

Genomic and Evolutionary Diversity of Long Terminal Repeat (LTR) Retrotransposons in Date Palm (*Phoenix dactylifera*)

Authors : Faisal Nouroz, Mukaramin Mukaramin

Abstract : Of the transposable elements (TEs), the retrotransposons are the most copious elements identified from many sequenced genomes. They have played a major role in genome evolution, rearrangement, and expansions based on their copy and paste mode of proliferation. They are further divided into LTR and Non-LTR retrotransposons. The purpose of the current study was to identify the LTR REs in sequenced *Phoenix dactylifera* genome and to study their structural diversity. A total of 150 *P. dactylifera* BAC sequences with > 60kb sizes were randomly retrieved from National Center for Biotechnology Information (NCBI) database and screened for the presence of LTR retrotransposons. Seven bacterial artificial chromosomes (BAC) sequences showed full-length LTR Retrotransposons with 4 Copia and 3 Gypsy families having variable copy numbers in respective families. Reverse transcriptase (RT) domain was found as the most conserved domain among Copia and Gypsy superfamilies and was used to deduce evolutionary analysis. The amino acid residues among various RT sequences showed variability in their percentages indicating post divergence evolution. Amino acid Leucine was found in highest proportions followed by Lysine, while Methionine and Tryptophan were in lowest percentages. The phylogenetic analysis based on RT domains confirmed that although having most conserved RT regions, several evolutionary events occurred causing nucleotide polymorphisms and hence clustering of Gypsy and Copia superfamilies into their respective lineages. The study will be helpful in identification and annotation of these elements in other species and genera and their distribution patterns on chromosomes by fluorescent in situ hybridization techniques.

Keywords : transposable elements, *Phoenix dactylifera*, retrotransposons, phylogenetic analysis

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