

MENTORS DIRECTORY

2022 SUMMER RESEARCH INTERNSHIP AND FELLOWSHIP PROGRAM

Offered by the

**West Virginia IDeA Network of Biomedical Research Excellence
(WV-INBRE)**

to be held at

**The Robert C. Byrd Health Sciences Center
Of West Virginia University**

And

**The Joan C. Edwards School of Medicine
at Marshall University**

Introduction

WV-INBRE is pleased to offer summer research internships to students from colleges and universities participating in the WV-INBRE program. In 2022, the internship period will be from May 31 through July 26, with the Summer Research Symposium to be held on July 27 in Huntington, WV. Listed in this directory are faculty members at the West Virginia University Health Sciences Center and at Marshall University who have agreed to participate as mentors in the summer internship program. Mentors have submitted a description of the projects that are available to interns in their laboratories. Please review these carefully so that you are aware of what is available for summer projects.

A listing of mentors with a short description of their research and the general area of their research is presented on pages 3-7. Mentors and project descriptions begin on page 8. Listed for each mentor is an e-mail address, phone number and, where available, a website address. The websites will allow you to learn more about the mentors and their research programs.

Application forms are available on the WV-INBRE web site (<http://www.wv-inbre.net>) at a link under **2022 Summer Program**. Applications may be submitted by mail or e-mail; however, **direct electronic submission is available and its use is encouraged.**

For general questions about the summer internship and fellowship program please contact one of the following individuals who are serving as summer research program coordinators.

Dr. Elsa Mangiarua
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Dr. Werner Geldenhuys
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WV-INBRE website: <http://www.wv-inbre.net>

Directory of Mentors – Mentors are listed by their location; the first list contains mentors at the West Virginia University Health Sciences Center and the second list contains mentors at Marshall University

Mentors at the West Virginia University Health Sciences Center

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Dr. Paul R. Lockman	Prevention of brain metastases in breast cancer	17
Dr. Kathleen E. Morrison	Understanding the cellular and molecular mechanisms of experience-dependent resilience and vulnerability to stress	18
Dr. Mohammed A. Nayeem	Assessment of genetic polymorphism in human population and in mouse models through their oxylipins profile for targeted therapy related to hypertension and cardiovascular diseases	19
Dr. Randy Nelson	Circadian Rhythm Disruption and Health	20
Dr. Timothy Nurkiewicz	Airborne particles and systemic microvascular endothelial dysfunction	20
Dr. Mark Olfert	Microvessel and vascular responses to E-cigarettes, nicotine and/or environmental stress	21
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Dr. Bradley Webb	Cell biology and biochemistry of intermediary metabolic enzymes	23
Dr. Zachary M. Weil	1. Energetic dysfunction in the brain following traumatic brain injury 2. Alcohol abuse after traumatic brain injury	24

WVU Mentor Listing According to Area of Research

Biochemistry: Webb

Bioinformatics: Hu

Cancer Research: Choi; DeVries; Hazlehurst; Ivanov; Lockman; Rojanasakul

Cardiovascular Research: Brown; Chantler; Hollander; Nayeem; Nurkiewicz; Olfert

Diabetes: Leonardi

Drug Development: Benedito; Geldenhuys

GI Research: Rajendran

Inflammation: Brown

Nanotechnology: Geldenhuys; Rojanasakul

Neuroscience Research: Brefczynski-Lewis; Brown; Choi; Geldenhuys; Hileman; Lewis;
Morrison; Nelson; Weil

Obesity: Leonardi

Pharmacology Research: Choi; Geldenhuys

Pulmonary Research: Hussain; Nurkiewicz; Rojanasakul

Reproductive Biology Research: Hileman

RNA Splicing: Robart

Mentors at Marshall University

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Dr. Subha Arthur	Regulation of intestinal bile acid absorption in obesity	26
Dr. Ji C. Bihl	1. The role of exosomes in strokes and diabetes 2. The protective role of ACE2/Ang-(1-7)/Mas in strokes and ageing by counteracting the effects of ACE/Ang II/AT1. 3. The role of exercise in vascular diseases by modulating the concentration and contents of exosomes.	27
Dr. Lydia Bogomolnaya	1. Identification of natural functions of drug efflux pumps during infection 2. Defining the role of secreted DUF1471-containing proteins in adaptation of bacteria to different environments	29
Dr. Piyali Dasgupta	1. Anti-cancer activity of nicotinic antagonists in lung cancer 2. Capsaicin and small cell lung cancer	30
Dr. Price Dickson	Systems genetics and recombinant inbred mouse panels for discovery of the mechanisms driving drug addiction	31
Dr. Richard Egleton	Opioid regulation of brain development	32
Dr. Lawrence Grover	Central nervous system consequences of prenatal opioid exposure	33
Dr. Brandon Henderson	Examining the effect of flavors on vaping-related behaviors	33
Dr. Jung Han Kim	Genetics of obesity and type 2 diabetes	34
Dr. Emine C. Koc	1. Detection of changes in MRP expression in ovarian cancer 2. Regulation of protein synthesis in mitochondria by acetylation in ovarian cancer	35
Dr. Wei Li	1. Examine the mechanistic role of thymidine phosphorylase in thrombosis 2. Examine the mechanistic role of thymidine phosphorylase in obesity and atherogenesis 3. Examine the mechanistic role of thymidine phosphorylase in the development of severe COVID-19.	36
Dr. Tim Long	New treatment strategies for multi-drug resistant infections	37
Dr. Yongke Lu	1. Peroxisomes and alcohol-related liver disease 2. Cell-cell interaction in liver	38
Dr. Swarup Mitra	1. Identify the role of dorsal striatal projections underlying heroin induced behavioral plasticity 2. How does controllable versus uncontrollable stress influence heroin relapse 3. Identify the neuronal circuit specific transcriptional and epigenetic changes that contribute to maladaptive plasticity during heroin relapse and or stress.	39

Dr. Daniel Morgan	1. Endocannabinoid signaling in human health and disease 2. Understanding the role of neuropeptide signaling in the regulation of pain and motivated behaviors 3. Impact of decursinol in acute, inflammatory, and chemotherapy-evoked chronic pain.	40
Dr. Sandrine V. Pierre	1. Cardioprotection by Na ⁺ /K ⁺ -ATPase ligands in acute myocardial infarction. 2. Role of α1 Na/K-ATPase in adverse cardiac remodeling and heart failure	41
Dr. Gary Rankin	Kidney and liver toxicology	42
Dr. Chris Risher	1. Synapse growth and maturation 2. Mechanism by which gabapentin and opioids interact	43
Dr. Louise Risher	How adolescent binge drinking influences brain function	44
Dr. Boyd Rorabaugh	Impact of Methamphetamine use during pregnancy on the cardiovascular function of adult offspring	44
Dr. Travis Salisbury	Environmental pollutants and breast cancer	45
Dr. Nalini Santanam	1. Adolescent vaping and behavior 2. Non-opioid analgesics and pain	45
Dr. Yevgeniy Shakirov	1. Genetic and epigenetic architecture of natural telomere length variation 2. Analysis of the interplay between telomere biology and ribosome biogenesis	46
Dr. Vincent Sollars	1. "What causes treatment failure in some cancer patients but not others? 2. "What are the molecular defects that promote age-related dysfunction?"	47
Dr. Jiang Tian	Na/K-ATPase Alpha 1 in Heart Failure and Cardiac Decompensation	48
Dr. Monica Valentovic	1. Reducing serious cancer chemotherapy side effects 2. Potential role of e-vape flavoring agents in renal impairment 3. Examination of the mechanism of renal damage by an antiviral agent used in treating HIV and hepatitis B patients	49
Dr. Mindy Varney	1. Elucidating the role of IRGM in the pathogenesis of Myelodysplastic syndromes (MDS) 2. Determining how obesity contributes to initiation and progression of MDS 3. Defining the mechanisms by which obese individuals are more susceptible to infection and have lowered vaccine efficacy	50
Dr. Hongwei Yu	1. Cystic Fibrosis Biofilms 2. Testing antimicrobials 3. SFB probiotics 4. New biopolymer development	51

Marshall University Mentor Listing According to Area of Research

Addiction: Dickson; Egleton; Grover; Henderson; Lu; Mitra; Morgan; C. Risher; L. Risher; Rorabaugh

Bioinformatics: Shakirov

Cancer Research: Amin; Dasgupta; Koc; Salisbury; Santanam; Sollars; Valentovic; Varney

Cardiovascular Research: Bihl; Li; Pierre; Rorabaugh; Tian

Diabetes: Bihl; Kim

Drug Action, Metabolism, and Resistance: Amin; Morgan; Santanam; Valentovic

GI Research: Arthur; Lu

Genetic Research: Kim; Shakirov; Sollars

Infectious Diseases: Bogomolnaya; Long; Yu

Neuroscience/Sensory Research: Egleton; Grover; Mitra; Morgan; C. Risher; L. Risher

Obesity Research: Arthur; Kim; Varney

Renal Research: Rankin; Valentovic;

Toxicology Research: Rankin; Valentovic

I. At The West Virginia University Health Sciences Center

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Unveiling the biosynthesis regulation of the antimalarial medicine, artemisinin in *Artemisia annua* L. through genomics, transcriptomics, and metabolomics

Introduction and rationale: *Artemisia annua* L. (Asteraceae family) is a medicinal herb native to temperate Asia and the main commercial source of the *anti-malarial drug artemisinin*. This sesquiterpene lactone compound is used in standard treatments worldwide. Given its complex chemical structure, artemisinin is difficult to synthesize *ex vivo*, which leads to high costs and makes it amenable to global shortages due to unfavorable climate variables. Therefore, to improve artemisinin yields, it is essential to understand the physiology and regulation of its biosynthesis. **Research goal and objectives:** *The main goal of our research is to understand the genetic regulation of artemisinin biosynthesis pathway.* At WVU, we have a unique germplasm collection of accessions differing in final yields of artemisinin and related compounds. *Our hypothesis is that artemisinin accumulation is a factor of carbon drain strength of sesquiterpenes towards the committed pathway, competitive enzymology, and the final-step conversion into the final product.* **Methods:** Artemisinin and related compounds are quantified through GC-MS and LC-MS. Biochemical and physiological parameters are being analyzed along with the expression levels of known terpenoid biosynthesis genes to understand the variance in artemisinin accumulation in the different accessions. We are also taking full advantage of the genome sequence of *Artemisia annua* to unveil the natural genetic variation and genomic rearrangements leading to increased artemisinin biosynthesis and accumulation. *This research is ideal for students who want to learn about metabolic flux of biochemical pathways, biosynthesis of natural compounds of pharmaceutical interest, functional genomics, and chromatography of fine chemicals.*

Julie Brefczynski-Lewis, Ph.D.

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Stress related to difficult personal encounters is very pervasive yet poorly understood. Such stress over time can lead to physical (e.g. cardiovascular) and mental health (e.g. depression/anxiety) issues. Compassion training is a simple and inexpensive way to help decrease the stressful reactions from difficult personal encounters. The project for the summer will be to examine brain responses (using PET (Positron Emission Tomography)) and heart rate variability and cortisol/alpha amylase responses to aversive stimuli (such as pictures of disliked political figures and narratives). The physiological and neural responses to stressful stimuli will be measured before and after compassion meditation or relaxation meditation training (active control) that participant access using a Smartphone app.

This project will provide opportunities to learn:

- how to work with human participants,
- how to do measure neural response to stimuli using PET
- how to combine physiological, behavioral, and neural measures.

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**Brain and immune system interactions in neurological disease**

Communication between the brain and the immune system is essential in human health and disease. Research in my laboratory is focused on brain-immune interactions that affect levels of brain inflammation, also known as neuroinflammation, in mouse models of neurological disorders such as ischemic stroke and Alzheimer's disease. In addition, my laboratory also studies the role of sepsis as a comorbidity in these two disorders. Current studies are focused on understanding the role of tissue nonspecific alkaline phosphatase – a ubiquitous enzyme whose physiological function(s) in the brain are poorly understood – in neuroinflammation. We integrate our studies on tissue nonspecific alkaline phosphatase with the study of sex differences in order to better understand how male brains and female brains respond differently in ischemic stroke and Alzheimer's disease.

INBRE summer students will have the opportunity to engage in projects aimed at understanding how the tissue nonspecific alkaline phosphatase enzyme which is localized in brain endothelial cells protects the brain during ischemic stroke and Alzheimer's disease. S/he will interact with graduate students, lab staff members, and the WVU neuroscience community. Skills and techniques to be learned during the internship may include: 1) tissue sectioning, immunohistochemistry, and imaging of mouse and human brain tissues; 2) handling and husbandry of transgenic mouse models; 3) animal behavior testing; 4) small animal surgical procedures, and 5) training in standard molecular biology techniques, including PCR and quantitative RT-PCR.

Dr. Paul Chantler

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Cardiovascular responses to disease states

INBRE program participants will work in conjunction with laboratory personnel on current projects. Current pre-clinical research is examining: 1) how chronic stress impacts cerebrovascular function and health as a pathway to dementia; 2) how adipose tissue regulates vascular dysfunction; and 3) how E-Cig exposure affects vascular dysfunction. INBRE participants will interact with graduate students and staff members to answer research questions, using both invasive and non-invasive approaches to examining cardiovascular function.

