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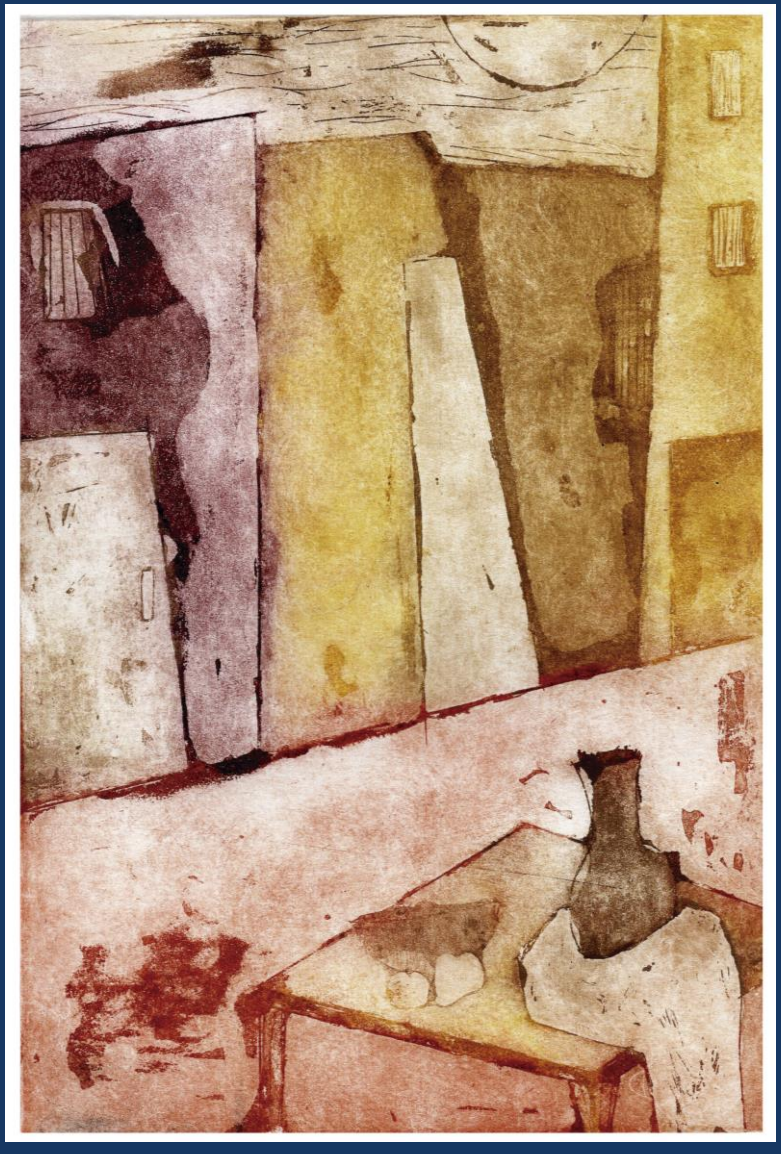

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La Tapa (Ver pág. 4)
Atardecer en la tarde
Antonella Ricagni

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VI Reunión Científica Regional de la Asociación Argentina de Ciencia y Tecnología de Animales de Laboratorio (AACyTAL)

con la participación de
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to the flagellar pocket of the parasite and there is evidence that it forms a homotrimer. Conversely to other trypanosomatids, no hemoglobin (Hb) receptor has been found in T. cruzi yet. Given these precedents, we investigated if TcHTE has a role in Hb uptake from the extracellular medium or in Hb-derived heme transport. At mRNA and protein level, TcHTE is higher in heme starved Wild Type epimastigotes, and it gradually decreases when increasing amounts of a heme source (hemin or Hb) are added to the media. However, this response is faster when hemin is used as heme source, which may be related to the different biodisponibilities and/or uptake mechanisms of both heme sources. Surprisingly, epimastigotes that overexpress rTcHTE.His-GFP incubated in media supplemented with Hb have a significantly higher intracellular heme content compared to control epimastigotes; as previously reported using hemin as heme source. Altogether, these results mean that TcHTE is also involved in Hb uptake. Conversely to Trypanosoma brucei ortholog rTbHRG, rTcHTE.His-GFP does not change its localization when Hb is used as heme source, which discards that TcHTE has a role in the salvage of Hb-derived heme in internal compartments. We concluded that T. cruzi is able to sense intracellular heme level and regulates TcHTE expression according to it. Based on these and our previous results we propose two models of heme uptake in T. cruzi. In the first one, Hb is endocyted via a non-canonical Hb receptor and Hb-derived heme is transported through an unknown protein, meanwhile heme enters the cell via TcHTE. In the other model, Hb is degraded by external proteases in the parasite's surface, heme is released and enters the cell via TcHTE.

