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Characterization of putative chromosomal rearrangements related to chromosomes ends between *Leishmania* species. An in silico approach.



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Short Abstract: In this study we are characterizing genomic rearrangements at chromosome ends in *Leishmania* spp. This comparative analysis could contribute to the understanding of genetic diversity of parasites and the identification of patterns associated with the molecular evolution process. An analysis pipeline and preliminaries results of recombination events will be presented.

Long Abstract:

The large number of complete and ongoing genome projects related to pathogenic organisms together with the advances of bioinformatics, permit not only a comparison between species on the basis of homologous proteins sequence differences but with respect to the rearrangements of groups of genes and large fragments of chromosomes.

In trypanosomatids the study of genomic rearrangements can contribute to the understanding not only of the genetic diversity among these organisms, but also to the knowledge of evolutionary aspects of the mechanisms involved in the control of the changes in genic order and gene distribution among the chromosomes. Genomic rearrangements can also play a key role in molecular evolution, since rearrangement of genes can either induce or reflect evolutionary changes.

Protozoan parasites of the genus *Leishmania* are the causative agents of leishmaniasis, a spectrum of diseases with different clinical manifestations ranging from mild cutaneous lesions to severe fatal visceral form. Leishmaniasis is widely distributed in Tropical and Sub-Tropical areas of the world and one of the major parasitic diseases targeted by the World Health Organization (WHO).

In this study, focusing on *Leishmania* (*Viannia*) *braziliensis* that is one of the causative agents of cutaneous leishmaniasis (CL) in Brazil and using information from the published *Leishmania* major genome and from *Leishmania infantum* and *Leishmania braziliensis* genome sequencing projects, currently underway, we are characterizing sequences involved in chromosomal ends rearrangements, the level of synteny (conservation of gene order) among these three organisms and analysing the location of *L.braziliensis* specie specific genes.

We are currently in the process of mapping genome chromosomal ends rearrangements events in the three *Leishmania* species and searching for retrotransposon-like elements associated with these regions. A comparative analyses pipeline using global and local

alignment search tools (FASTA and BLAST) together with specific PERL scripts for the parsing and analyses of the similarities results together with graphical representation of putative recombination events will be presented.

Preliminary results of mapped rearrangements and the genes families involved will also be presented, beyond the analysis of specie-specific genes.