U. Brandon Choi, Ph.D.

Assistant Professor - Department of Biochemistry

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Proteins govern a vast number of processes inside the cell, making them central to cellular function. Although high-resolution atomic structures are known for many proteins, relating a single static structure to its function is difficult. Many proteins are dynamic, changing shape thus affecting the function of the molecule. Therefore, it is important to develop methods to watch proteins in action. We will apply single molecule fluorescence resonance energy transfer (smFRET) to monitor protein motions and complex assemblies in real time on biologically relevant timescales (sub-milliseconds to minutes). The application of fluorescence at the single molecule level will allow us to distinguish molecular heterogeneity, monitor transient intermediates and rare events, as well as sequence of events.

Protein Quality Control—Mechanistic role of p97

p97 is a member of the superfamily of AAA+ ATPase, and its central role in protein quality control makes it an attractive target for cancer drug development. Malfunction of p97 is associated with various aggregation diseases including neurodegenerative diseases such as Alzheimer's and Parkinson's disease. At the molecular level, p97 is involved in the segregation of protein complexes, membrane fusion, endoplasmic reticulum associated protein degradation (ERAD) and activation of membrane-bound transcription factors. Although extensively studied, the molecular mechanisms underlying p97 function are still not fully understood. Our goal is to use combinations of single molecule approaches such as smFRET, single particle cryo-EM, single particle tracking to investigate the hidden conformational intermediates both *in vitro* and in live cells to understand the different biological pathways leading to distinct cellular responses. This investigation will provide mechanistic insight into cancer related research and therapeutic design for drug development.

Neuroscience—Single molecule imaging of presynaptic scaffolding network

The release of neurotransmitters relies on an active zone at the presynaptic nerve terminal consisting of a highly specialized network of scaffold proteins. Dysfunction of the presynaptic scaffolding network leads to many neurological disorders, including autism, schizophrenia and neurodegeneration. Our goal is to understand the role of scaffold proteins in the organization of the presynaptic active zone. Although the key factors and the physiological roles of the presynaptic scaffold proteins are identified, we lack a quantitative and mechanistic understanding of the scaffolding network due to the dynamic and transient assemblies. We will study the dynamic structures of the presynaptic scaffold proteins using single molecule fluorescence approach to observe the organization of the presynaptic scaffolding network in real time. This will allow us to characterize previously undetectable intermediate steps in assemblies.

Dr. A. Courtney DeVries

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John T & June R Chambers Chair of Oncology Research

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Affective Consequences of Breast Cancer and Chemotherapy

Among women, breast cancer is the most commonly diagnosed cancer type with an estimated 265,000 new diagnoses this year in the United States. Breast cancer survivors frequently display alterations in metabolism and sleep, elevated mood disorders (anxiety and depression), and increased cognitive disturbances. However, determining the underlying causes of these deficits has proven to be difficult, as very few studies have examined the effects of breast cancer and cancer treatment independently. Our research group studies the physiological and behavioral effects of breast cancer and chemotherapy. Summer interns and fellows would have the opportunity to assist with current projects in the lab which include: 1) the effects of breast cancer on sleep and metabolism 2) the effects of chemotherapy on depressive-like behavior and cognitive function. 3) the effects of social enrichment on tumor development and depressive-like behavior following chemotherapy administration.

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Discovery of compounds to treat Parkinson's disease

Parkinson's disease is an age-related neurodegenerative disease which affects the motor skills of patients. Unfortunately, no drugs are currently available to slow down the disease progression, and there is a great need to discover these types of compounds. In this study we will be screening a library of compounds which consist of FDA approved and novel compounds identified through computer aided drug design techniques in several enzyme and *C. elegans* models. Once the compounds are identified which show promise, we will test them for neuroprotective activity. During the period of the study, students will learn how to screen compounds for biological activity in a high throughput manner as well as how to utilize models of Parkinson's disease to screen for phenotypic improvement afforded by the compounds. The student will learn more about the drug discovery process and how new drugs are found and characterized.

Deliver of therapeutic proteins using nanoparticles

Parkinson's disease is an age-related neurodegenerative disease which affects the motor skills of patients. Unfortunately, no drugs are currently available to slow down the disease progression, and there is a great need to discover these types of compounds. In Parkinson's disease there are some mitochondrial proteins which we have found can be used to restore the damaged mitochondria seen in the disease. In this project we will work on developing a nanoparticle drug delivery system to deliver a therapeutic protein to the brain using several cell culture models. This project will introduce the student to the art of nanoparticle drug delivery formulation using biological therapeutic proteins as disease modifiers.

Dr. Lori Hazlehurst

Professor Pharmaceutical Science
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Development of novel therapeutic strategies for tumors that reside or home to bone

Background: Our laboratory has identified a novel target called Ero1-alpha for the treatment of lung cancer. Our data indicate that depleting Ero1-alpha using Crispr technologies inhibits the growth of lung cancer using cell culture as well as *in vivo* models. Ero1-alpha is critical for protein folding of secretory and membrane proteins. Our working hypothesis is that Ero1-alpha is critical for maintaining the tumor based secretome which drives growth and metastasis of lung cancer.

Project: The incoming INBRE student would work with graduate students in identifying secretory proteins that confer the observed phenotype in Ero1-alpha depleted cell lines.

Students that joined our laboratory will learn cell culture, RT-PCR, standard genetic and pharmacological approaches for inhibiting Ero1-alpha as well as exposure to analyzing microarray and proteomic data.

Dr. Stan Hileman

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The process of puberty can be defined as the process whereby an individual gains the capacity for reproduction. This process is dependent upon changes in the release of gonadotropin releasing-hormone (GnRH) from the hypothalamus of the brain. Prior to puberty, GnRH release is minimal and the reproductive system is largely quiescent. As the time of puberty approaches, GnRH secretion increases, eliciting a corresponding increase in the release of luteinizing hormone (LH) and follicle stimulating hormone from the anterior pituitary gland that causes follicular maturation and, eventually, the first ovulation. The neural mechanisms underlying the pubertal increase in GnRH secretion are not completely understood, but may involve a set of neurons in the arcuate nucleus of the hypothalamus that coexpress kisspeptin, neurokinin B, and dynorphin, thus termed KNDy neurons. Kisspeptin and neurokinin B are critical for puberty onset in humans and have been shown to stimulate LH secretion in a number of species. The aim of our current project is to define the role of the KNDy peptides in puberty using female sheep as the model animal. Since puberty is a process dependent upon sufficient nutrition, we have recently started looking at the relationship amongs KNDy peptides and neurons involved in regulating food intake, namely agouti-related peptide and proopiomelanocortin neurons with the arcuate nucleus of the hypothalamus. This is accomplished through *in vivo* pharmacology as well as immunohistochemical and immunofluorescent approaches.

Dr. John Hollander

Professor

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Cardiovascular Research (This project is appropriate for faculty and/or students)

INBRE program participants will work in conjunction with laboratory personnel on projects examining metabolic aspects of cardiac diseases. Projects in the laboratory focus specifically on understanding the role played by proteins thought to be protective against the development of heart failure during diabetes mellitus as well as the genetic regulation of these proteins. Our studies have a tremendous impact on Appalachia due to the high incidence rate of diabetes mellitus and obesity. The goal of these studies is to provide insight into the mechanism of action of these proteins and genes, with the goal of designing therapeutics to treat cardiac disease states. Our experimentation involves both basic research and analyses in patient populations.

INBRE participants will interact with graduate students and staff members to answer research questions, using a multidisciplinary approach that includes genetic modification of the heart in both cell and animal models as well as analyses in patient samples. Training will be provided to the participants, which includes molecular cloning, whole heart physiology, RNA, DNA, and protein manipulation, bioinformatics as well as biochemical analyses.

Dr. Gangqing (Michael) Hu

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Bioinformatics and Epigenome Biology

Dr. Hu's laboratory combines computational and experimental techniques to understand epigenetic gene regulation in cancer and immune systems. The epigenome of an eukaryotic cell consists of chemical changes to DNA sequence and histone proteins wrapped by the DNA, also known as chromatin. Chromatin modifying enzymes, transcription factors, and transcription machinery collectively modulate the epigenome, which instructs gene expression program. The overarching goal of the lab is to decode the function and regulation of epigenome of immune cells during cell fate decision and cell activation, and epigenetic mechanisms of drug resistance of cancer cells. The research programs will help to define the effects that microenvironment can have on the epigenome of immune cells and cancer cells, and thereby affect their functions, providing implications in human diseases such as autoimmune diseases and cancers.

Projects: 1) an integrative database to chart the epigenomic landscapes of multiple myeloma by collecting and processing public high-throughput sequencing data and 2) decoding cellular heterogeneity underlying drug resistance of multiple myeloma using single-cell epigenetic assays. During the internship, the trainees will learn basic concepts on the biology of epigenetic regulation and receive hands-on experience on the processing and integrating high-throughput genomic sequencing data.

Salik Hussain DVM, PhD

Assistant Professor

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We are interested in elucidating the role of environmental exposures in aggravation and/or susceptibility to chronic pulmonary disorders such as asthma and interstitial lung diseases. Lung diseases are among top five causes of global mortality (WHO). Almost 15% of the US population suffer from lung inflammatory diseases e.g., asthma effects 1-18% of global population (approximately 300 million individuals), including over 25 million people in the United States. Global asthma patient number is expected to reach 400 million by 2020 and asthma is implicated in one of every 250 deaths worldwide. Environmental and occupational agents (ground level ozone, particulate matter, nanomaterials) significantly impact the development as well as exacerbations of the respiratory disorders. The over-arching goal of our research is to identify novel therapeutic targets to treat pulmonary disorders. We elucidate cellular and molecular pathways implicated in pulmonary disease susceptibility by studying patient samples, *in vitro* and *in vivo* rodent models of pulmonary disease to elucidate molecular pathways.

Techniques:

- In vitro Organoid Cultures (air-Liquid Interface cultures, 3D Alveolar cultures)
- Lung Physiology Measurements (state of the art lung function measurements)
- Translational Studies (human clinical samples)
- Rodent Models (disease, transgenic, cell type specific gene deletions).

Available Projects:

- Role of Alveolar Progenitor/Stem cells in Lung regeneration after Acute Injury
- Role of Mitochondrial NOD-Like Receptors in Idiopathic Pulmonary Fibrosis
- Early life/Childhood Asthma (Environmental Exposures x susceptible gene interactions)

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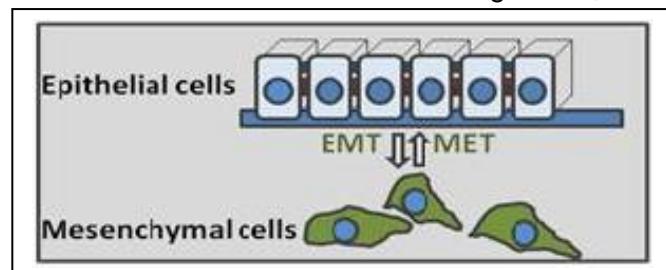
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Description of Research

Vast majority of human tumors are of epithelial origin, e.g. they derive from cells normally highly organized in specialized epithelial layers. At the same time, most cancer-related deaths occur due to tumor recurrence and spread to distant organs (metastasis), which are tightly linked to acquisition by cancer cells of mesenchymal properties such as increased motility, invasion and resistance to chemotherapy. The metastasis stage of cancer is associated with epithelial-to-mesenchymal transition (EMT). Normally acting only during early embryonic development, the EMT program is hijacked by cancer cells during evolution of individual tumors. EMT is activated by a handful of transcription factors referred to as the EMT master regulators, such as Snail and ZEB.

The goals of our research are to identify transcriptional network involved in activation of EMT during cancer metastasis. This knowledge will help to develop future therapeutic approaches in treating cancer and prevention of metastasis.



Available projects:

1. Negative control of EMT by epithelial-specific transcription factors.

EMT promotes cancer cell invasion, metastasis and drug resistance. Primary breast tumors largely maintain inherent epithelial status. However, cancer cells on the tumor periphery are believed to undergo partial EMT and disseminate to distant organs. The goal of this project is to define the roles of several transcription factors including OVOL, GRHL and FOXA1 responsible for the maintenance of the epithelial state in suppression of EMT.

2. Role of the TGF-beta pathway in partial EMT and drug resistance of triple-negative breast cancer.

Transforming growth factor beta (TGF-beta) acts as a tumor suppressor at the early stages of cancer development. Cancer cells evolve various mechanisms to overcome TGF-beta inhibitory effects, including silencing and mutation of TGF-beta receptors or silencing and deletion of TGF-beta target genes involved in growth suppression. The latter mechanism is often observed in triple-negative breast cancer (TNBC). TNBC cells show increased TGF-beta signaling leading to partial EMT and resistance to certain drug therapies. The goal of this project is to investigate if pharmacological inhibition of the TGF-beta pathway combined with standard cancer therapy will improve drug response in vitro.

3. Identification and characterization of prognostic markers for non-small cell lung cancer (NSCLC).

Lung cancer is the leading cause of cancer related deaths. Previously, we have identified several biomarkers, including gene ZNF71, which can predict lung cancer patient response to chemotherapy. The goal of this project is to characterize the molecular mechanisms of ZNF71 function in EMT and lung cancer metastasis.

Former WV-INBRE summer research interns in the lab

Year Name & College

2021 Austin Taylor & Linh Nguyen, Concord University

2019 Jessica Johnson, Fairmont State University

2018 Emily Means, WV Wesleyan College

Current position

still in school

still in school

earned DO in Lake Erie College of Osteopathic Medicine

environmental hazardous waste management

earned MD at WVU School of Medicine

earned MD at WVU School of Medicine

FBI Forensics Lab, Quantico, VA

2015 Brandon Trinh, Bethany College

2013 Morgan Johnson, Shepherd University

2012 Anna Alappat, Shepherd University

2009 Icel Cavis, Shepherd University

Roberta Leonardi, Ph.D.

