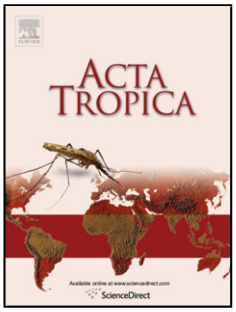

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Trypanosoma cruzi I: Towards the need of genetic subdivision?, Part II

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Abstract

Chagas disease is a complex zoonosis caused by the kinetoplastid parasite *Trypanosoma cruzi*. This protozoan exhibits remarkable genetic diversity evinced in at least six Discrete Typing Units (DTUs) with the foreseen emergence of a genotype associated to bats (TcBat). *T. cruzi* I is the DTU with the broadest geographical distribution and associated to severe cardiomyopathies. In 2011, we published a review questioning the need for genetic subdivision within TcI. However, after six years of intensive research herein, we attempted to determine if TcI should be subdivided or not in the light of the current genetic, biological, clinical and ecological data. The future perspectives are discussed.

Key-words: Chagas disease, TcI, genotypes, $\mathrm{TcI}_{\mathrm{DOM}}$, DTUs

1. Introduction

Chagas disease is a complex zoonosis caused by the kinetoplastid parasite *Trypanosoma cruzi*. This protozoan exhibits remarkable genetic diversity and has been subdivided into at least seven Discrete Typing Units (DTUs) from TcI to TcVI including a recent genotype called TcBat and associated to anthropogenic bats (Lima et al., 2015; Zingales et al., 2012). These DTUs present some associations with the ecology, transmission cycle (domestic/sylvatic) and clinical manifestations of the disease to some