Department of Global Health
MSPH Rotation Opportunities-Spring 2017

Adams Laboratory

(1) Malaria is one of the most deadly diseases in the world affecting vast areas of tropical and sub-tropical countries of the world. The causative agent is a parasite (Plasmodium) and disease is caused by a parasite (Plasmodium) and spread by the female *Anopheles* mosquito. Of the five species of Plasmodium that cause human malaria, *Plasmodium vivax* is the major cause of clinical disease outside of Africa. There are increasing reports of widespread drug resistance and clinical severity of disease due to emerging virulent forms of the parasite, but no vaccine exists that protects humans from infection. This emphasizes the need to create alternative prophylactic and therapeutic strategies including the development of a vaccine against this disease. Immunity to erythrocyte invasion ligands plays a critical role in controlling blood-stage infection of *P. vivax*. Invasion of human erythrocytes by the parasite is dependent on the interaction between the Duffy binding protein region II (DBPII) on the parasite surface and the Duffy blood group antigen (DARC) expressed on the surface of human erythrocytes. This makes DBPII an ideal vaccine target. A major obstacle in developing DBPII as a vaccine is that this region is highly polymorphic and these polymorphisms can compromise vaccine efficacy, creating a bias towards development of strain-specific immunity. The objective of this project is to overcome this obstacle by developing a vaccine that focuses immune response to conserved functional epitopes and boost immunogenicity. A student could join this project to work on developing antibody reagents to define and characterize the immunoreactive surface of DBPII to optimize an effective vaccine for *P. vivax* malaria. Techniques involved include PCR, recombinant DNA, expression and purification of recombinant proteins and ELISA.

(2) MS of exosomes collected from maturing RBC to identify reticulocyte receptor
The worldwide malaria strain Plasmodium vivax infects immature red blood cells (RBC) known as reticulocytes. It is important to determine the receptor/receptors which are involved in *P. vivax* attachment and invasion of reticulocytes. One of the possible approaches to clarify this process is to study exosomes, which are small vesicles (30-150 nm) that are secreted by maturing RBCs. It is one of the most reasonable ways for the RBCs to loose receptors on the surface, which aren't necessary and/or could cause a negative effect on function of mature RBC. These receptors could be CD36, CD44, and CD71, which may be involved in parasite invasion into reticulocytes. In contrast, mature RBCs are missing these receptors and are resistant to *P. vivax* invasion.
These work include isolation of exosomes and studying interaction with parasite. The line of methods for this research includes ultracentrifugation, electrophoresis of proteins, Western blotting, immunofluorescence, microscopy and related ones.

Students interested in either of the rotation opportunities above should contact Samantha Barnes (Adams Lab Project Coordinator) at sjones@health.usf.edu to set up an appointment to discuss the project.

Jiang Laboratory:

Systems Biology of Infectious Diseases

With rapidly advancing parallelization and miniaturization of genome technologies, the research of human diseases and pathogenic microorganisms is in a state of 'data deluge'. A new era of digital data-driving research will transform the field of infectious diseases and public health. Computational biology is instrumental to analyze and interpret these large-scale data sets. The Jiang lab is using an integrated approach involving systems biology to study liver infectious diseases. The lab focuses on

(i) Evolutionary study of eukaryotic pathogens. We are constructing the evolutionary trajectories of essential pathogenicity acquisition and adaptation from a genome science perspective. For the major pathogens that cause a heavy public health burden, such as malaria, we are using this approach to identify the most unique and amenable pathways for drug intervention.

(ii) Computational analysis of malaria parasite gene networks. Liver-stage is the first and an obligatory stage for malaria infection. We are actively developing methodologies to leverage existing genome, transcriptome, epigenome, and population genomics data to generate gene network modules of malaria parasites. We will target the gene modules that are critical for liver infection to treat diseases.

(iii) Liver host genetics study. Hepatocytes provide a cellular environment for pathogen growth. In addition, the pathogens extensively remodel the host cells to promote their own survival. We are utilizing human hepatocyte genomic and functional genomics resource to create a roadmap of host metabolic and signaling pathways. We are establishing a human hepatocyte-malaria interaction system, and aiming at disrupting the parasite's host dependence and host manipulation.