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Coenzyme A (CoA) is an essential and universally distributed cofactor that acts as the major acyl group carrier in the cell. Free CoA and acyl-CoAs are involved in hundreds of metabolic reactions, and are among a selected number of small molecules that have the ability to act as global regulators of cellular metabolism. Consistent with this key function, CoA levels are at the same time tightly regulated and flexible, so that the available supply is sufficiently adaptive to metabolic challenges such as fasting or a high fat diet. Regulation of CoA levels occurs through coordination of synthesis and degradation. In the liver, modulation of the amount of CoA contributes to the metabolic flexibility of this organ and to its ability to maintain glucose homeostasis during a fast. Conversely, in diabetic mice, hepatic CoA levels are abnormally high and unresponsive to changes in the nutritional state.

Not much is known about CoA degradation. The goal of our research is to establish the importance of CoA-degrading enzymes in the regulation of CoA levels and energy metabolism. In particular, we are interested in studying these enzymes in the context of diabetes, obesity and other metabolic diseases using a combination of biochemistry, animal studies and metabolomics.

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Description of Research (2020-2021): Neuroimaging and sensory processing of chronic headache and opioid use disorder.

Lewis laboratory activities:

Our lab generally studies mechanisms of sensory and multisensory perception, and understanding how this ties in with brain networks mediating cognition and language processing. We primarily use 3 Tesla functional magnetic resonance imaging (fMRI), but also evoked response potential (ERP) methods. Recent clinical-research projects include (1) mapping chronic pain in specific types of headache sufferers, with the goal of identifying where (or how) in the brain the sense of headache pain is mediated. Advances in this field could lead to novel techniques to relieve chronic pain. A second front (2) is mapping the brains of opioid use disorder (OUD) patients, examining resting state functional connectivity (rsfMRI) data at different stages of successful rehabilitation. We primarily use computational approaches and methods for studying brain function, and thus applicants with a solid background in computer sciences or engineering are preferred.

Potential projects include:

- (1) Identifying and mapping brain networks mediating chronic headache pain using fMRI.
- (2) Examining difference in resting-state functional connectivity patterns in OUD patients.
- (3) Examining rsfMRI data of individuals receiving transcutaneous electrical neural stimulation (TENS) as a treatment therapy.

Dr. Paul R. Lockman

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Significance and Translational Relevance

Brain metastases pose a life-threatening problem for women with advanced metastatic breast cancer. Of women who have been diagnosed with disseminated breast cancer, ~10-16% will develop symptomatic brain metastases and at least 20-30% will have micrometastatic lesions present at autopsy. Once lesions are established in the central nervous system, only one in five women survive one year. We have recently shown that chemotherapeutics do not reach effective concentrations in ~90% of CNS metastases. Therefore, our lab is working on ways to prevent the formation of metastases in brain.

Project Information

Our lab uses cutting edge microscopy to identify single breast cancer cells that can invade into brain tissue. Once the cells are found we have techniques that can remove the individual cancer cell. Once the cell is collected the goal of the project is to identify if there is a DNA signature that allows the cancer cell to get into brain (>99% of breast cancer cells do not enter into brain tissue). Once that signature is identified it is hoped we will find a molecular target that can be blocked by a drug, which should reduce penetration of the cancer cells into brain. It is hoped this project will be a first step in the prevention of brain metastases of breast cancer.

Skills and/or experiences the student will be exposed to

1. Cell culture of human and mouse cells
2. Fluorescent microscopy – to potentially include multi-photon imaging
3. Bioluminescence imaging of cancer cells in living animals.
4. Laser micro-dissection of cells in tissue
5. RNA amplification
6. Microarray data

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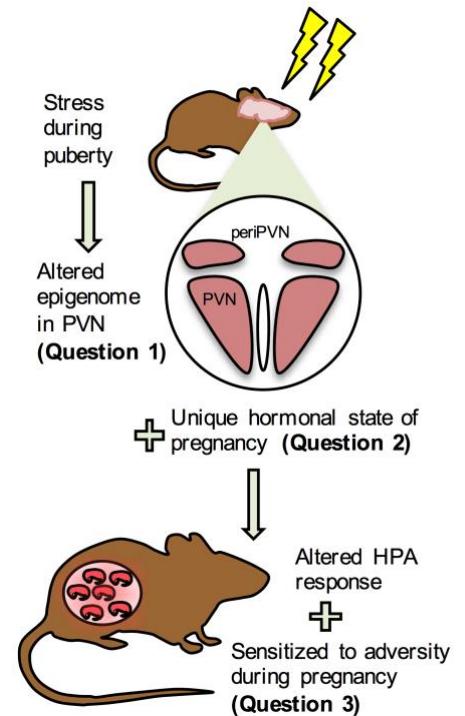
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Using stress as one of the common experiences that brings about neuropsychiatric disease, the Morrison lab works to understand the cellular and molecular mechanisms of experience-dependent resilience and vulnerability to stress, and how sex, developmental stage, and type of experience shape an individual's trajectory. We are particularly interested in women's mental health, as there has been little preclinical work to understand why women are more likely than men to suffer from mood disorders. Working with clinical collaborators, we have developed a translationally relevant mouse model that allows the lab to address how neuropsychiatric disease risk is compounded throughout the life of a woman, a process that is multifaceted and not well understood. The Morrison lab utilizes a variety of approaches, including advanced sequencing techniques, bioinformatics, molecular methods, and behavioral assays.

We have previously examined the hypothesis that female humans and mice would be susceptible to stress during the peripubertal period of development and that long-term outcomes would depend on hormonal state. We found that women exposed to adversity during peripuberty show a disrupted stress response during pregnancy and postpartum, as well as increased postpartum depression symptoms. Our mouse model completely recapitulates this phenotype, such that female mice exposed to stress during puberty demonstrate a disrupted stress response during pregnancy and postpartum. Subsequent work with this translationally-relevant **mouse model** suggests that long-term epigenetic reprogramming of the paraventricular nucleus of the hypothalamus by peripubertal stress may underlie this phenotype.

Projects in the lab revolve around three central questions, and students have some flexibility in contributing to a particular area of their interest:

1. *What is the epigenetic programming enacted by peripubertal stress?*
2. *What about pregnancy permits the expression of the stress dysregulation phenotype?*
3. *What are the consequences of a "second hit" stressor during pregnancy for mom and offspring?*



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<https://scholar.google.ru/citations?user=SYQwJY0AAAAJ&hl=ru>

Assessment of genetic polymorphism in human population (WV) and in mouse models through their oxylipins profile for targeted therapy related to hypertension and cardiovascular diseases: INBRE program participants will work with our laboratory staff (postdoctoral fellows, graduate student & technician) on projects including NIH funded project to understand the mechanisms involve in cardiovascular diseases including hypertension in humans having genetic variations (genetic polymorphisms) in CYP2J2, sEH and A_{2A}AR genes. The goal of this research project is to investigate the role plasma oxylipins, and to use oxylipins profile as a possible biomarker for human hypertension (HTN), which can be identified before clinical signs develop. In addition, we will investigate the mechanisms underlying the differential plasma oxylipins profile and their role in blood pressure (BP) response in HTN patients vs. age matched controls, mouse models (profiling oxylipins from plasma, heart & kidneys) of increased (Pro-HTN) vs. decreased (Resistant to HTN) susceptibility to HTN. Our lab research focuses on understanding the role of plasma oxylipins (5,6-, 8,9-, 11,12- and 14,15-EETs; 5,6-, 8,9-, 11,12- and 14,15-DHETs; 5-, 8-, 9-, 11-, 12-, 15-, 19- and 20-HETEs; 9,10- and 12,13-EpOMEs; 9,10- and 12,13-DiHOMEs; 9- and 13-HODEs; 6K-PG-F_{1α}, PG-F_{2α}, TxB₂, PGD₂, PGE₂, 8isoPGF_{2α}, PGB₂, 10,11-EpHep, 19,20-EpDPE, 17,18-EpETE, etc.) in human pre-HTN, HTN and CVDs cases related to endothelial dysfunction due to aging and polymorphisms in adenosine A_{2A} receptor (A_{2A}AR) and enzymes involved in epoxyeicosanoid synthesis and metabolism (CYP2J2 and soluble epoxide hydrolase, sEH) in humans. Our long-term goal is to identify the possible targets leading to the development of novel drugs to treat clinical problems of cardiovascular diseases including pre-hypertension, hypertension, salt-sensitive hypertension, coronary artery disease, heart failure, cardiac arrest, cardiac death, heart attack, etc., associated with the defect in the enzymes and receptors (CYP2J2, sEH, A_{2A}AR) in humans who have genetic variants that may possibly act similar to our genetically engineered mice. INBRE participants will interact with our lab staff (postdoctoral fellows, graduate student & technician) and learn the techniques to measure the cardiovascular response in vitro and in vivo.

Dr. Randy J. Nelson

Professor and Chair

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Hazel Ruby McQuain Chair for Neurological Research

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Circadian Rhythm Disruption and Health

Circadian rhythms are endogenous biological rhythms of about 24 hours and are a fundamental characteristic of life. Although life evolved over the past 3-4 billion years under bright days and dark nights, humans have been able to interrupt this natural light-dark cycle for the past 130 years or so with bright light at night. Our research group studies the effects of these disrupted circadian rhythms on several parameters including immune function, neuroinflammation, metabolism, pain, sleep, and mood. Summer interns and fellows would have the opportunity to assist with current projects in the lab which include: 1) the effects of light at night on metabolism, cognition, and pain sensitivity, and 2) the effects of circadian disruption on neuroinflammation associated with cardiac or cancer development and treatments.

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Airborne Particles and Systemic Microvascular Endothelial Dysfunction

Evidence indicates that acute exposure to airborne pollutants such as particulate matter (PM) and nanoparticles increases the risk of pulmonary and cardiovascular morbidity and mortality. This implies that PM affects extra-pulmonary tissues, as evidenced by the occurrence of cardiovascular dysfunction on high pollution days. However, the biological mechanisms by which PM evokes systemic effects remain to be defined. Despite its obvious importance in regulating the delivery of cells and molecules to all tissues, and in the etiology of most cardiovascular diseases, no research has investigated how systemic microvascular function is affected by pulmonary PM exposure. Our preliminary observations in the rat spinotrapezius muscle indicate that endothelium-dependent arteriolar dilation is significantly impaired after pulmonary particle exposure, and this impairment is associated with microvascular oxidative stress. Interestingly, this systemic microvascular effect can occur independent of pulmonary inflammation. My central hypothesis is that acute particle exposure affects peripheral microvascular function, and this effect is achieved by local reactive oxygen species production and/or altered neurogenic input to the systemic microcirculation. A fundamental understanding of these mechanisms is vital in preventing and treating the life-threatening events associated with air pollution. Our studies are further applied to the rapidly growing field of nanotoxicology. Wherein, it is acknowledged that nanotechnology has become a regular component of most every aspect of our daily lives, yet the toxicity of exposure to specific nanoparticles remains to be determined. Exposure to these nanoparticles carries just as much, if not more potential for generating profound effects on microvascular function. The student or faculty member will have the opportunity to develop surgical and experimental techniques associated with animal studies and isolated microvessels, as well as assist in exposing animals to various particle aerosols. These techniques include: inhalation exposure, animal surgery, microsurgery, intravital microscopy, in vivo measurement of oxidative stress and various micropipette-based techniques.

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Title: Microvessel and vascular responses to E-cigarettes, nicotine and/or environmental stress

INBRE program participants will work in conjunction with laboratory personnel on projects examining blood vessel responses to varied conditions, such as E-cigarettes, inhaled nicotine and/or other conditions (nano-material exposure, chronic disease states, etc.). Projects in the laboratory focus specifically on understanding the proteins and cell signaling responsible for regulating the function and formation of blood vessels in response to environment stress (e.g. inhaled toxicants, electronic cigarettes), biological stresses (e.g. exercise), and/or the loss of blood vessels in disease (e.g. obesity, heart failure, lung disease, diabetes, etc.). The goal of these studies is to provide insight into the mechanism(s) involved with the ultimate goal of designing therapeutics to treat abnormal vascular pathology. INBRE participants will interact with graduate students and staff members to answer research questions, using a multidisciplinary approach that includes genetic modification, whole animal clinical and metabolic testing, and bench top tools for DNA, RNA and protein analyses. Training provided to the participants will include whole animal physiology, basic surgical and microscopy techniques, along with molecular and biochemical analyses.

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Inflammatory bowel disease (IBD) includes Crohn's disease and ulcerative colitis. Crohn's disease affects any part of the intestine (small and large intestine). Ulcerative colitis affects only the large intestine/colon. Both Crohn's disease and ulcerative colitis are chronic inflammatory diseases. Ulcerative colitis that affects young adults is most prevalent in developed countries. This laboratory focuses on identifying the cause of the disease and on developing drugs for its prevention and cure.

Molecular Basis of Ulcerative Colitis

Ulcerative colitis occurs as a result of inflammation of the mucosal cells that line the inner surface of the colon. This mucosal inflammation results in a reduced rate of nutrient, electrolyte and water absorption, leading to diarrhea. In addition, inflammation also reduces nutrient metabolism that produces energy needed to maintain healthy mucosal cells. An overactive immune system is one of the major reasons for mucosal inflammation in ulcerative colitis. The overactive immune reaction constantly produces free radicals (reactive oxygen species) that inhibit water absorptive processes and damage the mucosal cells.

