

## Poster 14

### Review of Phylogenetic and Phylogeographic Evolution of *Trypanosoma cruzi* Based on Two Partial Sequences of Mitochondrial Genes.

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**Introduction:** Introduction: Genetic analyses from sequences of *Trypanosoma cruzi* strains are increasing. However, publications generally focus on limited geographic scales or very specific matters –such as clonality vs. genetic exchange– thus providing an incomplete outlook of *T. cruzi* genetic structuration within its entire endemic area.

**Objectives:** The aim of the current analysis is to update previous and current phylogenetic and phylogeographic information on *T. cruzi* at a major geographic scale based on mitochondrial DNA.

**Methodology:** A total of 225 Cyt b and 199 COII partial gene sequences were downloaded from GenBank, aligned and resolved for 490 bp and 386 bp respectively. Within both data sets there were sequences from the six *T. cruzi* discrete typing units (DTU). Phylogenetic reconstruction was performed using median-joining network algorithm (MJ) (<http://www.fluxus-engineering.com>). Geographic origin and the assignment to DTUs were distributed among the network haplotypes for interpretation.

**Results:** For both markers, the network topologies showed that (i) few changes in tree skeletons were observed, (ii) the most ancestral hypothetical *T. cruzi* node separates TcII from other DTUs, (iii) TcI is well differentiated by plenty of mutations, (iv) haplotypes of TcIII and TcIV appeared closely related and (v) their origin remains unclear. Some incongruent haplotype DTU assignments were depicted and may correspond to mitochondrial introgression.

After geographic assignment of the haplotypes, the networks showed that (i) the haplotypes from South Cone countries were the most spread out through the networks (Brazil, Chile and Bolivia in the data set), (ii) TcII haplotypes are not sampled in the countries further north Amazon,

(iii) numerous haplotypes are shared among countries tracing dispersion routes, (iv) most other country specific haplotypes are derived ones, showing more recent local expansions.

**Conclusion:** Based on both previous evolutionary dating and the current revision at a higher geographic scale previously done, important guidelines on *T. cruzi* evolution can be proposed: (i) very long evolution process, (ii) ancient broad dispersion in South America associated with remarkable genetic diversification and (iii) more recent selective dispersion towards the north (Central and North America).

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# II

## WORKSHOP INTERNACIONAL DE LA ENFERMEDAD DE CHAGAS, VECTORES TRIATOMINOS, *Trypanosoma cruzi* Y TRIATOMA VIRUS



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Del 17 al 20 de SEPTIEMBRE DEL 2012

COCHABAMBA - BOLIVIA

**II International Workshop on Chagas Disease,  
triatomine vectors,  
*Trypanosoma cruzi*, and Triatoma virus**



## II International Workshop on Chagas Disease, triatomine vectors, *Trypanosoma cruzi*, and Triatoma virus

In memoriam of Dr François Noireau

Facultad de Medicina, IIBISMED-CUMETROP, Universidad Mayor de San Simón,  
Cochabamba, Bolivia

September 17-20, 2012

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### Workshop objectives

- To inform interested stakeholders about the current Chagas disease burden and control strategies.
- To discuss current and future methods and technologies oriented to control triatomines and other insect vectors.
- To get feedback from associations, industry sector, and research organizations about using *Triatoma* virus as biological control agent.
- To assess research needs and cooperation opportunities between scientists working on human and animal trypanosomiasis, insect vectors and viruses.

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