

Cytogenetic and molecular analysis of LINE-1 sequences in *Tatera gambiana* and *Acomys* sp. rodents

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It have been demonstrated that repetitive DNA elements contribute to the evolution of Eutherian genomes. Their dynamic nature represents a major force that shapes genome's size, configuration and plasticity. Almost half of the mammalian genome derives from ancient transposable elements, an interspersed repetitive DNA. "Long Interspersed Nuclear Elements" (LINEs) are an ancient family of autonomous non-LTR retrotransposons, being the LINE-1 (L1) the most recent lineage and the only autonomous non-LTR retrotransposons in rodents. L1 have shaped and expanded mammalian genomes through their own retrotansposition; the assistance in retrotransposition of other mobile elements (providing the machinery necessary for their retrotransposition); transduction (promoting the shuffling of non-L1 sequence throughout the genome); and by affecting gene expression. Different authors suggested that L1 are not transposed randomly and the target sites might be conserved among mammalian species, making them non-homoplastic markers, what increased the use of L1 insertions as phylogenetic markers. In order to make a phylogenetic analysis in the rodents *Acomys* sp. (Rodentia, Muridae, Deomyinae) and *Tatera gambiana* (Rodentia, Muridae, Gerbillinae), we isolated a fraction of L1 sequence from these genomes and analysed its physical distribution. The same chromosome preparations were then submitted to classical C-banding, allowing its precise chromatin distribution. The isolated sequences were then sequenced and molecularly analysed and compared with LINE-1 sequences available on the NCBI Nucleotide database.