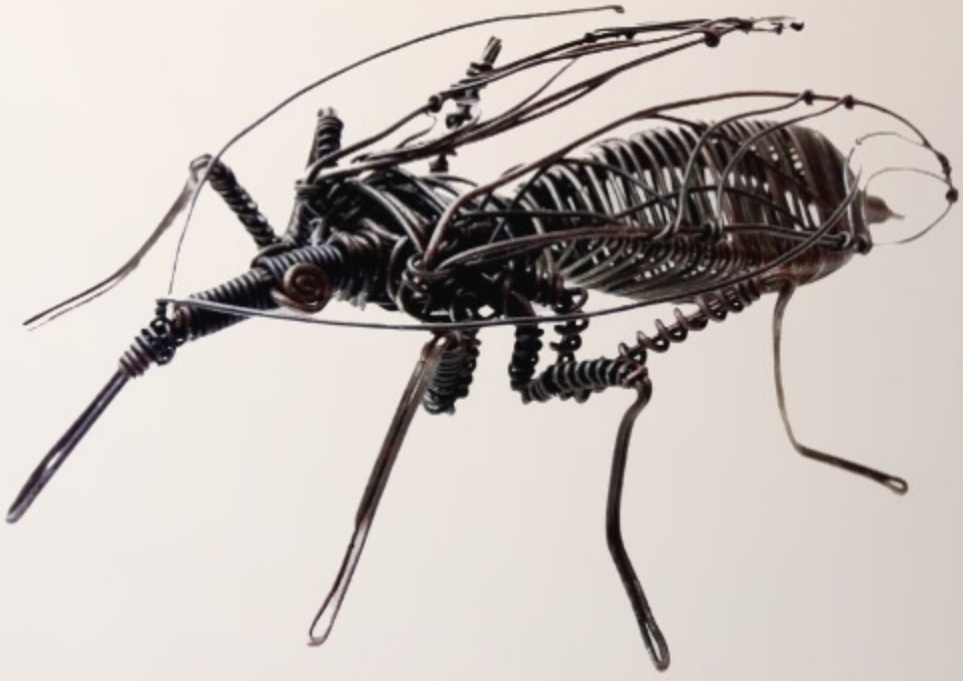
XL Annual Meeting of the Brazilian Society of Protozoology

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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PV – 055 - **FAZ10 at the FAZ: Structural Insights from Computational Prediction to Experimental Validation in *Trypanosoma brucei***

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Trypanosoma brucei, the causative agent of African trypanosomiasis, relies on the flagellum attachment zone (FAZ) to maintain cell morphology and ensure proper coordination during cell division. Among the FAZ components, FAZ10 is a high-molecular-mass protein localized at the FAZ and is implicated in cleavage furrow positioning and cytoskeletal organization. Despite its recognized functional importance, the structural characteristics of FAZ10 remain largely unexplored. In this study, we focus on the FAZ10 central region as an entry point to uncover new insights into its structure and potential mechanisms of action. *In silico* analyses using AlphaFold2, MARCOIL2, and IUPRED2A revealed a low-disorder region consisting of a coiled-coil with dimeric conformation, flanked by two globular domains. To investigate this architecture, we expressed and purified the full central region (~67 kDa), the isolated coiled-coil domain (~33 kDa), and one globular domain (~11 kDa) using Ni-NTA affinity chromatography followed by size-exclusion chromatography (SEC). SEC-MALS confirmed dimer formation for both the central region and the coiled-coil domain, while the globular domain remained monomeric. Circular dichroism spectroscopy supported the predicted secondary structure, and electron microscopy revealed an elongated, filament-like structure of approximately 40nm in length. Altogether, our findings demonstrate that the central region of FAZ10 adopts a dimeric filamentous conformation driven by its coiled-coil architecture. This supports the notion that full-length FAZ10 exists as a dimer and may assemble into higher-order structures, potentially serving as a structural scaffold within the FAZ of *Trypanosoma brucei*. Such oligomeric organization is likely crucial for maintaining cytoskeletal integrity, cellular polarity, and morphogenesis. A deeper understanding of the biochemical and biophysical properties of FAZ10 is therefore essential to elucidate the architecture and function of the FAZ. Given that African trypanosomiasis remains a neglected tropical disease, targeting structural proteins like FAZ10 could also contribute to the development of novel therapeutic strategies.

Supported by: FAPESP, CAPES, FAEPA
Keywords: Flagellum attachment zone;Trypanosoma brucei;coiled coil proteins.

PV – 056 - **Is dissolved organic carbon a main factor affecting testate amoebae diversity in shallow-water restinga habitats?**

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Planktonic protozoa have often been neglected as a pivotal group in energy flow in aquatic ecosystems. Due to resistant decay shells, testate amoebae are considered an important group to understand ecosystem changes. Since testate amoebae are often found in moist, organic-matter-rich environments, they can be used as tools to understand the carbon cycle as a whole. Especially in light of current climate change scenarios, unveiling the interaction of biodiversity with carbon may help planning and decision making. Dissolved organic carbon (DOC) is one of the forms in which carbon can directly or indirectly affect biodiversity in aquatic systems. Thus DOC can influence a variety of environmental parameters, changing the planktonic communities composition. Our objective was to observe the relationship of testate amoeba communities and environmental factors in aquatic ecosystems of the northern region of Rio de Janeiro, with emphasis in their relation with a broad DOC gradient found in these environments. Our initial hypothesis is that the testate amoebae community structure will respond due to its expected closer relation with organic matter concentrations and it will also respond negatively to salinity increase, due to oxidation stress. We applied multivariate statistical analyses to environmental variables (conductivity, DOC, pH, [O2]; salinity, temperature, turbidity) measured during environmental sampling campaigns conducted at Restinga de Jurubatiba (Macaé, RJ) during the year of 2017, in order to assess their influence on the diversity of testate amoebae. Our results show that DOC increase had no direct effects in community structure. On the other hand, the community composition and abundance was influenced by salinity in the shallow-water restinga habitats analyzed.

Supported by: CNPQ, CAPES
Keywords: environmental gradient;restinga;biological indicators.