Research Initiation Program
Award Recipients
2010-2011

The Research Initiation Program received an outstanding response to the call for proposals. The quality and quantity of proposals for this year's competition were generally great! The RIP Committee would like to have had sufficient funds available to award everyone, but due to the lagging economy only the following proposals have been selected for FY 2010-2011 funding.

Dr. John Adeyeye
Mathematics
College of Arts and Sciences
Award: $10,000.00

Proposal Title: **"Dynamical Systems over Finite Fields and Molecular Network Modeling"**

Abstract: Discrete dynamical systems are ubiquitous not only in engineering but also the life sciences. Especially during the last decade finite dynamical systems, that is, discrete dynamical systems with a finite-phase space have been used increasingly in systems biology to model a variety of biochemical networks, such as gene regulatory networks and signal transduction networks. In many cases, the available data quantity and quality is not sufficient to build detailed quantitative models such as systems of ordinary differential equations, which require many parameters that are frequently unknown. In addition, discrete models tend to be more intuitive and more easily accessible to life sciences.

Over the last several years polynomial dynamical systems over finite fields have been studied as a modeling framework for molecular networks. These represent a very general class of multi-level time-discrete dynamical systems that generalize Boolean networks. Large arrays of theoretical and computational tools from computational algebra are available for their study. The goal of the proposed projects is to establish results that relate their structure to their dynamics. To obtain strong results it is necessary to focus on specific families of such systems. We focus on systems that are constructed from monomials only, the generalization of Boolean networks constructed using only the AND operator. We will derive results relating dynamics and structure for such networks with specific dependency graphs.

Dr. Johanna Porter-Kelley
Life Sciences
School of Health Sciences
Award: $10,000.00

Proposal Title: "**Cultured Sporozoites, A Pre-erythrocytic Malarial Vaccine**"

Abstract*:* Plasmodium, the causative agent of malaria, is a major cause of morbidity and mortality on the world population. Although major efforts have been made toward finding a vaccine, one has not been made available. All major morphological forms of the mosquito phases have been observed in culture for several Plasmodium species. In our cultured

P.yoelii sporozoites. Our thought was that since cultured sporozoites produced much lower parasitemias the possibility exists that these sporozoites could be used as a vaccine. Our preliminary data show that cultured sporozoites are attenuated and are protective in mice later challenged with mosquito derived P. yoelii sporozoites.
Our hypothesis is that a vaccine composed of attenuated sporozoites produced in mosquito phase cultures protects against clinical blood stage malaria. To investigate the validity of our hypothesis we propose to:
Specific Aim 1: Show that cultured P. yoelii sporozoites produced protective immunity in mice. Mice will be inoculated using P. yoelii sporozoites produced in culture and challenged using mosquito derived sporozoites. Protection will be assessed by the lace of parasitemias in Giemsa-stained blood smears. Antibodies in the immunized mice will be assessed by antibody productions against sporozoites; P. yoelii infected hepatocytes, and infected blood.
Specific Aim 2: To determine which antigens are protective in the cultured sporozite vaccine. Antibodies derived from cultured sporozoite immunized mice will be used to screen sporozite lysate, infected hepatocyte lysates, and infected blood lysate. We will assess the reactivity of the antibodies in the mouse serum by western blot analysis. Reactivity in the western blot analysis against any of the three lysate will be further characterized by immunoprecipation and LCMS/MS.

Dr. Dionne Roberts
Nursing
School of Health Sciences
Award: $10,000.00

Proposal Title: "Building Community-Academic Partnership to Address Cardiovascular Disease Risk Factor in African Americans"

Abstract: Building on the principal investigator's previous research on culturally appropriate intervention for blood pressure control in African Americans, the primary goal of the proposed study is to obtain preliminary data to design a community-driven intervention that is culturally appropriate, sustainable and effective in reducing cardiovascular disease risk in Guilford County, North Carolina. In Guilford County, the death rates from heart disease and stroke have been disproportionately affected among African Americans than white Americans. Frequently cited in the literature, the community-based participatory research (CBPR) approach has been identified as fostering an equitable, cooperative, participatory co-learning environment between the community and academic institutions to promote health issues undergirded by racial/ethically influences.