(iv) Cloud-based computational pipelines. We will tackle human infectious diseases with new diagnostic, tracking, and analyzing tools. We are implementing programs, such as PathSeq, to identify potential pathogens from large amounts of sequencing data of human tissues. Together with our collaborators, we are working toward realizing personalized medicine in disease prevention, detection, and treatment.

Please contact Dr. Rays Jiang at (jiang2@health.usf.edu) to explore potential research opportunities and set up an appointment for projects discussion.

Shaw Laboratory

Work in the Shaw lab focuses on the drug resistance and virulence mechanisms of bacterial pathogens. A major focus of our work is to understand the disease causation pathways of Methicillin Resistant Staphylococcus aureus (MRSA) using molecular tools and 'omic approaches. Projects in this area center on regulatory circuits within MRSA, and include the control of transcription, translation and post-translation as it relates to pathogenesis. Our group also engages in antibacterial drug discovery, searching for novel therapeutics targeting the ESKAPE pathogens. In these studies we work with both natural products and synthetic medicinal chemists to generate new treatment options for drug resistant bacterial infections. Students should contact Dr. Shaw directly (Shaw@usf.edu) to discuss rotation opportunities and projects.

Suvorova Laboratory:

In the Suvorova lab, we work with *Toxoplasma gondii*, an important human pathogen that causes life-long infection in millions of people. People at severe risk for this infection include individuals with a weak immune system and women that acquire the infection during pregnancy. *T. gondii* is a member of the Apicomplexa phylum of obligate protozoan parasites that also includes other pathogens that cause malaria and cryptosporidiosis. Apicomplexan parasites have peculiar cell cycles that are in many ways more complex than our own cells. It is not unusual for these parasites to produce a few to thousands of daughter parasites seemingly all at once. They are able to do this by suspending cytokinesis while they produce multiple copies of their chromosomes and then coordinately assembling daughter parasites at the end of their life cycle. The molecular basis for how these parasites can accomplish such unusual cell cycles is unknown and solving the mystery of Apicomplexa replication is the major interest of our laboratory. We are tackling this problem using an array of genetic, biochemical and cell biological approaches in the tachyzoite growth model of *T. gondii*. It is the ultimate goal of these studies is to uncover molecular vulnerabilities upon which new treatments to combat these pathogens can be developed.

Please contact Dr. Suvorova at essuvorova@gmail.com to explore opportunities in the Suvorova lab.

Unnasch Laboratory

TResearch in the Unnasch lab focuses upon arthropod borne infectious diseases, ranging from the human filarial infections to arboviruses. Projects range from basic biochemistry and molecular biology (studies of gene regulation and drug discovery in filarial parasites) to domestic field research (ecology of Eastern Encephalitis virus) to applied international research (remote sensing, development of novel insect traps and assisting international control programs in certifying elimination of onchocerciasis). Rotation projects are available in all of these areas.

Please contact Dr. Unnasch or Hassan Hassan (hhassan@health.usf.edu) in the Unnasch lab to explore potential project opportunities.

White Laboratory:

Research in the White laboratory is focused on how the malaria-related protozoa, grow and develop in its human host using the model organism *Toxoplasma gondii*. *T. gondii* is an environmental pathogen of the central nervous system (class B bioterrorism agent), which causes an often fatal disease in people who are immunocompromised including those suffering AIDS. Projects in our laboratory focus on how these parasites interact with their host cell to produce new progeny and establish persistent infections that are life-long in humans. Our studies employ a diverse and extensive array of genetic and biochemical approaches with an emphasis on whole-cell strategies that enable a global understanding of the biochemical pathways involved in parasite growth and development. From forward genetic approaches that allow us to pin-point essential genes required for parasite growth to be identified by genetic complementation to deciphering the key transcriptional changes within the parasite transcriptome that are responsible for parasite expansion and transduction of the parasite life cycle, we are uncovering novel pathways that hold the key to important parasite biology.

Please contact Dr. White at mwhite.usf@gmail.com to explore opportunities in the White lab.