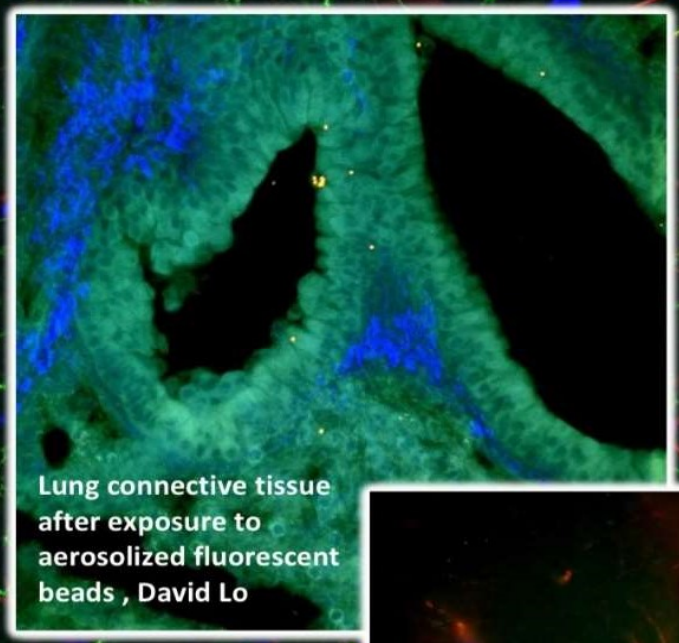
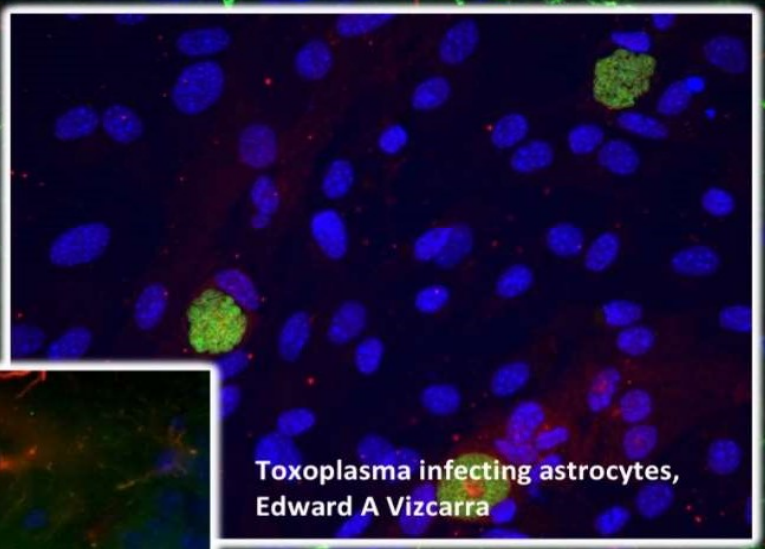
UC RIVERSIDE
School of Medicine

