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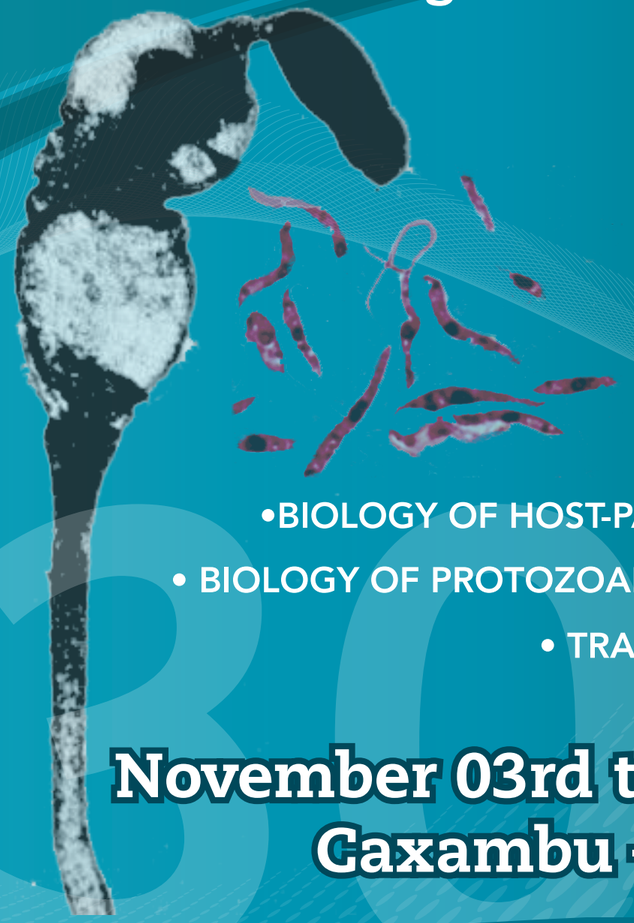
XXX Annual Meeting of the Society of Protozoology

# XXX ANNUAL MEETING of the Society of Protozoology

## XLI Annual Meeting on Basic Research on Chagas' disease



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- BIOLOGY OF HOST-PARASITE INTERACTION
- BIOLOGY OF PROTOZOAN AND THEIR VECTORS
- TRANSLATIONAL BIOLOGY

**November 03rd to 05th , 2014**
**Caxambu – MG – Brazil**

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**TB27 - EVALUATION OF PARASITE BURDEN AND MOLECULAR TYPING OF TRYPANOSOMA CRUZI IN BLOOD SAMPLES FROM PATIENTS WITH CHRONIC CHAGAS DISEASE FROM BRAZIL**

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Chagas disease is a major public health problem in many Latin American countries. Currently, it is estimated that 7 to 8 million people are infected and 75 to 90 million are exposed to the disease. Trypanosoma cruzi, the etiological agent of disease, is represented by a set of strains or isolates that circulate in mammalian hosts and insect vectors, with large heterogeneity of biological behavior and different levels of virulence in humans and animal models, besides distinct levels of drug sensitivity and prognosis of the disease. Thus, one major challenge for the scientific community is to identify T. cruzi genetic markers capable to divide the isolates into discrete groups, searching for a surrogate marker for the pathogenesis of Chagas disease. In this work, we selected 144 patients from the National Institute of Infectious Diseases Evandro Chagas, 72 with positive serology and 72 with negative serology, from different regions of Brazil and presenting distinct clinical manifestations of the disease. For each patient, two blood samples were collected before the beginning of the treatment. To estimate parasitemia, DNA was extracted from blood samples using QIAamp DNA Mini Kit (Qiagen). The parasite load was estimated by TaqMan qPCR assay. Briefly, this multiplex assay comprises one target to T. cruzi nuclear satellite DNA and one target to human RNase P gene, as an internal control. So far, qPCR was performed for 278 samples, which 89 were positive for T. cruzi. Parasite load varied from 0.005 ± 0.003 to 336.09 ± 48.59 parasite equivalents/mL. In parallel, we are conducting the standardization of T. cruzi genotyping directly from blood samples, based on the methodologies based on conventional described by Burgos et al., (2010) and Ramirez et al., (2010), in order to investigate the correlation between parasite load, T. cruzi genotype and progression of Chagas disease. **Supported by:**CAPES/FAPERJ/IOC-FIOCRUZ

**TB28 - EFFECT OF 1,2,3 TRIAZOLE DERIVATIVES AGAINST *LEISHMANIA* SPECIES ASSOCIATED TO CUTANEOUS LEISHMANIASIS.**

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Leishmaniasis is a parasitic diseases caused by the flagellate protozoa of the genus *Leishmania*. The first-line treatment in Brazil is based on meglumine antimoniate (Glucantime). Other drugs used as second choice are amphotericin B and pentamidine. All these drugs have a large number of problems, including considerable toxicity, adverse effects, and high cost of production. So, is urgent the necessity of new drugs for chemotherapy of the leishmaniasis. The objective of this work was to evaluate the leishmanicidal activity of 1,2,3 triazole derivatives against promastigote of L. *amazonensis* and *L. major*. The anti-promastigote activity and cytotoxicity in peritoneal macrophages were evaluated by the MTT colorimetric method after 72 hours of treatment. Results were expressed as $IC_{50}$ (molecular concentration that inhibits 50% of the parasite growth). Among the five compounds evaluated, four compounds exhibited a strong leishmanicidal activity (the $IC_{50}$ < 1,0 µM). The compounds 1, 3, 4 and 5 exhibited a very significant leishmanicidal activity with $IC_{50}$ of 0.16; 0.69; 0.10; 0.20 µM for *L. amazonensis*, respectively and $IC_{50}$ of 0.25; 0.30; 0.13; 0,25 µM for *L. major,* respectively. Regarding the cytotoxicity in macrophages all compounds showed a toxic effect, which shows the low selectivity for the parasite. Modifications in the structure will be conducted to improve the selectivity of these compounds. **Supported by:**FAPEMIG; CNPq; UFJF