Approach to Cure and Prevent Ulcerative Colitis

To prevent ulcerative colitis, simultaneous reduction of the overactive immune system and improvement of mucosal cell health are essential. Overactive immune reactions could be controlled by supplying antioxidants. Mucosal health could be improved by supplying butyrate (a short chain fatty acid), which is the major nutrient of colonic mucosal cells. Butyrate is not present in food, but is produced from non-absorbed carbohydrates by bacteria present in the colon. Therefore, this laboratory is designing non-digestible carbohydrate (resistant starch) and free radical scavenger derivatives that, upon fermentation, deliver butyrate and an antioxidant right on target at the colon.

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**Structure and Function of Non-coding RNAs and RNPs**

Although many human diseases are caused by mis-splicing of genes, we still do not fully understand the fundamental mechanisms that drive the function of the splicing machinery or how non-coding RNAs propagate and spread within our genome.

Group II introns are mobile genetic elements that are the likely evolutionary ancestors of both the spliceosome and active human retrotransposons. Thus, these ribozymes offer a simplified system to study these fundamental cellular processes. These primitive ribozymes often contain an intron-encoded protein (IEP) that assists splicing to form ribonucleoprotein (RNP) complexes, which act as selfish retroelements that copy and integrate into new genomic locations. In humans, retroelement mobility cause disease by disrupting open reading frames, altering gene regulation, and triggering genomic rearrangements. ***Long term, we aim to harness the highly sequence specific properties of these movements for biotechnology and gene therapy applications.***

The overall goal of our lab is to determine the detailed molecular mechanisms of how intron RNPs form and how these RNPs spread introns to new locations in DNA by combining biochemical and structural biology approaches. Our lab is currently using multiple structural biology methods to understand the structure of the intron ribozyme and the RNP complex, including X-ray crystallography, cryo-electron microscopy (cryo-EM), and small angle X-ray scattering (SAXS). Structural studies are aided and complemented through biochemical, molecular, and bacterial genetic approaches.

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Cancer Cell Biology and Nanotechnology

Major research interest is in the area of cancer development and chemotherapy. Our laboratory is particularly interested in the carcinogenic effects of engineered nanomaterials and environmental agents. We also investigate drug resistance mechanisms and new therapeutic strategies for cancer treatment. The student will learn research techniques for 1) growing and manipulating cells in culture, 2) assessing cellular responses to carcinogenic and anticancer agents, 3) identifying biomarkers and drug targets for lung cancer using various molecular biology techniques.

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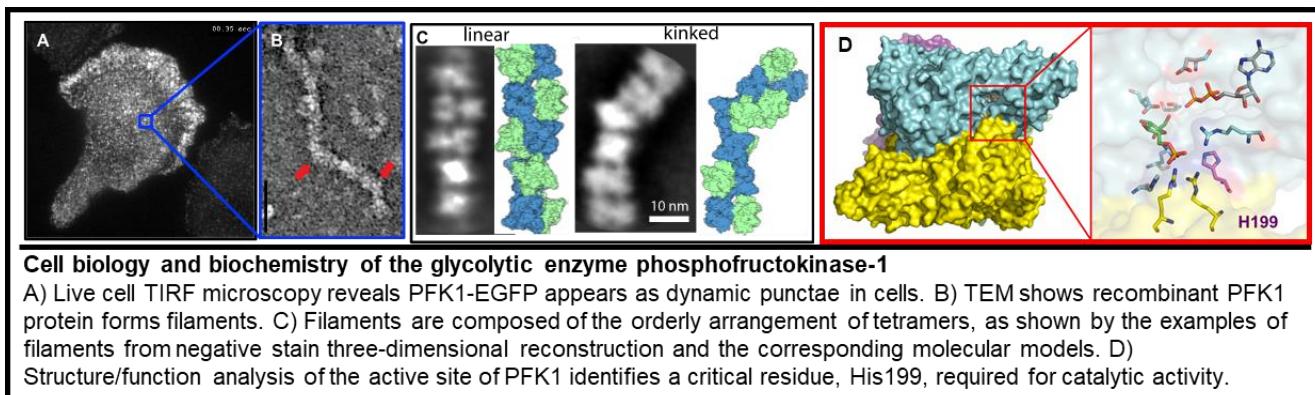
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Cell biology and biochemistry of intermediary metabolic enzymes

The enzymes and pathways controlling intermediary metabolism for energy production, nutrient utilization, and biomass synthesis play critical roles in cellular homeostasis. Dysregulated metabolic enzymes and pathways are now considered central to diseases such as cancer, diabetes, and neurodegenerative disorders. Despite being studied for half a century, we still have limited knowledge of the spatial and temporal dynamics of metabolic enzymes in cells, which is critical for understanding metabolic flexibility in normal cells and aberrant metabolism in diseases. We are currently addressing questions regarding the localization, regulation, and structure/function of enzymes in the glycolytic pathway. Using biochemical, cell biological, and cell imaging techniques, INBRE students will enhance our understanding of the spatial and temporal regulation of the glycolytic enzyme phosphofructokinase-1. In particular, the INBRE student will study how metabolites, post-translational modifications, or disease-associated mutations regulate the enzymatic activity and localization of phosphofructokinase.



Publications:

<https://www.ncbi.nlm.nih.gov/sites/myncbi/bradley.webb.2/bibliography/46426825/public/?sort=date&direction=descending>

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The Weil Lab at West Virginia University is focused on understanding the basic biology and long-term consequences of traumatic brain injuries (TBI). Traumatic brain injury (TBI) is a serious public health issue costing Americans over 75 billion dollars annually in health care costs and lost productivity. One prominent feature of TBI is that injuries make future injuries more likely and more devastating. Moreover, individuals with a history of TBI are more likely to develop substance abuse issues. Our lab is interested in understanding the molecular and biochemical basis of these phenomena.

There are two lines of research in our lab that students can become involved with:

- 1) Energetic dysfunction in the brain following traumatic brain injury. This project investigates how brain injuries can impair the brain's ability to process and utilize energy and how this can make the brain more vulnerable to other kinds of injuries, like repeated brain injuries, later on.
- 2) Alcohol abuse after traumatic brain injury. Traumatic brain injuries early in life can increase the likelihood of developing alcohol abuse issues later on in life. Our lab is interested in trying to understand how a brain injury can lead to increases in drinking behavior.

II. Mentors at Marshall University

A.R.M. Ruhul Amin, B.Pharm., M.Pharm., Ph.D.

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1. Investigating the mechanism of drug resistance

Cancer is the second leading cause of deaths in the United States accounting over 600K deaths per year. Intrinsic as well as acquired resistance to anti-cancer drugs are continuously posing challenges toward the success of cancer treatments. Understanding the molecular mechanism of drug resistance is the key to overcoming drug resistance and developing new treatment regimen using combinatorial approach. Keeping this objective upfront, my laboratory is utilizing *in vitro* cell culture and *in vivo* animal models of lung and head and neck cancers to better understand the molecular mechanism of resistance to targeted therapy. My laboratory has identified that some head and neck cancer cell lines overexpress p-Met downstream of Src family kinases (SFK) and these cell lines are resistance to apoptosis induced by the combination of erlotinib (EGFR inhibitor) and BKM120 (PI3K inhibitor). Addition of SFK inhibitor or Met inhibitor sensitizes these cells to apoptosis. The laboratory is currently exploring the downstream targets of SFK-Met signaling.

2. Chemoprevention using natural compounds

Chemoprevention means pharmacological intervention before the development of invasive cancer (full blown cancer) at a precancerous stage with the hope to slow down or reverse the carcinogenesis process. However, drug-associated toxicity is one of the major concerns in using drugs in prevention settings since the recipients of the chemopreventive drugs are normal subjects with high risk for developing cancer. Therefore, those agents with non-toxic or minimal side effects would be ideal candidates as chemopreventive agents. Because of their proven high safety margin through centuries of human consumptions as food or as traditional medicines, natural compounds presents in fruits, vegetables and spices have drawn special attention for chemoprevention. With this objective in mind, my laboratory is investigating the potential of diet derived natural compounds such as green tea EGCG, luteolin, resveratrol, curcumin etc. for chemoprevention of head and neck cancer and lung cancer. The project includes testing of *in vitro* and *in vivo* efficacy as well as exploring their molecular mechanism of action.

These projects will provide opportunities to learn:

- Mammalian cell culture and maintenance
- Cell proliferation and cell death assays
- RNA and plasmid DNA isolation
- Gene expression analysis by PCR
- Protein expression analysis by western blotting
- Flow cytometry analysis
- Measuring protein and nucleic acid concentrations

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Regulation of intestinal bile acid absorption in obesity.

Obesity is a national epidemic, and even more so in West Virginia with adult obesity rate of 39.5%. Dyslipidemia is central to most of the complications of obesity e.g. heart disease, fatty liver, and stroke, type 2 diabetes etc. Increased absorption of dietary fat, which is one of the primary causes of obesity leading to dyslipidemia, has been further attributed to increased bile acid levels in the intestine, leading to dysregulation of bile acid and lipid homeostasis in obesity. Apical sodium dependent bile acid co-transporter or ASBT located only in the brush border membrane of villus cells, and only in the distal ileum, is exclusively responsible for the reabsorption of bile acids in the mammalian intestine. Despite the importance of ASBT in the maintenance of bile acid homeostasis and in turn lipid steady state, the altered regulation of ASBT, which may lead to dyslipidemia of obesity, is unknown. The ongoing research involves understanding the physiological and molecular regulation of intestinal bile acid absorption mediated by ASBT in Zucker rat and diet induced rat models of obesity. Better understanding of the regulation of bile acid absorption that directly affects lipid absorption in obesity may result in novel and efficacious treatment modalities.

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The Bihl lab studies the role of extracellular exosomes (EXs), stem cell therapy, and the renin-angiotensin system in ischemic stroke, hemorrhagic stroke, and diabetic vascular complications. Our goal is to develop new therapeutical avenues addressing cerebrovascular diseases based on stem cells and their-released exosomes. The research approaches include transgenic mouse models in combination with animal surgeries, such as telemetric probe implantation for recording blood pressure and heart rate, minipump/microinjection for chronic/acute drug administration, and animal modeling for MCAO-induced ischemic stroke and brain injection for hemorrhage stroke.

Project 1. The role of exosomes in strokes and diabetes.

Exosomes (EXs) are small vesicles of cellular membrane released from almost all types of cells in response to physiological and pathological stimuli. EXs represent a novel way of cell-to-cell communication by transferring their molecular signatures (proteins and miRs) to target cells and tissues. Thus, extracellular EXs could be the novel therapeutic target or avenue for stroke; and could be the biomarkers for stroke and diabetes patients. These studies emphasize the protective effects of EXs derived from endothelial progenitor cells (EPC-EXs) on vascular cells and neurons. We have discovered the function of EXs from different origins by carrying different molecular signatures. We also have established the approach to identify the size, concentration, and origins of EXs by using the Nanosight Tracing Analysis system (NTA). Our recent study reported that EPC-EXs could provide the therapeutic effects on ischemic stroke by alleviating the acute injury and promoting long-term neurological function recovery. Further studies are needed to investigate the mechanisms that are related to their carried proteins and miRs, such as miR-126, miR-210, etc.

The approaches used for this project include *in vitro* cell culture and *in vivo* animal models. For the *in vitro* model, vascular cells (endothelial cells and smooth muscle cells) and neuronal cells (neurons and astrocytes) under hypoxia/reoxygenation condition (*in vitro* stroke model) or oxHb stimulation (*in vitro* hemorrhage stroke model) will be treated with a different type of EXs. For the *in vivo* model, we have middle cerebral occlusion (MCAO) surgery to induce ischemic stroke, and brain microinjection model to induce a hemorrhagic stroke. After surgery, the mice will be treated with different types of EPC-EXs. Neurological behavior will be tested before collecting the brain samples for further analysis. Moreover, we have human blood samples from stroke and diabetes patients. These samples will be used to identify the biomarker for the outcome of these diseases by using NTA.

Project 2. The protective role of ACE2/Ang-(1-7)/Mas in strokes and ageing by counteracting the effects of ACE/Ang II/AT1.

The renin-angiotensin system (RAS) participants in the pathogenesis of stroke, primarily through the actions of the vasoactive peptide angiotensin II (Ang II) and its pathway ACE/Ang II/AT1. Angiotensin-converting enzyme 2 (ACE2) is a homolog of ACE that is abundantly expressed in the cardiovascular-related areas of the brain and blood vessels. The primary function of ACE2 is to metabolize the deleterious Ang II into Ang-(1-7), a heptapeptide with vasoprotective actions. ACE2/Ang-(1-7)/Mas, a newly identified member of RAS, has been demonstrated to counteract the effects of ACE/Ang II/AT1. Therefore, activation of the ACE2/Ang-(1-7)/Mas pathway might represent a novel target and strategy for treating strokes. Our previous publications demonstrate that ACE2 and Ang-(1-7) protects the brain from ischemic and hemorrhagic stroke. These studies also discuss the protective effects of ACE2 on EPC function and how ACE2 improves the therapeutic efficacy in ischemic stroke. We recently found that ACE2 be carried by EPC-EXs and provide an additive beneficial effect on ageing cells by decreasing apoptosis and promoting cell viability. Further studies are needed to verify

the protective effects of ACE2 on ageing animal models. In addition, the modulation of exercise on the balance of these two pathways and its implications in strokes will be studied.

