

Genome-Wide Analysis of Long Terminal Repeat (LTR) Retrotransposons in Rabbit (*Oryctolagus cuniculus*)

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Abstract : European or common rabbit (*Oryctolagus cuniculus*) belongs to class Mammalia, order Lagomorpha of family Leporidae. They are distributed worldwide and are native to Europe (France, Spain and Portugal) and Africa (Morocco and Algeria). LTR retrotransposons are major Class I mobile genetic elements of eukaryotic genomes and play a crucial role in genome expansion, evolution and diversification. They were mostly annotated in various genomes by conventional approaches of homology searches, which restricted the annotation of novel elements. Present work involved de novo identification of LTR retrotransposons by LTR_FINDER in haploid genome of rabbit (2247.74 Mb) distributed in 22 chromosomes, of which 7,933 putative full-length or partial copies were identified containing 69.38 Mb of elements, accounting 3.08% of the genome. Highest copy numbers (731) were found on chromosome 7, followed by chromosome 12 (705), while the lowest copy numbers (27) were detected in chromosome 19 with no elements identified from chromosome 21 due to partially sequenced chromosome, unidentified nucleotides (N) and repeated simple sequence repeats (SSRs). The identified elements ranged in sizes from 1.2 - 25.8 Kb with average sizes between 2-10 Kb. Highest percentage (4.77%) of elements was found in chromosome 15, while lowest (0.55%) in chromosome 19. The most frequent tRNA type was Arginine present in majority of the elements. Based on gained results, it was estimated that rabbit exhibits 15,866 copies having 137.73 Mb of elements accounting 6.16% of diploid genome (44 chromosomes). Further molecular analyses will be helpful in chromosomal localization and distribution of these elements on chromosomes.

Keywords : rabbit, LTR retrotransposons, genome, chromosome

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