



NIMBioS

National Institute for Mathematical
and Biological Synthesis



NIMBioS Interdisciplinary Seminar 3:30 p.m.*, Tuesday, November 5, 2013

Dr. Clemente Aguilar
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“Computational characterization of GPI-anchored proteins in *Trypanosoma cruzi* and their potential use as vaccine candidates”

The plasma membrane of the causative agent of Chagas' disease, the parasite *Trypanosoma cruzi*, is covered with a dense, protective surface coat. This surface coat is a monolayer of millions of variant surface glycoproteins (VSG) that protect the parasite from the innate immune system and, through antigenic variation, against the specific host immune response. Most VSGs in the parasite are proteins attached to the cell membrane via glycosylphosphatidylinositol (GPI) anchors. A better understanding of GPIs could lead to the discovery of new anti-trypanosome drugs or a preventive vaccine against the disease. Liquid chromatography tandem mass spectrometry (LC-MS/MS) is often the technique of choice for characterizing GPIs. However, experimental samples consist of thousands of MS spectra, each of which is a complex piece of data that must be analyzed to extract relevant information about the biomolecules. These data sets are often noisy and therefore require sophisticated and robust tools that are capable of efficiently processing the information. No computational tool for characterizing the chemical structures of GPI is available to date. In this talk I will describe a proposed computational approach for the identification and characterization of GPIs in LC-MS/MS datasets. Additionally, the role of GPIs as vaccine candidates will be discussed.

Location: Room 105 at NIMBioS, Claxton Education Bldg, 1122 Volunteer Blvd.

**Join us for refreshments at 3 p.m.*

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