The approaches for this project include *in vitro* cell culture and *in vivo* animal models as well. For the *in vitro* model, ageing cells induced by Ang-II treated with EPC-EXs w/wo ACE2 overexpression. For the *in vivo* model, we have the Renin-transgenic hypertensive mice. We also have mice with age over six-month-old. The mice will be treated with different types of EPC-EXs.

Project 3. The role of exercise in vascular diseases by modulating the concentration and contents of exosomes.

It is well-known that exercise induces beneficial impacts on vascular diseases and diabetes. We have confirmed that long-term exercise could provide beneficial effects on blood pressure, body weight, and diabetic metabolic parameters. Recent studies suggest that exercise could modulate the levels of circulating exosomes and miRs, which are known to be majorly carried by EXs. We have recently demonstrated that exercise could modulate the level and contents of circulating EPC-EXs. Further studies will focus on the effects of exercise on different organs, such as adipose tissue, vessels, and the brain through the communication of EXs. The correlations of the level and contents of EXs after exercise with the outcome of strokes and diabetes will also be explored.

The approaches for this project will test the effects of long-term exercise on different animal models, such as hypertensive and type-2 diabetic mice.

Dr. Lydia Bogomolnaya

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Our research focuses on characterization of molecular mechanisms utilized by Gram-negative bacteria *Salmonella enterica* ser. Typhimurium and *Serratia marcescens* to survive host response and to develop better treatment options. In particular, we are interested in the following important questions:

Project #1: Identification of natural functions of drug efflux pumps during infection

Non-typhoidal *Salmonella enterica* serotypes including Typhimurium are the leading cause of bacterial food-borne enteritis in the United States. Until recently, *Salmonella* isolates were highly susceptible to most of the commonly used antibiotics but in the last decade the emergence of multidrug resistant *Salmonella* has been reported worldwide. *Serratia marcescens* is an opportunistic pathogen with increasing clinical importance. *S. marcescens* can cause meningitis, endocarditis, infections of airway and urinary tract, especially in immune-compromised patients. Efficiency of antibiotic therapy for these patients in some cases is extremely low due to the high intrinsic antibiotic resistance of *S. marcescens*. One mechanism for resistance of bacteria to antibiotics is through antibiotic efflux via multidrug efflux pumps. However, little else is known about the natural functions of these pumps during infection. We found that at least one pump called MacAB present in both bacterial species protects them against reactive oxygen species (ROS). We are interested in identification of natural substrates of this pump; how these substrates protect bacteria from ROS and how substrate production is regulated. Our studies will advance our understanding of the natural functions of bacterial efflux pumps beyond excretion of antibiotics and will aid to develop alternative strategies to control bacterial infections and augment conventional antimicrobial therapy.

Project #2: Defining the role of secreted DUF1471-containing proteins in adaptation of bacteria to different environments

Bacteria are able to successfully exist in ever-changing environment. For a quick adaptation to a new niche, bacteria rely on secondary metabolites, peptides and secreted proteins. These molecules can participate in a number of important biological processes: signal transduction within population, production of new compounds (for example, antibiotics), formation of biofilms, and also play an important role in virulence. Gram-negative bacteria from *Enterobacteriaceae* family secrete in the environment a number of proteins containing DUF1471 domain with unknown function and a similar structure. The physiological role of these proteins in maintaining of bacterial viability remains unexplored. We hypothesize that bacteria utilize DUF1471-containing proteins as a network of signals to accelerate adaptation to a new environment. Our studies will be focused on identification of DUF1471-containing proteins needed for survival during infection and during antibiotic exposure.

WV-INBRE participants will receive training in standard microbiological techniques, molecular cloning, generation of mutants, DNA and protein analysis, and animal handling.

Dr. Piyali Dasgupta

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The following projects are available in my laboratory:

1. **Anti-cancer activity of nicotinic antagonists in lung cancer:** Smoking bears a strong correlation to the development of a type of lung cancer called lung adenocarcinoma. In our laboratory we study the signaling pathways of how nicotine and NNK (components of cigarettes) promote the growth of lung cancer. Specifically, students working on this project will examine whether compounds which block the effect of nicotine can be useful for lung cancer therapy. Other techniques the students will learn are (i) to measure the effects of nicotine on the growth of human lung cancer cells (ii) to measure the anti-cancer activity of compounds (that inhibit the effects of nicotine) in human lung adenocarcinoma.
2. **Capsaicin and small cell lung cancer:** Capsaicin is the major active ingredient of chilli peppers. Preliminary data in our laboratory shows that capsaicin can inhibit the growth of human small cell lung cancer cells. We are interested in investigating molecular pathways contribute to this process. If you are interested in this project, you will learn (i) to perform specific assays to determine whether capsaicin can cause cell death in human small cell lung cancer cells (ii) to examine the biochemical mechanisms underlying this growth-inhibitory activity of capsaicin.

TECHNIQUES:

The techniques that are routinely performed in our laboratory:

1. Cell culture techniques
2. Preparation of lysates, nuclear, membrane and cytosolic fractions
3. Assays to study cell growth and cell cycle progression
4. Detection of proteins using Western Blotting
5. Measurement of tumor angiogenesis.
6. Animal studies: anti-cancer studies on nude mice models

Price E. Dickson, Ph.D.

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Systems genetics and recombinant inbred mouse panels for discovery of the mechanisms driving drug addiction

Drug addiction is a critical public health issue with genetic and environmental causes for which the underlying biological mechanisms remain largely unknown. To uncover these mechanisms, the Dickson Lab uses construct-valid behavioral techniques within the context of a systems genetics approach. Systems genetics using experimental mouse populations enables discovery of novel genetic and genomic mechanisms influencing disease by associating genetic and phenotypic variation. The intravenous drug self-administration paradigm is the gold-standard of volitional drug use assessment in rodents due to its ability to index drug taking and seeking at many stages of drug use including initiation, maintenance, and relapse. Through integration of a systems genetics approach and construct-valid behavioral techniques such as intravenous drug self-administration, novel and unexpected genetic mechanisms underlying the complex psychological phenotype of drug addiction and behaviors that predict drug use and addiction can be discovered.

Students in the Dickson lab can expect to learn about:

- Systems genetics as an approach to biological discovery
- The importance of genetic diversity in the laboratory mouse in the context of systems genetics
- The use of recombinant inbred mouse panels in the context of systems genetics
- Intravenous drug self-administration as an approach to identify biological and psychological mechanisms driving addiction

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My research focuses on how opioids regulate various cells in the brain during development. I have projects that look at cells in tissue culture and also in whole animals. My studies focus on how opioids given in utero alter the development of the brain.

Opioid regulation of brain development

In West Virginia we have one of the highest levels of opioid abuse in the whole country. Unfortunately this also includes among pregnant women, with approximately 10% of all neonates having exposure to opioids during pregnancy. The long term consequences of this exposure are not currently known. Studies with other drugs of abuse have shown that there can be significant developmental issues for the child when given during pregnancy. Our lab investigates how opioids can regulate the development of the brain. This project will investigate the effects of opioid exposure on the regulation of oligodendrocytes and brain myelination. Changes in myelination can have a significant effect on brain development, and lead to long term developmental delay. Methods that will be used will include dissection, Western blot analysis, immunofluorescence microscopy, and real-time PCR.

Instrumentation:

This project may involve using fluorescent and UV plate readers, real-time PCR, microscopy, gel rigs, centrifuges, balances and other standard lab equipment.

Dr. Lawrence M. Grover

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Central nervous system consequences of prenatal opioid exposure. Fetal exposure to opiate drugs due to maternal drug use has both immediate and long-term consequences due to effects on the central nervous system. Immediate consequences include neonatal abstinence syndrome (NAS), which is caused by drug withdrawal after birth. Symptoms of NAS may include hyperexcitability, high-pitched cry, tremor, diarrhea, vomiting, sweating, rapid breathing, feeding and sleep problems, and seizures. The symptoms of NAS reflect disturbances in nervous system development and function as a consequence of opiate exposure. Infants exposed prenatally to opiates also have a long-term risk for neurobehavioral problems lasting at least through childhood. The mechanisms through which prenatal opiate exposure produces these adverse consequences are still poorly understood. We are investigating the hypothesis that neurotrophic factors, which play critical roles in development and plasticity of the nervous system, are altered by prenatal opiate exposure leading to both immediate symptoms of NAS and longer term alterations in the nervous system and behavior.

Methods and instrumentation. Students participating in these projects will have the opportunity to learn animal handling, techniques for *in vitro* analysis of neuron function (dissection of CNS tissue samples, electrophysiological measurement of neural functions), techniques for measuring protein expression (Western blotting, enzyme-linked immunosorbent assay or ELISA), and techniques for analysis of emotional and cognitive behaviors in laboratory animals. For tissue preparation and analysis of neural function, we use *in vitro* incubation chambers, micromanipulators, amplifiers, stimulators, and oscilloscopes; data is collected and analyzed using software running on personal computers. For Western blotting and ELISA we use gel electrophoresis equipment, chemiluminescence, a digital imager, and a plate reader. Animal behavior is recorded and analyzed using a computer-based animal tracking and measurement system. Students will use standard lab equipment (scales, pH meter, osmometer, pipetters, sonicator, centrifuge, etc) for preparing solutions, reagents and samples.

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Examining the effect of flavors on vaping-related behaviors

While nicotine is the primary addictive component of all tobacco and vaping products, flavor additives have now been found to alter the neurons that are critical for addictive behaviors. As the use of electronic cigarettes continue to grow, it is critical that we understand how all constituents of vaping e-liquids effect the neurons that mediate addiction. The Henderson lab directly studies how nicotine and flavors trigger addiction. We use mice that are trained to use vaping devices to model human smoking and vaping behaviors. In these experiments we directly study how combining flavors with nicotine can increase drug reinforcement and vaping initiation. We then conduct follow-up experiments to examine changes in neurobiology and neurophysiology. These include the use high-powered fluorescence microscopy to examine structural changes in the dopamine neurons that play a major role in addiction neurocircuitry and electrochemistry to examine functional changes in the release of dopamine in the brain. Together, these experiments allow us to determine how entire brain circuits are modified by vaping constituents and trigger changes that reinforce vaping-related behaviors. For more information, visit the Henderson lab website: www.hendersonlab.org

Dr. Jung Han Kim

Professor

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Genetics of Obesity and Type 2 Diabetes

My research interest is in understanding the etiology and pathogenic mechanisms underlying type 2 diabetes and obesity, concomitantly related diseases. Type 2 diabetes is the most common form of human diabetes, accounting for over 90% of cases and obesity at such epidemic proportions creates serious public health problems. There is substantial evidence demonstrating that genetic factors are strongly involved in the development of type 2 diabetes and obesity, and I have focused my attention on the link between gene dysfunction and these diseases and its interaction with diets. As an internship project in our laboratory for the WV-INBRE Summer Research Program, I propose to study candidate genes for diabetes and obesity loci identified in a genetic mouse model of obesity and type 2 diabetes and their interactions with diets. This study will ultimately provide ready targets for diabetes and obesity therapies in humans. Experimental methods involved in this internship research will include enzyme-linked immunosorbent assay, colorimetric assay, polymerase chain reaction (PCR), western blot analysis, and real-time quantitative PCR. DNA, RNA and protein will need to be isolated from mouse tissues. Instruments involved in this project include gel electrophoresis, western blotting apparatus, microplate readers, spectrophotometer, imaging system, thermal cyclers, EchoMRI, and comprehensive lab animal monitoring system.

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WV-INBRE SUMMER RESEARCH PROJECTS

Ovarian cancer, worldwide, is the most common cause of gynecologic cancer death. Primary treatment consists of a combination of surgical and platinum-based therapy. Despite success in attaining remission in many cases of ovarian cancer, over half of women with ovarian cancer experience of recurrence with chemoresistance and metastasis, specifically in high grade serous ovarian cancer (HGSOC). Interestingly, mitochondrial dysfunction is emerging as one of the major contributors of aggressiveness and chemoresistance in HGSOC due to its central role in energy metabolism.

In humans, mitochondria are responsible for providing over 90% of the energy in the form of ATP, which is generated by the process of oxidative phosphorylation. They have their own 16.5 kb circular genome and translation machinery/ribosomes essential for the synthesis of 13 essential proteins of the oxidative phosphorylation complexes. The mammalian mitochondrial ribosome (55S) is composed of ~80 mitochondrial ribosomal proteins (MRPs), accumulating data suggest that alterations in expression levels, mutations, and post-translational modifications of MRPs, such as acetylation and phosphorylation, affect disease states, apoptosis and cancer. Our multidisciplinary research takes advantage of biochemical, molecular and biological, and mass spectrometry (MS)-based proteomics technologies in a "systems biology" approach. The following studies will be aimed at understanding the role of mitochondrial translation and protein acetylation in HGSOC.

Project 1: Detection of changes in MRP expression in ovarian cancer. Apoptosis, also known as programmed cell death, is an essential process for normal development, tissue maintenance and aging. The failure in this process can cause tumor formation. Two pro-apoptotic proteins, DAP3 (Death Associated Protein 3) and PDCD9 (Programmed Cell Death Protein 9), were identified in our proteomics analysis of the mitochondrial ribosome as MRPS29 and MRPS30, respectively. We have characterized a DAP3 splice variant with an upstream open reading frame (uORF) that is involved in regulation of its expression in different cell lines. Alterations in MRPS29 and MRPS30 transcript levels are also observed in tumors; however, regulation of their expressions and contributions to tumor formation is not yet understood. Expression of pro-apoptotic MRPs and the other functionally significant MRPs will be screened at the transcript and protein levels by quantitative RT-PCR and immunoblotting analyses using HGSOC biopsies.