The proposed study will examine the increase mortality rates of CVD among geographically defined community of African Americans in Guilford County, North Carolina through CBPR. To maintain the tradition of CBPR, a community advisory board (CAB) will be formulated to collaborate with the principal investigator to address the specific aims: 1) explore the perceptions of CAB about the CVD in the community, 2) evaluate the existing data about CVD in the community, and 3) design a recruitment and membership plan for community focus groups to examine the community perceptions about the CVD problem, the importance of cardiovascular health, and ideas and suggestions to reduce the CVD risk in the community.

Dr. Xiuping Tao
Chemistry
College of Arts and Sciences
Award: $10,000.00

Proposal Title: "Needle in a Haystack: Sifting through Predicted Protein Structures for Correct Folds"

Abstract: A protein is a sequence of amino acids folded into a unique 3-dimensional (3D) shape – native structure. Protein native structures are closely related to their biological functions, and knowing them helps make medicine to cure diseases. Scientists know almost 5 million proteins ("words") by their amino-acid sequences ("spelling") but only 1% by their 3D structures. It is cost prohibitive to find native structures from sequences. Prompted by the obvious disparity, researchers have been using computers to predict protein structures. Only a fraction of predicted structures are correct folds, i.e. similar to native structure, and scientists generally do not know how to select correct folds from large pools. This is considered a bottleneck in protein structure prediction research. I propose to select correct folds from many predicted protein structures by a so-called Kernelling Method. It is based on a hypothesis backed by physics energy theories: the correct folds are structurally similar to each other, and if clustered, they form the largest cluster than ones formed by incorrect folds. It searches for amino acid pairs neighboring in space for each predicted fold and makes a list of them. The common part of the lists is called a kernel and the method is named after it. The largest kernel is hypothesized to be from correct folds.
My initial results are promising: the method out-performed in 10 out of 28 cases of protein structure prediction compared to an eminent research group's work. The requested support can further develop the method.

Dr. Steven Viscido
Life Sciences
College of Arts and Sciences
Award: $9,926.00

Proposal Title: "Quantitative Analysis of Animal Group Movement under Field Conditions"

Abstract: The overall goal of my research is to discover the underlying mechanisms that give rise to animal group behaviors. To achieve this goal, computational software must be created to track and measure animal movements. Therefore, I propose this 1-year project for the purpose of beginning to create the necessary software for motion analysis. I will develop software in MatLab that performs two key functions of motion analysis (background subtraction and individual detection). To test the software, I will record video sequences of fiddler crab flocks and ant social groups under field conditions. I will then use the software to help reconstruct the trajectories of the animals and estimate their movement parameters. Upon completion of the project, I will be able to quantify the characteristics of animal movement and group behavior, and will have a prototype computer program ready for future use in larger projects.

Dr. Gregg Ward
Life Science
College of Arts and Sciences
Award: $10,000.00

Proposal Title: **"The in vivo (CB1 cannabinoid receptor deficient mice) investigation of drugs of abuse on the expression of atypical genetic markers."**

Abstract: The broad goals of this research are to determine the existence and function of atypical genes which may cause pronounced neuroadaptation to drugs of abuse. Preliminary data indicate that the cannabinoid CB1 receptor regulates genes that control neuronal function and influence drug-seeking behavior. Using cDNA microarray analysis of the cannabinoid CB1 receptor-deficient mouse mesolimbic system (the brain region that mediates the addictive effects of drugs of abuse), multiple genes have been either upregulated or downregulated, including Cyclin-dependent kinase 5-regulatory subunit 2 (Cdk5/p39). Although Cdk5/p39 promotes functional synapse formation in NG108-15 cells (combination of N18TG2 mouse neuroblastoma and C6-BU-1 rat glioma cells), the molecular mechanism(s) responsible for this synaptic plasticity change is unknown. Therefore, the following will be done. First, perform real-time RT-PCR validation of Cdk5/p39. This will be accomplished by eliminating the effects of the CB1 receptor in the nerve cells in culture. Subsequently, the mRNA will be extracted and the amount of Cdk5/p39 mRNA measured. Second, correlate Cdk5/p39 mRNA expression and conversion to protein using Western immunoblotting. This can be accomplished by the isolation of proteins from the previously used nerve cells. After separating the proteins according to their size, Cdk5/p39 protein levels will be measured. Third, investigate the molecular mechanism(s) responsible for CB1-mediated control of Cdk5/p39-mediated synaptic plasticity changes. This can be accomplished by utilizing multiple techniques including real-time RT-PCR, neurite outgrowth assays (measures synaptic plasticity), Western immunoblotting and coimmunoprecipitation analysis (identifies signaling proteins that interact with each other in the intracellular pathway).