being transcribed. Some families were also identified in other Solanaceae genomes, indicating possible evolutionary relationships among the genomes of *Solanum lycopersicum*, *Solanum pimpinellifolium*, *Solanum tuberosum*, and *Nicotiana tabacum*. Overall, the framework of an experimental MITE amplification system has been laid while *de novo* characterization of MITEs in eukaryotic genomes will contribute to a more complete understanding of MITE amplification in eukaryotic genomes.