Project 2: Regulation of protein synthesis in mitochondria by acetylation in ovarian cancer. Changes in expression of various histone deacetylases and sirtuins have been associated with metastasis in ovarian cancer. We have shown that the reversible acetylation of MRPL10 regulates protein synthesis in mitochondria. To investigate the role of protein acetylation on mitochondrial translation and cell proliferation in HGSOC, OVCAR3 cell lines will be treated with small inhibitors of these deacetylases.

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Project 1. Examine the mechanistic role of thymidine phosphorylase in thrombosis.

Our recent study revealed, for the first time, that thymidine phosphorylase (TYMP), an enzyme in the DNA salvage pathway, plays important mechanistic roles in facilitating platelet activation and thrombosis (Li et al. Circ Res. 2014, Belcher et al. ATVB 2021). Thrombosis, namely, clot formation in the vascular system, is a fatal complication for many diseases, which causes myocardial infarction, stroke, or pulmonary embolism. Various anti-platelet and anti-thrombotic drugs have been developed; however, in addition to that they cause severe side effects, such as bleeding, some patients do not respond to those drugs well. Therefore, developing novel mechanism-mediated anti-platelet and anti-thrombotic therapy is a top priority. We believe that TYMP is a promising target because TYMP deficiency significantly inhibits arterial thrombosis but does not disturb systemic hemostasis. Furthermore, TYMP inhibitor has been approved by the FDA for clinical use, which makes it possible to be repositioned as a novel and systemically safe anti-platelet drug. For this, it is first necessary to elucidate the detailed mechanistic pathways of TYMP in platelet activation and thrombosis. Our hypothesis is that *TYMP plays an important mechanistic role in platelet activation via signaling pathways involving platelet glycoprotein VI (GPVI) and G-protein coupled receptors (GPCRs)*.

In this project, we will use basic laboratory techniques including cell lysate preparation, protein concentration quantification, Western blotting and immunohistochemistry, as well as platelet aggregation assay, flow chamber assay, among others. The intern will have opportunities to participate in platelet isolation, stimulation, cell lysate preparation, measurement of protein concentration and Western blot assays etc.

Project 2. Examine the mechanistic role of thymidine phosphorylase in obesity and atherogenesis.

Dysregulated lipid metabolism and chronic inflammation have been recognized as key contributors to the development of obesity and atherogenesis. All of these are risk factors for causing thrombosis, which leads to myocardial infarction and stroke. TYMP is an enzyme in the pyrimidine salvage pathway. Our recent study revealed, for the first time, that TYMP possesses signaling functions and is essential for platelet activation and thrombosis, suggesting a novel function of TYMP in the cardiovascular system. TYMP is present in the lipid rich core of human atherosclerotic lesions, yet its function remains unknown. By searching Gene Expression Omnibus, we have found that TYMP is potentially correlated with the development of obesity. We thus hypothesize that TYMP participates in lipid metabolism and is essential for obesity and atherogenesis.

In addition to the basic laboratory techniques mentioned in project 1, student involved in this project will have opportunities to learn histological study including tissue sectioning, staining and quantitative analyses etc.

Project 3. Examine the mechanistic role of thymidine phosphorylase in the development of severe COVID-19.

As mentioned in project 1 and 2, we have found that thymidine phosphorylase (TYMP) plays important mechanistic role in platelet activation, thrombosis, as well as in the development of obesity. Obesity is one of the high-risk cohorts for developing severe COVID-19, which is also characterized by combination of thrombotic events. Using the **MGH (Massachusetts General Hospital) Emergency Department COVID-19 Cohort with Olink Proteomics**, we have found that TYMP levels in COVID-19 patients increased in an acuity-

dependent manner. Studies conducted in our lab also demonstrated that TYMP was significantly increased by SARS-CoV-2 spike protein, and TYMP inhibition attenuated SARS-CoV-2 spike protein enhanced thrombosis. We hypothesize that increased TYMP expression induced by SARS-CoV-2 spike protein plays an important mechanistic role in the development of severe COVID-19.

Student involving in this project will have opportunities to evaluate platelet function, thrombosis, lung inflammation, western blotting of inflammatory markers and signaling transduction molecules, etc., using tissues harvested from animal models as well as in vitro cell culture.

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Since 2013, my lab at Marshall University has focused on discovering new treatment strategies for multi-drug resistant infections. We are currently investigating the use of disulfiram (Antabuse) and other FDA-approved drugs as antibiotic adjuvants for the treatment of vancomycin-intermediate *Staphylococcus aureus* (VISA) infections. It was discovered that disulfiram reduces the MIC of vancomycin in VISA to levels observed in vancomycin-susceptible MRSA. Mechanistic studies suggest that disulfiram and its primary metabolite disrupt energy production in MRSA and cause perturbations in bacillithiol-mediated redox homeostasis. Following discovery that disulfiram decreases intracellular bacillithiol levels, we are now evaluating its potential therapeutic application to counteract the resistance mechanism employed by Gram-positive and Gram-negative bacteria to inactivate fosfomycin. Researchers will learn techniques to evaluate antibiotic synergy between disulfiram and fosfomycin using the checkerboard assay and time-kill studies. Hands-on experience using plate readers and flow cytometer may also be employed for additional pharmacodynamic studies.

Yongke Lu, PhD

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1. Peroxisomes and alcohol-related liver disease

Chronic alcohol consumption may cause metabolic liver disease designated alcohol-related liver disease (ALD), which ranges from simple steatosis (fatty liver) to steatohepatitis (liver inflammation), fibrosis and cirrhosis, and even liver cancer. About 90% alcohol drinkers have liver fat accumulation, i.e., fatty liver. Peroxisomes are organelles can oxidize fatty acid, which is regulated by a transcriptional factor peroxisome proliferator activated receptor α (PPAR α) and PPAR α agonist WY-14,643 can induce peroxisome proliferation, enhance peroxisomal fatty acid oxidation, and ameliorate alcoholic fatty liver. We are examining how peroxisome influence the development of alcoholic fatty liver in mouse model.

In this project you will learn about scientific experiment design, data collection and analyses, and result interpretation. You may practice the following techniques: general protein quantification, specific protein detection by immunohistochemistry staining, Western blot analysis, or enzyme-linked immunosorbent assay (ELISA), liver disease judgement by biochemical assays (serum levels of lipid, glucose, and ALT) using spectrophotometers and histopathology (liver section H&E staining) using microscopes.

2. Cell-cell interaction in liver

As an organ, liver contains multiple cell types like hepatocytes, Kupffer cells, hepatic stellate cells (HSC), etc. Hepatocytes are liver parenchymal cells. Most of liver functions are carried out by hepatocytes. Kupffer cells are immune cells protecting liver against insults from pathogens or pathogen-derived endotoxins. HSCs usually store vitamin A and are quiescent. When HSCs are activated by liver injury (mainly damaged hepatocytes), HSCs are transformed to fibrogenic cells to synthesize and release collagen, which causes liver fibrosis and cirrhosis. We will apply cell co-culture system to study hepatocyte-HSC interaction in liver fibrosis. In this project you will learn how to design an experiment, how to treat the cells, how to collect cultured cells for biochemical and molecular biological assays. You will practice sterile operation under hood.

Dr. Swarup Mitra

Assistant Professor of Biomedical Sciences
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The main theme of my research laboratory is to examine sex specific epigenetic and circuit plasticity underlying heroin induced neuroadaptations. There are three primary questions that we intend to examine under this theme.

1) Identify the role of dorsal striatal projections underlying heroin induced behavioral plasticity

The striatum forms a critical neural substrate underlying habitual behaviors and is often implicated in reinforcement learning and the development of compulsive habits, a behavioral characteristic of heroin addiction. Habit formation has mostly been attributed to the DS and time-dependent intensification of habit formation is thought to occur due to neuroadaptations in the DS. Dorsal striatal (DS) sub-structures (dorsolateral striatum-DLS and dorsomedial striatum-DMS) receive inputs from several essential brain areas including the thalamic nuclei (TN) and prefrontal cortical (PFC) regions. Selecting and generating appropriate actions for execution of a behavior involves integrating associative and sensory information. The DS, TN, and the PFC structures form a key hub where such integration occurs. We will examine how projections from TN and PFC substructures to DLS and DMS mediate heroin-induced behavioral plasticity.

2) How does controllable versus uncontrollable stress influence heroin relapse

Stress plays an important role in drug use and relapse. Specifically, daily life stress during abstinence is linked to increased craving for heroin in individuals with OUD, which is predictive of higher risk of relapse. Most importantly, emotional response over a stressful experience is an important determinant of behavioral adaptation to future stressful events. Modulation of stress responses to stressful experiences is a common pathology observed in several psychiatric diseases. The control dimension has most often been examined by using an escapable (controllable) versus non-escapable (non-escapable) foot shock paradigm. While it is well established that the DS mediates stimulus-response learning, the role of DS in influencing freezing or escape responses to aversive stimuli (foot shock) is less understood. We will examine how projections in DS substructures (DMS and DLS) modulate aversive learning in a controllable versus non-controllable stress behavioral paradigm, and how pairing such stressors influence drug-taking and relapse assays.

Sex differences are an essential determinant of neuroadaptations underlying addiction and stress mechanisms and warrants further exploration. Ovarian hormones regulate DS plasticity through its receptors present on the DS neurons. We will therefore examine questions 1 and 2 between males and females. We will utilize retrograde tracing followed by immunofluorescence and in-situ-hybridization to characterize PFC and TN projections to DS substructures in heroin addiction and/or stress. We will then chemogenetically activate or inhibit these circuits to examine their role in these behaviors. Finally, we will deplete ovarian hormones in females through ovariectomy and examine the sex-specific circuit plasticity underlying stress and/or heroin exposure.

3) Identify the neuronal circuit specific transcriptional and epigenetic changes that contribute to maladaptive plasticity during heroin relapse and/or stress.

Opioids are thought to alter transcriptional and chromatin processes in brain reward regions modulating synaptic plasticity underlying the addicted state. Experiences and cues associated with learning have been observed to induce distinct neural gene expression patterns in a temporal and pulsative manner, which is analogously referred to as the genomic action potential (gAP). Mechanistically, gAP has cascading consequences that influence long term functioning required for behavioral adaptations, which is achieved through governing of sex and cell-type-specific transcriptome and the translatome. Such gAP-mediated transcriptional and translational changes over a period of time enable experience-dependent modification of the synaptic circuitry to catalyze behavioral adaptations. There is emerging evidence that gAP underlies experience-dependent neuroplasticity through immediate early genes (IEG). However, the characteristics and functions of such neuroadaptations within specific neural substrates and between sexes in stress and opioid induced plasticity remain unclear. We will examine time-dependent changes in IEGs in the DS in rodents that will undergo heroin self-administration, relapse and stress assays. This will be addressed through biochemical approaches, including RNAscope and Catfish. To determine cell-type specific (i.e. the D1 and D2 expressing medium spiny neurons) IEG changes in the DMS and DLS, we will utilize RiboTag capture using Cre-inducible RiboTag in transgenic D1 and D2 cre lines. RiboTag will allow isolation of ribosomal RNA for sex and cell-type-specific quantification of IEGs. We will then do viral manipulation of IEGs in specific cell types in DMS and DLS will enable dissecting the role of D1 and D2 MSN in the DMS and DLS in stress, drug-taking and relapse. To examine the patterns of genomic enrichment of IEGs, we will use Chromatin immunoprecipitation (ChIP) followed by RNA-seq to examine patterns of gene expression that may be related to IEG binding.

INBRE participants will work closely on one of the research questions and get trained on preclinical models of substance use disorder, biochemical approaches, and imaging techniques. Data obtained during the training duration will be analyzed and formulated into poster presentations, grant proposals, and manuscripts for publications.

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1. The primary focus of my laboratory is to understand the mechanisms responsible for endocannabinoid signaling in human health and disease including cannabinoid tolerance, drug addiction, and metabolic homeostasis. Currently my group is funded by NIDA to assess the mechanisms responsible for cannabinoid tolerance (DA044999). This work involves assessing the contribution and molecular mechanisms of c-Jun N-terminal kinase (JNK) signaling in tolerance for different cannabinoid drugs. We are also actively engaged in work to understand the mechanisms responsible for sex differences between male and female mice in the response and tolerance to cannabinoids. This work involves using different strains of mutant mice that express either desensitization or internalization-resistant forms of the cannabinoid type 1 receptor. Members of my group commonly use methods in behavioral pharmacology to assess acute, inflammatory, and chronic pain in mice and molecular pharmacological approaches to assess cannabinoid receptor function and signaling. These pain testing approaches include the tail-flick and hotplate tests to measure acute pain, the formalin test to measure inflammatory pain, and the von Frey, Hargraeve's, and acetone tests to measure mechanical and thermal sensitivity in mice with chronic pain from chemotherapy exposure or nerve injury. We also use the elevated plus maze, forced swim test, conditioned place preference, and ultrasonic vocalizations to measure affective components of chronic pain. Lab members use molecular approaches such as qRT-PCR, Western Blotting, radioligand binding, and agonist-stimulated G protein activation to probe receptor expression and function.

