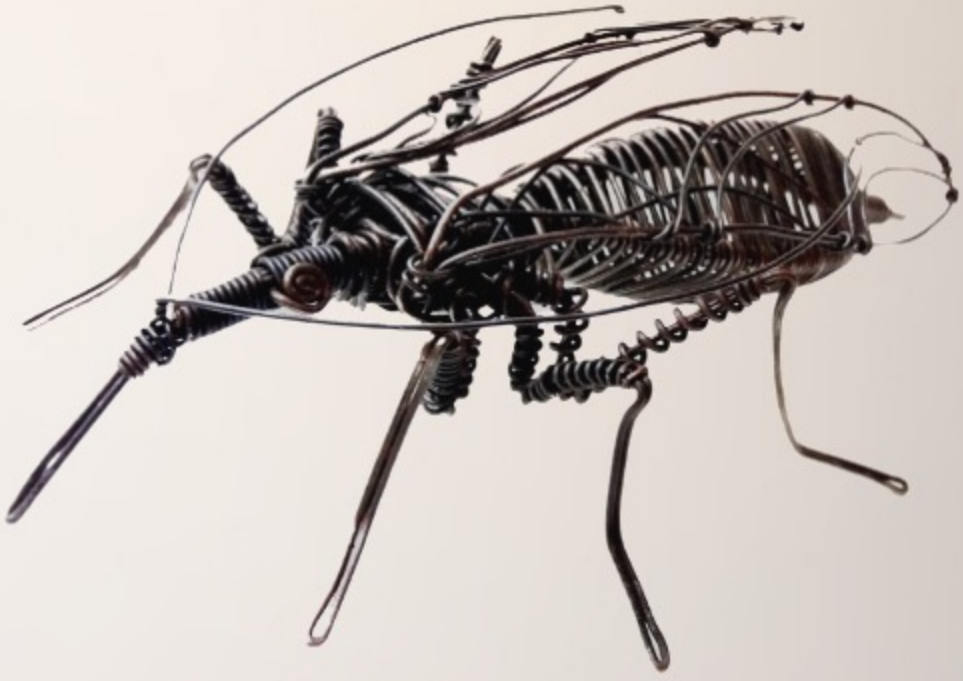
XL Annual Meeting of the Brazilian Society of Protozoology

LI Annual Meeting on Basic Research in Chagas' Disease



Hotel Glória – Caxambu (MG), Brazil

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PROCEEDINGS
XL Meeting of the Brazilian Society of Protozoology
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*Hotel Glória, Caxambu, MG, BRASIL- C*axambu
10-12 November, 2025

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CO – 009 - **Beyond the Genetic Code: Insights into Trypanosome Epigenome on Gene Regulation**

DA CUNHA, J.P.C..
LABORATÓRIO CICLO CELULAR, INSTITUTO BUTANTAN, SÃO PAULO - SP - BRAZIL.

In *Trypanosoma cruzi*, gene expression of protein-coding genes is regulated mainly post-transcriptionally due to polycistronic transcription and the absence of canonical promoters. However, our group and others have accumulated evidence suggesting that gene expression is also reflected in chromatin marks, genome accessibility, and three-dimensional genome structure. Here, I will show that these features are dynamically modulated across the parasite's cell and life cycle, correlating with its gene expression patterns and phenotypic differences. I will focus on our recent findings on the dynamics of histone variants and post-translational modifications, nucleosome occupancy, 3D genome interactions, and nascent transcription profiles, using different omics strategies such as high-resolution proteomics, transcriptomics, epigenomics, and Hi-C. I will also present the characterization of H4.V, a novel histone variant in *T. cruzi*, enriched at telomeres and convergent strand-switch regions (cSSRs), and strongly associated with chromatin in metacyclic forms. Together with H2B.V—previously characterized by our group—these variants show stage-specific expression, distinct chromatin affinities, and an association with regions enriched in virulence genes. Finally, integrative Hi-C and tRNA-seq analyses revealed that 3D chromatin folding, codon usage, and anticodon availability further shape gene expression and translational efficiency in these organisms.
Supported by: FAPESP, CAPES and CNPq. **Keywords:** chromatin;histone, epigenetics,;T;cruzi.

CO – 010 - **Synchrotron light: can it help my research?**

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The investigation of different biological samples depends on the physical techniques employed for their analysis, the correct interpretation of the resulting data, as well as on the knowledge of their limitations and potential artifacts. A powerful set of techniques involves the acquisition of images of biological samples. Incredible advances in light and electron microscopy have revealed increasingly greater details of cellular and tissue architecture. In parallel, modern synchrotron light sources have established a diverse range of beamlines with different optics and capabilities that can be used to analyze biological material. By using synchrotron radiation at different intensities and wavelengths, it is possible to scrutinize the cellular structure without causing physical damage to the material necessary for tissue preparation. Focusing on the beamlines currently in operation at the SIRIUS synchrotron in Campinas (Brazil), we intend to present the potential capabilities of beamlines such as CATERETÊ, CARNAÚBA, MOGNO and IMBUIA, and present preliminary results that illustrate the applications that can be considered for cellular investigation as well as its limitations.
Keywords: Synchrotron;3D image;Cellular structure, Tissue structure.

CC – 001 - **What DNA Replication Tells Us, So Far, About the Biology of *Trypanosoma cruzi***

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Trypanosoma cruzi is a generalist parasite that completes its life cycle across multiple host species. In both mammalian and insect hosts, it alternates between a proliferative form and a specialized, non-replicative one—likely as a strategy to preserve its genome, similar to what occurs in differentiated cells. The balance between genome maintenance and the generation of genetic variability is essential for adaptability. For *T. cruzi*, this is particularly critical, as the parasite must overcome diverse host-imposed challenges while remaining capable of performing its key function: host cell infection. Our group has been investigating proteins involved in DNA replication and its dynamics in this parasite, aiming to understand the extent to which DNA duplication contributes to genetic diversity during replicative stages, and how this process is silenced in non-replicative forms, where genome integrity must be maintained. In this talk, I will present proteins involved in the pre-replication complex that license replication origins, highlighting differences in their expression and DNA-binding capacity between replicative and non-replicative stages. Additionally, I will show that distinct *T. cruzi* genome compartments exhibit different replication dynamics, which impact the mutation rates of each genomic region, evidencing the DNA replication contribution to the diversification of fast-evolving genomic regions while preserving the conserved core compartment. Therefore, we suggest that infection success relies on a regulated transition from a proliferative, diversity-generating stage to a non-replicative, genome-preserving one, highlighting how parasites can harness core biological processes not only for survival, but as active strategies for adaptation. **Supported by:** FAPESP
Keywords: DNA replication;Trypanosoma cruzi;genetic variability.