

Project

Multi-omics approaches to unveil host-parasite interactions

Synopsis

Schistosomiasis (*Bilharzia*) is a vector-borne disease, ranking third only to malaria and COVID-19 in terms of number of infected individuals worldwide. It is caused by parasitic worms capable of adapting to both invertebrate and mammalian hosts, hijacking their immune systems to ensure their own perpetuation.¹ These parasites require permissive temperatures, which, due to global warming, are expanding the disease into previously unsuspected regions, such as the Mediterranean.²

Effective surveillance relies on reliable diagnostic tests and drug prophylactics, as the disease shares early clinical symptoms with several other pathogens. In this regard, the search for suitable biomarkers and new drug targets is of utmost importance. In the last decade, numerous studies on genomics and transcriptomics have emerged to unravel the complexity of the *Schistosoma* parasite.³ However, little is known about the interface between the parasite's tegument and its host.

In this research project, we aim at characterizing the molecular composition of the tegument, which is rich in lipids—including both phospholipids and glycolipids—as well as the intra-tegumental space, where most soluble antigens are found. Using lipidomics, proteomics, and metabolomics, the PhD candidate will map the chemical entities present in the tegument by high-resolution mass spectrometry (HRMS).

Additionally, through an international collaboration with the Faculty of Medicine at Rostock University (Germany), teguments extracted from *Schistosoma* eggs—both circulating and trapped in the liver of infected mice—will be analyzed, and comparisons will be made across various field and laboratory strains.

Finally, the biomarkers present in the highest concentrations will be isolated and analyzed using both biophysical techniques and HRMS methods combined with ion mobility.

The project will be hosted at the Institute of Analytical Sciences (ISA), located on the university campus. ISA comprises approximately 100 researchers and is one of the largest analytical science centers in Europe. The thesis project will be conducted within the ATHEXIM axis (A.E. Miele), whose laboratories are fully equipped for heterologous protein expression and purification, as well as state of the art instruments for structural and functional analyses, including NMR spectrometers, circular dichroism (CD), and dynamic light scattering (DLS).

Furthermore, the project will benefit from the expertise of the spatial multi-omics platform at the IHU Hepatology Institute of Lyon, hosted at ISA (S. Ayciriex, MDMC axis).

The successful candidate should have completed (or be in the final stages of completing) an M.Sc. degree with skills in analytical chemistry, sample preparation, biochemistry, or physical chemistry.

References

1. Schistosomiasis: epidemiology, diagnosis and treatment. Editor A.E. Miele. Nova Publisher, NY. ISBN: 978-1-63117-186-4.
2. Bisoffi Z, et al. Schistosomiasis transmission in Europe. *Lancet Infect Dis*. 2016; 16:878–880.
3. Anderson L, et al. *Schistosoma mansoni* Egg, Adult Male and Female Comparative Gene Expression Analysis and Identification of Novel Genes by RNA-Seq. *PLoS Negl. Trop. Dis*. 2015;9:e0004334.



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Proposed collaboration within ArchiFun network:

Prof. Tito Cali, University of Padua (IT)

FidaBio technologies (Copenhagen, NL)

Proposed list of secondments:

Prof Martina Sombetzki, Faculty of Medicine, Rostock University (DE)

Dr Patrick England, Institut Pasteur, platform of Biophysics (Paris, FR)

BIFI Lacrima, University of Zaragoza (ES)

NovAlix (Strasbourg, FR)

Main ArchiFun theme involved:

- Host-pathogen interactions;
- Mechanisms of bacterial resistance and cancer onsets;
- Neurodegenerative and autoimmune diseases;
- Translational research in prevalent diseases;
- Physiology and ecology;
- Neurosciences and cognition.