CLONING AND SEQUENCING OF THE TRNA LIGASE FROM *LEISHMANIA MAJOR*

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Visceral and cutaneus leishmaniosis are diseases that affect millions of people in the whole world, mainly in Central America, South America, Africa and Asia. These illnesses are caused by the tripanosomatid *Leishmania major*. The present study is concentrated on the tRNA ligase of this protozoa (Trl1-like). This enzyme shows a narrow spectra of distribution among the three Kingdoms of life, being present only in the trypanosomatids and some fungi, as such, it is a promising target for drug development. The tRNA ligases are responsible for the ligation of the two halves of the tRNA molecule after the intron editing by an endonuclease. In the absence of a tRNA ligase, functional tRNA molecules are not synthesized and the protein synthesis of the organism is stalled. In order to perform our studies, the gene of the tRNA ligase from *Leishmania major* was amplified from the genomic DNA and cloned into pET15b with an N-terminal His-tag for its easier overexpression and purification. The sequencing of the amplified gene didn't show any mutations when compared to the gene present in the *Leishmania major*'s genome database (www.sanger.ac.uk/projects/l_major). Now we will be able to continue our studies by performing an "in vitro" biochemical characterization of the recombinant enzyme.

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