

Identification and Imaging of Selected Proteins Predicted to Be Secreted into the Host Macrophage by *Leishmania mexicana*

Leishmania is a parasitic protozoan that infects millions of people annually. It has a digenetic life cycle where it lives inside the sandfly vector and mammalian host macrophages. The process by which *Leishmania* manages to survive inside the phagosome of the host macrophage is not well understood. Multiple studies have shown that the parasite changes macrophage activity when it infects, for example, suppressing the pro-inflammatory response of macrophages. These changes to host cells and the parasite's ability to survive inside a hostile environment could be due to it secreting proteins that modulate macrophage activity. This study aims to identify secreted *Leishmania* proteins that help the parasite survive. An integrative approach was taken by using secretome studies and bioinformatics tools to identify *Leishmania mexicana* proteins that are likely to be secreted into the host macrophage. Laboratory work focused on proteins secreted into the culture medium by both promastigotes and amastigotes. Bioinformatic analysis of all hypothetical proteins in *Leishmania mexicana* identified those that are the most likely to be secreted. From these separate approaches, candidate proteins were selected and then the CRISPR-Cas9 system was used to endogenously tag the genes of interest. This marked the proteins they encode with mNeonGreen and enabled their tracking in *Leishmania* infected THP-1 derived macrophages.