0778 - FUNCTIONAL ROLES OF AMP-ACTIVATED PROTEIN KINASE (AMPK) COMPLEXES CONTAINING TCAMPKA1 OR TCAMPKA2 IN ENERGY HOMEOSTASIS REGULATION AND CELL CULTURE PROGRESSION IN TRYPANOSOMA CRUZI

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INGEBI-CONICET (1); INGEBI- CONICET- UBA (2)

Abstract/Resumen: The AMP-activated protein kinase (AMPK) is a heterotrimeric enzyme involved in maintaining energy homeostasis in response to different stresses in many organisms. During the transition between the mammalian host and the insect vector, Trypanosoma cruzi, the causative agent of Chagas disease, faces different types of environmental fluctuations, all of which prompt the parasite to remodel its metabolism. Recently, it was shown that Trypanosoma brucei AMPK is involved in the differentiation from the bloodstream slender to stumpy stage and in surface protein expression changes in response to nutritional stress. This underscores the relevance of AMPK for parasite life cycle progression. We identified four candidate genes for the AMPK subunits of T. cruzi (alpha1 and alpha2 catalytic subunits, beta and gamma regulatory subunits). The beta and gamma subunits are largely conserved in their domain structure relative to the mammalian orthologs. However, the alpha subunits show significant sequence and structure differences from the human counterparts. The presence of these subunits in T. cruzi epimastigotes was confirmed by RT-PCR, Western blot using a phospho-AMPKa specific antibody, mass spectrometry and by kinase activity assays using the specific AMPK substrate SAMS. TcAMPKa1 over-expressing epimastigotes showed a lower growth rate in basal culture conditions compared to the control. On the other hand, alpha2 over-expression had the opposite effect. Additionally, we observed upregulation of AMPK activity under epimastigote starvation, and that dorsomorphin, a specific AMPK inhibitor, also inhibits T. cruzi AMPK. Moreover, each of these subunits could complement S. cerevisiae conditional mutants lacking the respective subunit of the AMPK ortholog SNF1. Finally, starving assays with AMPKa over-expressing parasites also showed a possible role of AMPK in autophagy. Overall, our results show for the first time, the presence of a functional AMPK orthologue in Trypanosoma cruzi.

0688 - THE GENOME OF THE SYLVATIC SPECIES ECHINOCOCCUS OLIGARTHRUS: PHYLOGENETIC HISTORY OF ECHINOCCOCUS THROUGH WHOLE GENOME VARIANTS ANALYSIS

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IMPAM (UBA-CONICET) (1); INSTITUTO DE MEDICINA TROPICAL "DR. FELIX PIFANO" (2); INSTITUTO TECNOLÓGICO VALE (3)

Abstract/Resumen: The first parasitic helminth genome sequence was published in 2007, since then only ~200 genomes have become available, most of them being draft assemblies. Nevertheless, despite the medical and economical global impact of helminthic infections, parasites genomes in public databases are under-represented. Recently, through an integrative approach involving morphological, genetic and ecological aspects, we have demonstrated that the complete life cycle of Echinococcus oligarthrus (Cestoda: Taeniidae) is present in South America. The neotropical E. oligarthrus parasite is capable of developing in any felid species and producing human infections. Neotropical echinococcosis is poorly understood yet and only a few cases of echinococcosis have been unequivocally identified as consequence of E. oligarthrus infections. Regarding phylogenetics, the analyses of mitogenomes and nuclear data sets have resulted in discordant topologies and there is no unequivocal taxonomic classification so far. In this work, we sequenced and assembled the genome of E. oligarthrus that was isolated from agoutis (Dasyprocta azarae) naturally infected and performed the first comparative genomic study of a neotropical Echinococcus species. The E. oligarthrus genome assembly consisted of 86.22 Mb which showed □90% of identity and 76.3% of coverage with Echinococcus multilocularis and contained the 85.0% of the total expected genes. Genetic variants analysis of whole genome revealed a higher rate of intraspecific genetic variability (23,301 SNPs; 0.22 SNPs/Kb) rather than for the genomes of E. multilocularis and Echinococcus canadensis G7 but lower with respect to Echinococcus granulosus G1. Comparative genomics against E. multilocularis, E. granulosus G1 and E. canadensis G7 revealed 38,762; 125,147 and 170,049 homozygous polymorphic sites respectively, indicating a higher genetic distance between E. oligarthrus and Echinococcus granulosus sensu lato species. Phylogenetic analysis using whole genome SNPs demonstrated that E. oligarthrus is one of the basal species of the genus Echinococcus and is phylogenetically closer to E. multilocularis. This work sheds light on the Echinococcus phylogeny and settles the basis to study sylvatic Echinococcus species and their developmental evolutionary features.

SAP SYMPOSIUM III

IMMUNOLOGY AND VACCINES

Chair: Karina Gómez

ROLE OF THE ARYL HYDROCARBON RECEPTOR (AHR)-INDOLEAMINE 2,3 DIOXYGENASE (IDO) AXIS IN THE REGULATION OF IMMUNITY AND IMMUNOPATHOLOGY DURING TRYPANOSOMA CRUZI INFECTION

CRISTINA MOTRAN