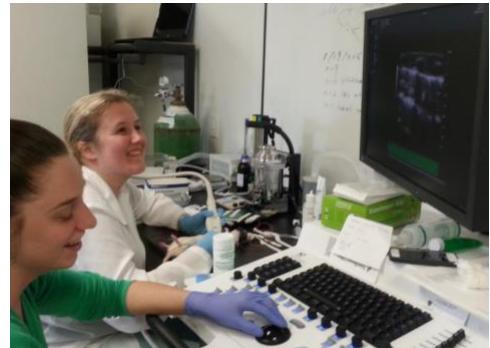
2. A second project that we are interested in involves understanding the role of neuropeptide signaling in the regulation of pain and motivated behaviors such as drug addiction and feeding. This work focuses on assessing the role of small neuropeptides derived from a protein precursor protein called proSAAS. ProSAAS-derived peptides have been shown to signal through two recently deorphanized G protein-coupled receptors, GPR171 and GPR83, to modulate body weight, feeding behavior, morphine tolerance and reward, and anxiety behaviors. Our current work involves examining acute, inflammatory, and chronic pain as well as morphine tolerance in mutant mice lacking proSAAS.

3. Finally, a third project involves assessing the impact of decursinol, the active anti-inflammatory and antinociceptive natural product component from the Korean Angelica Gigas Nakai plant, in acute, inflammatory, and chemotherapy-evoked chronic pain. Current work on this project involves assessing whether tolerance develops to the pain-relieving effects of decursinol and also whether co-administering this natural compound with chemotherapy might prevent development and "chronification" of neuropathic pain.

Dr. Sandrine V. Pierre

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The Pierre lab studies specific intracellular pathways involved in the integrated response of the myocardium to hemodynamic and metabolic disturbances. Our goal is to develop new paradigms to therapeutically address cardiovascular diseases based on the Na/K-ATPase signaling complex. We examine these issues by combining techniques of molecular and cell biology with *ex-vivo* (biochemistry and cell physiology, isolated heart perfusion, primary cardiac cell cultures, histology) and *in-vivo* assessments of cardiac function in genetically altered mice (echocardiography, measurement of blood pressure by tail-cuff and telemetry, cardiac and vascular catheterization).



Echocardiographic assessment of rodent cardiac function by Dr. P. Marck and undergraduate fellow A. Bryant.

In the interdisciplinary environment provided by MIIR, interns are exposed to the pre-clinical models and key techniques that are currently available to cardiac and vascular physiologists and pharmacologists.

Project 1. Cardioprotection by Na/K-ATPase ligands in acute myocardial infarction

Rationale: In addition to pumping ions, Na/K-ATPase interacts with neighboring membrane proteins and takes part in signaling complexes to send messages to various intracellular organelles. We believe that understanding these pathways and targeting the Na/K-ATPase receptor function will lead to novel interventions for the treatment and prevention of ischemia and reperfusion injury.

Method: the INBRE fellow will learn the isolated Landendorff-perfused mouse heart preparation and expose it to novel compounds targeting the Na/K-ATPase cardioprotective signaling pathway. This includes analysis of contractile function in real time and assessments of activation of the Na/K-ATPase cardioprotective pathway biochemically. The effectiveness of promising compounds will be further tested *in vivo* following experimentally-induced acute myocardial infarction (AMI). Mice will be subjected to an acute occlusion of the left descending anterior artery (LAD) for 30 min, and cardiac function and remodeling will be monitored after 1 and 2 weeks of reperfusion. In addition to functional echocardiographic assessments, the fellow will conduct morphometric and histological studies as well as biochemical (western blot) and qPCR evaluation of fibrosis, inflammation, and hypertrophy markers.

Project 2. Role of $\alpha 1$ Na/K-ATPase in adverse cardiac remodeling and heart failure

Rationale: Heart failure (HF), a chronic incurable illness, is the common end-stage of heart diseases caused by an array of highly prevalent conditions such as hypertension and coronary heart diseases. A greater and broader protection must be achieved to face the unmanageably high HF morbidity and mortality rates amidst the exploding incidence and prevalence of the condition worldwide. Targeting the Na^+/K^+ -ATPase receptor function may lead to novel interventions

Method: Using our newly developed model of cardiac-specific KO of Na^+/K^+ -ATPase $\alpha 1$, we will assess the role of Na^+/K^+ -ATPase $\alpha 1$ in the development of hypertrophy, fibrosis and heart failure in mice subjected to Angiotensin II infusion by osmotic minipumps. In addition to functional echocardiographic assessments, the students will conduct morphometric and histological studies as well as biochemical (western blot) and qPCR evaluation of fibrosis, inflammation, and hypertrophy markers.

Dr. Gary O. Rankin

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The following projects are available in my laboratory:

Project #1: Chloroanilines are commonly used chemical intermediates in the manufacture of dyes, drugs, agricultural herbicides and fungicides and thousands of other products. Exposure to a chloroaniline can result in a number of toxicities including toxicity to the blood, liver and kidney. This project seeks to determine the chemical species (parent compound or metabolite) responsible for liver and kidney damage and the mechanism by which toxicity occurs.

Project #2: Halogenated benzenes and phenols are common intermediates in the synthesis of a wide range of commercial products and appear as environmental pollutants in many parts of the world. Many of these compounds and/or their metabolites target the kidney and can induce kidney injury. This project will examine the nephrotoxicity induced by these compounds, examine structure-toxicity relationships as well as mechanisms by which these important chemicals harm the kidney.

Assays and Instrumentation: Projects that will investigate nephrotoxicity will use in vitro assays that involve isolation of rat kidney cells, measurement of enzyme release from treated and control cells, and potentially, the measurement of cellular ATP levels and other mitochondrial functional parameters. Additional techniques may involve Western blotting, quantifying urinary contents (protein, glucose), and measuring blood urea nitrogen and glucose levels. Instrumentation will primarily involve the use of balances, centrifuges and UV-visible spectrophotometers. High pressure liquid chromatography and thermocycler use is also possible.

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Recently, much progress has been made towards understanding how neurons, the cells responsible for the processing and transfer of information in the central nervous system (CNS), interact with non-neuronal brain cells. However, we have still only begun to scratch the surface about how non-neuronal cells contribute to the structural and functional maturation of the neuronal junctions known as synapses. Our work focuses on identifying and elaborating the genes, molecules, and signaling pathways that are crucial for linking non-neuronal cells with the synaptic structures that have been shown to be severely disrupted in nearly all known neurodevelopmental and psychiatric disorders. The long-term goal of our research is to contribute to novel therapeutic strategies to prevent or repair the impaired synaptic connectivity that occurs during abnormal brain development and following CNS injury or insult.

Two primary projects are currently ongoing in the Risher lab:

- 1) Astrocytes, the primary glial cell type in the brain, secrete a variety of factors that promote synaptogenesis during development and after injury. One family of synaptogenic proteins, the thrombospondins (TSPs), acts through a neuronal receptor, calcium channel subunit $\alpha 2\delta$ -1, which is known to be altered in some patients with epilepsy, intellectual disability, and autism. Our recent work showed that the interaction between TSP and $\alpha 2\delta$ -1 promotes downstream signaling via the actin cytoskeleton-regulating protein, Rac1, to facilitate synapse growth and maturation. In transgenic mice lacking $\alpha 2\delta$ -1 throughout the body, the dendritic spine structures that commonly receive synaptic input in the brain are severely disrupted, showing reduced density and structural maturity. We are currently investigating whether these brain abnormalities are present in a cortex-specific $\alpha 2\delta$ -1 knockout mouse line, as well as determine the mechanism by which TSP/ $\alpha 2\delta$ -1 triggers Rac1 activation.
- 2) Neonatal abstinence syndrome (NAS) is a devastating consequence of the national opioid epidemic that is showing striking incidence rates in West Virginia and Central Appalachia. NAS infants are essentially born with an addiction to opiates, and they enter an intense state of withdrawal after being cut off from the mother's nutrient supply. The babies require constant supervision and, approximately 50% of the time, pharmacological intervention before being able to be discharged from the NICU. The long-effects of NAS on cognition and behavior are predicted to be numerous, but there is currently not much known about how prenatal opioid exposure affects brain development. Recently, at Cabell Huntington Hospital, a subset of NAS infants have been described with a particularly harsh form of the condition; these infants were born to mothers who co-abused opioids and the drug gabapentin. Gabapentin is a ligand for the synaptogenic receptor $\alpha 2\delta$ -1 which prevents the binding of TSP and subsequent synapse-promoting effects. We are now conducting experiments to try to understand the mechanism by which gabapentin and opioids interact to affect the formation and maturation of synaptic circuitry in animal and human models of NAS.

In the Risher lab, students will be exposed to a variety of cellular, molecular, genetic, and imaging techniques. Commonly used methods include animal handling (mouse/rat), primary cell culture, organotypic brain slice culture, Western blotting, immunohistochemistry, plasmid DNA transformation and transfection, confocal microscopy, electron microscopy, 3D reconstruction-based image analysis, genotyping, and viral vectors including CRISPR/Cas9. Students will have the opportunity to meet regularly with Dr. Risher as well as in a group setting such as our biweekly lab meetings/journal clubs.

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Our laboratory is interested in understanding how adolescent binge drinking influences brain function and contributes to the development of alcohol use disorder. Using a rodent model of adolescent binge drinking, our laboratory and others have demonstrated that there are acute and long-term changes to neuronal structure, function, and behavior across multiple cognitive domains.

Over the last few decades it has become apparent that non-neuronal cells called astrocytes which outnumber neurons and ensheathe many neuronal connections, play an important role in synapse formation, synapse maintenance across the life-span, and synaptic recovery following injury. However, how astrocytes contribute to neuronal and synaptic remodeling following ethanol exposure is not fully understood. Understanding how astrocytes contribute to the long-term effects of adolescent binge drinking in a rodent model is crucial for understanding the impact that underage alcohol exposure can have on the adult brain and how early onset drinking may contribute to the development of alcohol dependence later in life.

We have three ongoing projects: 1. Investigating the acute and long-term effects of binge drinking on astrocyte function. 2. Investigating the role of astrocytes in the development of addiction. 3. Investigating how changes in astrocyte function following adolescent binge drinking influence recovery from secondary injury later in life, e.g., following stroke and/or traumatic brain injury. Techniques used to answer these questions include: intracranial survival surgery, immunohistochemistry, Western blot, qPCR, organotypic slice culture, confocal microscopy, 3D morphometric analysis of astrocytes, and a battery of behavioral paradigms including conditioned place preference, open field, social interaction, and plus maze.

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Impact of Methamphetamine use during pregnancy on the cardiovascular function of adult offspring

My laboratory studies the impact of methamphetamine use during pregnancy on cardiovascular outcomes in adult offspring. We have found that prenatal exposure to methamphetamine leads to myocardial hypersensitivity to ischemic injury, induces long-lasting changes in cardiac gene expression, and alters vascular function in adult offspring. Importantly, some of these effects are sex-dependent. Our data suggest that individuals that were prenatally exposed to methamphetamine may be at increased risk of developing cardiovascular diseases. We are currently trying to understand the mechanisms by which prenatal exposure to methamphetamine induces these cardiovascular changes.

INBRE participants will have the opportunity to participate in the identification of methamphetamine-induced changes in cardiac gene expression (analysis of RNA sequencing data, real time PCR, western blotting), conduct experiments with isolated tissues (hearts and blood vessels), interact with other investigators in the department (faculty, graduate students, postdoctoral fellows, and undergraduate students), assess scientific literature, and learn to present their data to a scientific audience.

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The aryl hydrocarbon receptor (AHR) is a ligand-activated transcription factor that binds environmental toxicants, pharmaceutical drugs and endogenous ligands. We have and others have discovered that the AHR promotes or inhibits breast cancer depending on the ligand that it binds. We hypothesize that the AHR modulates breast cancer progression by regulating the activity of embryonic pathways that have become oncogenic in breast cancer cells. We hypothesize that a better understanding of the mechanisms by which AHR regulates signaling in breast cancer cells will lead to novel therapies to treat this disease. Students in my lab would have the opportunity to study these questions in several lines of human breast cancer cells. Our methods are largely molecular biology based; therefore, students would have the opportunity to use real time PCR machines, electrophoresis equipment, and laminar flow tissue culture hoods. Students will also have a choice as to what technique they would like to learn during their intern. Techniques in lab will include, but are not limited to, real-time PCR, western blot, chromatin immunoprecipitation analysis, interfering RNA approaches to gene knockdown and proliferation assays.

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The following projects are available in my laboratory:

Project 1: Adolescent vaping and behavior: Vaping is highly rampant among adolescents. This study will use mouse models to assess behavior changes due to vaping. My laboratory is interested in studying effects of environmental stress on cardiometabolic end points.

Project 2: Non-opioid analgesics and pain: Opioid addiction is high among people who suffer from chronic pain. My laboratory is interested in understanding the physiology of pain, in order to test non-opioid analgesics to alleviate this pain. We will use cell culture and animal models of pain and test the analgesic compounds that work through non-opioid signaling.

