KinetoUTR: a tool for visualization and analyses of mRNA regulatory elements in kinetoplastids

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Background
Kinetoplastids are a group of flagellate protozoa, including parasites responsible for serious diseases in human and other animals, such as Chagas' Disease, Sleeping Sickness and Leishmaniasis. They diverged early in eukaryote evolution and consequently display unique cellular properties: Protein-coding genes are transcribed polycistronically by RNA polymerase II; Individual mature mRNAs are generated from polycistronic precursors by 5' trans-splicing of a leader RNA and 3' polyadenilation. A few cis-acting RNA elements in 3'-untranslated regions (UTRs) of mRNAs have been identified in trypanosomatids, which affect the mRNA stability or translation rate. This work aims to develop a tool for visualization and analyses of putative cis-regulatory elements in UTRs in the five kinetoplastid species with genome information available.

Materials and Methods
We have implemented a local database using an ad hoc schema in PostGreSQL, uploaded with genomic information from Trypanosoma brucei, T. cruzi, Leishmania major, L. braziliensis and L. infantum (RefSeq NCBI); and the orthologs group information from OrthoMCLDB (http://www.orthomcl.org/cgi-bin/OrthoMclWeb.cgi). We have also determined and uploaded the 5' and 3' UTR sequences for each gene. The web interface has been done in XHTML and CSS, running in an Apache server. Browser-server connections have been developed in CGI-PERL and figures were done with Bio::Graphics module from Bioperl project (http://www.bioperl.org/wiki/Main_Page).

Results
We have developed a prototype web tool for visualizing and analyzing cis-regulatory elements in trypanosomatids UTRs. We have implemented the following functionalities in the system: precomputed analyses of putative regulatory elements in UTRs using MEME and FIRE; visualization of precomputed regulatory elements in the UTRs of orthologous groups of genes in the five trypanosomatid species; visualization of genomic context for a specific gene using Gbrowse; search for a specific interest gene using ID or text search; statistical test for enrichment of a specific putative regulatory sequence in CDS, 5'UTR, 3'UTR in a global genome analysis and in a dataset provided by the user (results from ribonomics assays for example) for each species; prediction of trans-splicing and polyadenilation sites for T. cruzi based in short reads from 454 FLX and SOLiD.

Conclusions
KinetoUTR is capable of performing data comparison across genes and species, which improves determination of cis-acting elements involved in post-transcriptional gene expression control. This tool is being integrated with other high-throughput dataset that are being generated in our Institution, aiming to create an initial map of gene expression regulation.

References
http://www.orthomcl.org/cgi-bin/OrthoMclWeb.cgi
http://www.bioperl.org/wiki/Main_Page