

Transposons like selfish and domesticated elements in *Rhynchosciara americana* genome

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Rhynchosciara americana became a valuable model system for the research of developmental biology, due to the peculiar biological characteristics which allowed the association of the molecular biology with morphological aspects. From the analysis of sequences of a cDNA library constructed with mRNA of larval salivary glands of *Rhynchosciara americana* it was possible to identify the presence of different families of transposable elements, in a larval period when genomic DNA is under the last endoreplication cycle, just before the metamorphosis and tissue regression. The transposable elements are discrete sequences that can move around to different positions in the genome, and constitute a significant part of eukaryotic genome. They consist of two main classes, Class I elements transpose by reverse transcription of a RNA intermediate (retrotransposons), and Class II elements transpose via a DNA “cut-and-paste” mechanism (transposons), encode their own transposase and are flanked by short inverted terminal repeat. Class I member was characterized in molecular and cytological aspects, and some interesting data were obtained by *in situ* hybridization on salivary gland polytene chromosomes and by interference RNA experiments. The localization of a non-LTR retrotransposon in chromosome ends and its homology with *Drosophila* telomeric elements suggested an association to telomere on diptera *Rhynchosciara americana*. The non-LTR retrotransposon knockdown effect resulted in speeded up in the larval development; this result represents an interesting relationship between the non-LTR retrotransposon and the control of development timing. The present results are the first evidence of transposable elements in the genome of *Rhynchosciara americana*. The characterization of non-LTR retrotransposon that apparently has a defined biological process function it challenges the basic definition of selfish element.

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