Searching trypanosomatid genomes for deubiquitinating enzymes

Olmo,R.P.[1], Oliveira,L.G.[1], Souza,D.M.[1], Gomes,M.S.[1], Martino,N.C.[1], Queiroz,K.B.[1], Guerra-Sá,R[1]

[1]NUPEB/ICEB, Universidade Federal de Ouro Preto-UFOP, Ouro Preto/MG, Brazil.

The genome sequences of *Leishmania braziliensis*, *L. chagasi* and *Trypanosoma cruzi* revealed that each genome contains 8300-12000 protein-coding genes, of which approximately 6500 are common to their genomes. In this study, we focused the mining the trypanosomatid databases looking for proteins involved in ubiquitin metabolism. There are basically five distinct subfamilies of enzymes involved in this pathway and denominate DUBs: ubiquitin C-terminal hydrolases (UCHs), ubiquitin-specific processing proteases (USPs), Machado-Joseph disease protein domain proteases (MJDs), ovarian tumour proteases (OTUs) and JAMM motif proteases. In this work we used bioinformatic approaches to identity these set of enzymes in public databases. Our *in silico* search retrieved 106 putative entries coding to DUBs among *L. infantum*, *L. chagasi* and *T. cruzi* databases when compared to known GenBank ortholog proteins through BLASTx. Of these, 59 belong to USP subfamily, 23 to JAMM, 6 to UCH, 11 to OTU, and where not found entries to MJD. In *T. cruzi* genome was also observed the presence of duplicated genes, where the 58 entries might be resumed, with at least 95% of similarity, in 28 sequences. However, in each *Leishmania* genome studied were found 24 entries for DUBs, but most of them have its orthologues into the same genus. Comparative analysis of genes responsible for ubiquitin removal showed significant difference in their respective nucleotide sequence lengths as well as amino acid composition, especially with regards to regions outer conserved domains, suggesting maintaining of function, but different substrate specificity. These results evidence the complexity and diversity of DUBs in tripanosomatids and open the possibility to explore the relevance of their interactions in regulation of ubiquitin-mediated pathways in these parasites.

Financial support: CNPq, UFOP.