TECHNIQUES:

Techniques that will be used in the above projects are:

1. Animal studies: rodent models of vaping or pain
2. Behavior assessments
3. Cell culture systems to study pain
4. Isolation and quantification of RNA (including miRNA) and DNA
5. Detection of genes using quantitative PCR/Real time PCR and Western Blotting
6. Detection of cardiometabolic endpoints

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Our research interests focus on telomeres, the evolutionarily conserved protein-DNA complexes that cap linear eukaryotic chromosomes, promote genome maintenance and regulate cellular lifespan. Telomere length shortens with each somatic cell division and is often viewed as the most accurate cellular marker of biological age. Proper maintenance of telomere length has important implications for aging, stem cell-related diseases and cancer. Although considerable variation in mean telomere length exists in yeast, plants and humans, mechanisms underlying telomere length homeostasis are largely unknown.

Project 1. Genetic and epigenetic architecture of natural telomere length variation.

The main objective of current research in the lab is to elucidate the genetic and epigenetic causes of telomere length variation using the genetically facile plant *Arabidopsis thaliana* as a model. To achieve this goal, we use a plethora of cutting edge natural variation resources available for this organism and a collection of powerful molecular, genomic and epigenetic tools. We recently identified a major effect QTL that explained 48% of telomere length variation in recombinant inbred Arabidopsis populations, with the underlying natural polymorphism mapping to the *NOP2A* gene. Mutations in mammalian *NOP2* orthologs lead to uncontrolled proliferation of cancer cells, and their expression serves as a prognostic marker of tumor development. INBRE program participants will work with laboratory personnel on understanding the role played by *NOP2A* and other genes in telomere length control. Our studies will have an impact on understanding genetic differences in telomere length between individuals and populations, and may provide novel insight into the molecular basis for different rates of aging and predisposition to telomere-associated stem cell, cancer and age-related diseases.

Project 2. Analysis of the interplay between telomere biology and ribosome biogenesis.

We have recently identified several components of rRNA maturation machinery, including *RPL5*, that impact species-specific telomere length set point in plants. Interestingly, human *RPL5* inhibits tumorigenesis, and its inactivation is the most common (11-34%) somatic ribosomal protein defect in multiple tumor types. Indeed, important similarities exist between human diseases known as telomeropathies and ribosomopathies, and our findings argue that components of rRNA maturation machinery may impact species-specific telomere length set point across eukaryotic evolution. IMBRE participants will work with mutants of ribosome biogenesis genes in plants to uncover specific mechanisms linking telomeres with ribosome biogenesis.

All participants will receive training in molecular cloning, RNA, DNA and protein analysis, aspects of genetic manipulations and bioinformatics.

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Project 1:

The Question: “*What causes treatment failure in some cancer patients but not others?*” Cancer cells can be viewed as a separate organism within the host that is continually evolving in order to survive. Applying evolutionary theory in this context will help us understand how cancers can reoccur after going into remission or not respond to chemotherapies. The process that cells in our bodies undergo to become cancer cells end up producing a cell that ceases to listen and cooperate with its neighbors, which is necessary for the complex mixture of cell our bodies are. This project will investigate an ability of cells known as phenotypic plasticity, where a cell can change its characteristics in order to adapt to the physiological situation. Our previous investigations have shown that heat shock protein 90 (HSP90) has a critical role in epigenetic gene regulation through histone acetylation and phenotypic plasticity. HSP90 is over-expressed in multiple cancers with poor prognosis. Thus, we propose to investigate the role of HSP90 in the ability of cancer cells to use phenotypic plasticity to adapt to chemotherapy.

Research Goals: The approach is to test the effects of inhibition of HSP90 on phenotypic plasticity *in vitro* on a panel of cell lines. We will determine if inhibition of HSP90 can prevent the adaptation to chemotherapies of lung cancer cells newly derived from patient samples, as well as established cell lines. The two adaptive phenotypes we will examine include epithelial to mesenchymal transition (EMT) and expression of drug transporters in a multi-drug resistant (MDR) phenotype. The major tools of investigation will be flow cytometry and functional assays for the phenotypes.

Specific Project: Students will induce EMT and MDR in a variety of lung cancer cell lines and study the expression of various protein markers on the surface of the cells using flow cytometry to determine the effects. HSP90 inhibitors will be used to determine how these influence phenotypic plasticity.

Project 2:

The Question: “*What are the molecular defects that promote age-related dysfunction?*” Our understanding of the processes associated with aging now includes dysfunction associated with epigenetic gene regulation. Understanding the mechanisms that promote evolution of the epigenome and its increasing dysfunction with age in stem cells are critical to therapeutic strategies targeting aging. The results of our investigations in the *Drosophila* and murine model systems indicate a very important gene in epigenetic gene regulation, heat shock protein 90 (HSP90), is well connected to phenotypic plasticity. We propose to investigate if the loss of phenotypic plasticity associated with epigenetic drift and clonal hematopoiesis can be ameliorated by inhibition of HSP90.

Research Goals: This project is designed to test the hypothesis that inhibition of HSP90 results in changes in histone acetylation that in turn prevent epigenetic drift and loss of phenotypic plasticity in hematopoietic stem cells. The approach is to test the hypothesis *in vitro* in a stem cell model of blood cell differentiation.

Specific Project: Students will induce epigenetic drift in our stem cell model and study the production of various markers on the surface of cells using flow cytometry. HSP90 inhibition will be performed via small molecule inhibitors to determine if this inhibition can prevent and reverse epigenetic drift of these cells.

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Na/K-ATPase Alpha 1 in Heart Failure and Cardiac Decompensation

Initial hypertrophic growth of cardiac myocyte is a compensational process in response to reduced cardiac output due to pressure overload or myocardial infarction. Clinical data showed that about 50% of hypertrophic patients eventually become decompensated which lead to heart failure and death. Earlier studies found that heart failure patients exhibit significant reduction of Na/K-ATPase in their heart tissue, and their preserved contractile function is correlated with the amount of Na/K-ATPase. Our recent work demonstrated that specifically reducing Na/K-ATPase $\alpha 1$ causes cardiac cell death, reduces cardiac hypertrophy, and decompensates muscle contraction in animal models of cardiomyopathy. The current project is to study the mechanisms of Na/K-ATPase $\alpha 1$ in regulation of cardiac cell survival and metabolic activity through mitochondria-mediated signaling pathways. Specifically, we will investigate the relationship between Na/K-ATPase $\alpha 1$ reduction and mitochondria-mediated cell apoptosis. In addition, we have identified a specific Na/K-ATPase inverse agonist, MB5 (a hydroxyxanthone compound), that can preserve cell membrane Na/K-ATPase by blocking ouabain-induced endocytosis. We will continue to test if MB5 can be used as a potential rescue for Na/K-ATPase in animal models of cardiomyopathy. Students participate in this project could learn basic laboratory techniques including Western blot, RT-qPCR, cell culture, and tissue collection from animal studies. It is also expected for the students to practice experimental design and manuscript writing.

Dr. Monica Valentovic

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Our laboratory is focused on exploring new interventions that will reduce the adverse effects of drugs. We have recently focused on examining ways to reduce the toxicities of cancer chemotherapy agents, antiviral agents and radiocontrast agents. Projects available in my lab:

Project #1. Reducing serious cancer chemotherapy side effects. This is an ongoing project that has been funded by a federal grant from NIH. Our laboratory is evaluating new compounds that may reduce the adverse effects experienced by individuals treated with cancer chemotherapy drugs. All cancer chemotherapy agents induce side effects and reducing these side effects will allow a better quality of life for the individual and potentially improve the success of the cancer chemotherapy agent. A long term goal is to develop methods to improve the effectiveness of the cancer chemotherapeutic agents while lessening the side effects. This project has clear clinical relevance and is translational. The drugs we are exploring are used in controlling breast, lung, ovarian cancer and leukemia. An individual involved in this project will investigate cellular changes in toxicity, specifically we want to explore changes in the mitochondria as well as post-translational modifications of proteins caused by exposure to cancer chemotherapy drugs including doxorubicin, cisplatin camptothecin or irinotecan.

Project #2. Potential role of e-vape flavoring agents in renal impairment. E-cigarettes and e-vaping have a complex series of flavoring aldehydes. Recent studies have shown alterations in genetic expression in the lung, kidney, brain and liver following vaping in rodent models. We will examine changes mediated by flavoring aldehydes on human renal proximal tubules. This project will examine the impact of flavoring aldehydes on mitochondrial proteins critical in generation of ATP.

Project #3. Examination of the mechanism of renal damage by an antiviral agent used in in treating HIV and hepatitis B patients. Patients with HIV or hepatitis B must take antiviral agents to slow the progression of their disease. These drugs are taken for very long period of time even years. Side effects often occur after someone takes an antiviral agent for over 1 year. We are examining the mechanism of damage to the kidney by a commonly used antiviral agent. We are using a normal human proximal tubular epithelial cell culture model for this study. We have preliminary results to suggest certain agents can reduce the side effects of the antiviral agents but would not impact the pharmacologic activity.

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- 1. Elucidating the role of IRGM in the pathogenesis of Myelodysplastic syndromes (MDS).** – MDS are blood and bone marrow cancers that are often caused in part by overactive inflammation in hematopoietic stem and progenitor cells. I have already determined that loss of expression of 2 genes in a commonly deleted genomic region for MDS (Tifab and miR-146a) are involved in the pathogenesis of disease. IRGM lies in between these two genes and has been established to have anti-inflammatory and antimicrobial properties. I want to determine if loss of IRGM can lead to MDS initiation or can lead to progression of MDS at a faster rate in an MDS mouse model that also has deletion of Tifab and miR-146a. If our hypotheses are supported, the long-term goal of the lab regarding this project would be to create a small molecule mimic of IRGM to treat MDS patients. See the papers below for more background information.
<https://pubmed.ncbi.nlm.nih.gov/26143580/>
<https://pubmed.ncbi.nlm.nih.gov/26458771/>
<https://pubmed.ncbi.nlm.nih.gov/27733775/>
- 2. Determining how obesity contributes to initiation and progression of MDS.** Obesity has been linked to leukemia, but has not been studied in our double knockout (Tifab and miR-146a KO) MDS mouse model of disease. We will perform studies such that MDS susceptible mice are subjected to control and Western diet to determine mechanisms by which obesity contributes to initiation and progression of disease. We anticipate mechanisms to involve diet/obesity-driven changes in hematopoietic stem and progenitor cell differentiation. We will also plan to determine if this can exist as an epigenetic effect (Do offspring of parents on poor diet have increased susceptibility to MDS initiation and/or progression?)
<https://pubmed.ncbi.nlm.nih.gov/27733775/>
<https://pubmed.ncbi.nlm.nih.gov/21038084/>
<https://pubmed.ncbi.nlm.nih.gov/19296839/>
- 3. Defining the mechanisms by which obese individuals are more susceptible to infection and have lowered vaccine efficacy.** We hypothesize that this occurs through dietary and obesity-driven effects on hematopoietic stem cells, which we have found to be important in providing immune protection against pathogenic threats. We will also determine if this can exist as an epigenetic effect (Do offspring of parents on poor diet have decreased vaccine-induced immune protection against infectious disease?).
<https://pubmed.ncbi.nlm.nih.gov/21038084/>
<https://pubmed.ncbi.nlm.nih.gov/19296839/>
<https://pubmed.ncbi.nlm.nih.gov/30405604/>

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My research focuses on bacterial biofilms, lung infections and gut microbiota. Four projects are ongoing in the Yu lab.

Project #1: Cystic Fibrosis Biofilms. Individuals afflicted with cystic fibrosis (CF) are susceptible to recurrent lung infections with a bacterium called *Pseudomonas aeruginosa*. During the infection in CF, this bacterium forms a capsule (biofilms) by producing a polysaccharide called alginate. Alginate is a virulence factor that allows greater adhesion to lung epithelial cells, as well as protection from antibiotics and the host's immune system. We study how alginate production is regulated. Elucidation of the alginate pathways will lead to better understand the pathogenesis, and development of novel therapeutics for treatment in CF.

Project #2: Testing Antimicrobials. Most of bacterial lung infections starts with the colonization of upper respiratory tract. Aspiration of oropharyngeal secretions containing colonizing bacteria deep into the lung allows for the establishment of lower respiratory tract infections. We are using an inhalation exposure system to introduce bacteria into the distal airways of the mouse lungs, causing the development of pneumonia. This model is being utilized to test the safety and efficacy of novel antimicrobials against the multiple drug-resistant (MDR) lung infection. The goal of this project is to develop novel therapeutics against the MDR Lung infections and pneumonia.

Project #3: SFB Probiotics. Gut microbiota, a bacterial community made up of 1,000 different species, are important to human health. Among all the species, there is a morphologically-distinct symbiotic member known as segmented filamentous bacteria (SFB). The SFB belongs to a group of clostridia bacteria, which cannot be grown *in vitro*. However, the SFB play a vital role in the development of the immune system in mice. More specifically, SFB have been shown to attach to the apical epithelium of the small intestine to induce the interleukin-17-producing T helper (TH₁₇) cells. TH₁₇ cells are important for the protection against intestinal pathogens as well as in maintaining gut homeostasis. In this project, we will examine possibilities of how to develop the SFB into a novel probiotic to prevent and control the gastrointestinal diseases in children.

Project #4: New Biopolymer Development. Through removal of major pathogenicity genes from genome and validation via the genome resequencing, we created a non-pathogenic strain of *P. aeruginosa* that produces large amounts of alginate. Alginate is a polysaccharide widely used in biomedical applications. It consists of an unbranched linear biopolymer comprised of two sugar monomers, β-D-mannuronate and its C5 epimer α-L-guluronate. Through introduction of changes of genetic codes for the alginate biosynthetic enzymes, we hope that we may be able to use the non-pathogenic strain to produce alginate with custom compositions.