

PHILOGENY OF *LEISHMANIA* SPECIES BY ANALYSIS OF CODING SEQUENCES FOR TRYPANOTHIONE REDUCTASE

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Leishmania are protozoan parasites that cause a variety of diseases in human. It is estimated that 12 million people are infected worldwide, with 2 million new cases reported annually. Although a variety of approaches have been used in the identification of these parasites, few methods have provided comparative data suitable for investigating the evolutionary relationships among them. Over the last years contradictory hypothesis for either a Neotropical or a Palearctic origin of the genus *Leishmania* have been proposed. The formulation of a robust phylogenetic framework for these organisms is needed for the built up of a consensus picture based on extensive analyses of molecular sequences from several unlinked *loci*. In this work we determine the partial gene sequence encoding the enzyme trypanothione reductase (TR) from New World and Old World *Leishmania* species. TR is a NADPH-dependent oxidoreductase flavoprotein, central to thiol metabolism in all the trypanosomatids. This molecule has a crucial role in the parasite's defense against the oxidative stress inside the macrophage phagocytic vacuole, and therefore in the survival of the parasites during the host immune response. The data obtained in this work with gene amplification and sequencing was used to infer a phylogenetic relationship between the studied species in order to contribute for the solution of the geographic origin of the genus *Leishmania*.