

Tetracycline-inducible gene expression system in *Leishmania mexicana*

Natalya Kraeva¹, Aygul Ishemgulova¹, Drahomíra Faktorová², Lucie Podešvová¹, Julius Lukeš^{2,3,4}, Vyacheslav Yurchenko^{1,2,5,6}

¹ Life Science Research Centre, Faculty of Science, University of Ostrava, Ostrava, Czech Republic, ² Biology Centre, Institute of Parasitology, Czech Academy of Sciences, České Budějovice (Budweis), Czech Republic, ³ Faculty of Sciences, University of South Bohemia, České Budějovice (Budweis), Czech Republic, ⁴ Canadian Institute for Advanced Research, Toronto, Canada, ⁵ Department of Pathology, Albert Einstein College of Medicine, Bronx, NY, USA, ⁶ Institute of Environmental Technologies, Faculty of Science, University of Ostrava, Ostrava, Czech Republic.

Leishmania mexicana is a flagellated protist of the family Trypanosomatidae causing cutaneous leishmaniasis in humans. The genome sequence of this medically important parasite is available, but our understanding of its biology still critically depends on functional analysis of the *L. mexicana* proteins. At the moment, set of genetic tools for functional analysis is limited. In this work we established a T7 polymerase-driven Tetracycline-inducible protein expression system in *L. mexicana* (isolate MNYC/BZ/62/M379). We used this system to analyze gene expression profiles during *Leishmania* development in procyclic-, metacyclic promastigotes, and amastigotes. The transcription of the gene of interest was significantly reduced upon cell differentiation. This was explained by the reduced transcription of the T7 polymerase and Tet repressor. The regulation was not locus-specific and depended on untranslated regions flanking open reading frames of the analyzed genes. This system can be broadly used by the parasitology community to assess effects of certain genes on biology, physiology and virulence of parasites causing cutaneous leishmaniasis. However, it may not be suitable for *Leishmania* differentiation studies.