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In silico characterization of sequence conservation in the 5' and 3' untranslated regions between Leishmania species

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Short Abstract: In this study we are characterizing sequence conservation in the 5' and 3' untranslated genomic regions between Leishmania species. The study of these regions could shed light on the understanding of the post-transcriptional control mechanisms in these parasites. A sequence analysis pipeline and preliminary results of motifs conservation will be presented.

Long Abstract:
The recent availability of the Tritryp (Leishmania major, Trypanosoma brucei and Trypanosoma cruzi) genomes is a marker for the knowledge of the biology of these three pathogens.
Whereas analysis of a single genome provides remarkable biological insights on any particular organism, comparative analysis of multiple genomes provides considerably more information. Regarding Leishmania it expands our ability to: (i) understand the genetic and evolutionary bases of the shared and distinct parasitic modes and lifestyles and (ii) better assign putative function to predicted coding sequences.
In Leishmania protein-coding genes are grouped in long polycistronic units and the lack of transcriptional control in trypanosomatids suggests that other control mechanisms may have evolved in order to regulate mRNA levels.
Sequence conservation analysis in the 3' and 5' untranslated regions of protein coding genes between Leishmania species could be the computational key to a more complete understanding of the post-transcriptional control mechanisms that remains not fully elucidated in these organisms.
Leishmania (Viannia) braziliensis is one of the causative agents of cutaneous leishmaniasis (CL) in Brazil and its infection leads to a broad spectrum of clinical, histopathological, and immunological manifestations. In this study, taking L. braziliensis as model organism, we are characterizing sequence conservation in the 5' and 3' untranslated regions between Leishmania species.
Taking into accounting that intercoding regions are composed by sequences with low functional constraint and high mutation levels compared to CDSs (Coding DNA Sequences), we are currently in the process of identification and statistical validation of intercoding sequence motifs associated with the three parasite genomes. A sequence analysis pipeline will be presented together with motifs associated to gene ontology families assigned to predicted proteins in the genome annotation of the parasites.