Nucleic Acids Research 2018 vol.46 N2, pages 765-781

Trypanosomatid mitochondrial RNA editing: Dramatically complex transcript repertoires revealed with a dedicated mapping tool

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Abstract

© The Author(s) 2017. RNA editing by targeted insertion and deletion of uridine is crucial to generate translatable mRNAs from the cryptogenes of the mitochondrial genome of kinetoplastids. This type of editing consists of a stepwise cascade of reactions generally proceeding from 3' to 5' on a transcript, resulting in a population of partially edited as well as pre-edited and completely edited molecules for each mitochondrial cryptogene of these protozoans. Often, the number of uridines inserted and deleted exceed the number of nucleotides that are genome-encoded. Thus, analysis of kinetoplastid mitochondrial transcriptomes has proven frustratingly complex. Here we present our analysis of Leptomonas pyrrhocoris mitochondrial cDNA deep sequencing reads using T-Aligner, our new tool which allows comprehensive characterization of RNA editing, not relying on targeted transcript amplification and on prior knowledge of final edited products. T-Aligner implements a pipeline of read mapping, visualization of all editing states and their coverage, and assembly of canonical and alternative translatable mRNAs. We also assess T-Aligner functionality on a more challenging deep sequencing read input from Trypanosoma cruzi. The analysis reveals that transcripts of cryptogenes of both species undergo very complex editing that includes the formation of alternative open reading frames and whole categories of truncated editing products.

http://dx.doi.org/10.1093/nar/gkx1202

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