The Research Division of Biomedical Sciences Presents

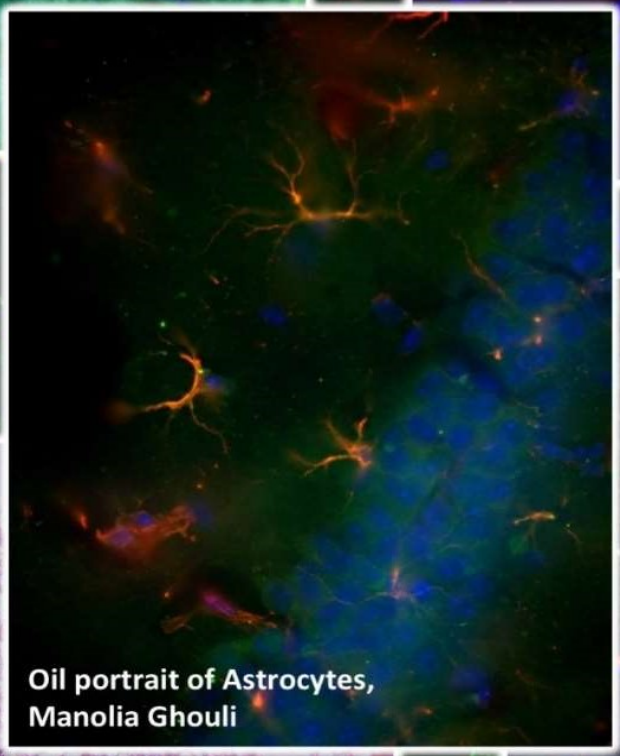
3RD ANNUAL ULTIMATE BIOMED RETREAT



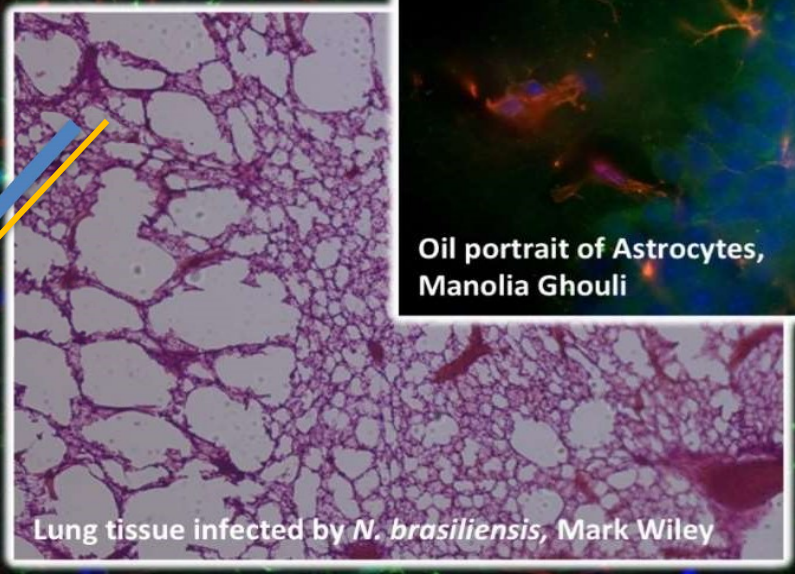
Lung connective tissue after exposure to aerosolized fluorescent beads , David Lo



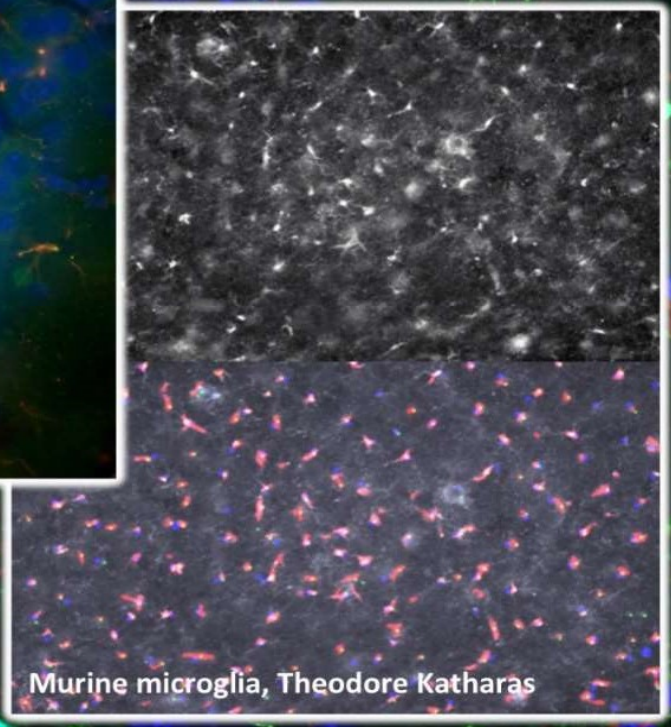
Toxoplasma infecting astrocytes, Edward A Vizcarra



Oil portrait of Astrocytes, Manolia Ghouli



Lung tissue infected by *N. brasiliensis*, Mark Wiley



Murine microglia, Theodore Katharas

Friday Oct 9th 2020, virtual

adult mouse hippocampus, Min Zhang

T A B L E – of – C O N T E N T S

Cover image winner:
"Adult mouse hippocampus"

CA1-glia+astrocyte-1

adult mouse hippo. CA1, blue- DAPI for nucleus, red- GFAP for astrocytes and green- Iba1 for microfilm.

Creative cover design by Min Zhang – Postgraduate Research Scientist
University of California, Riverside
–Zheng lab, Biomedical Sciences

A special thank you to our retreat committee, volunteers, and Biomed Grad Program Faculty for their hard work, time, and effort with coordinating this event.

Without your contributions, this event would not be possible.

Committee Co-Chairs:

Dr. Lukasz Jaroszewski

Dr. Patricia Pirbhoy

Rebecca Ruggiero

Division Chair: Dr. Monica Carson

Retreat Committee

Jeffrey Koury

Dr. Min Zhang

Kelly Radecki

Courtney Wood

Biomed Grad Program Faculty

Nicholas DiPatrizio

Anandasankar Ray

Cover image first runner-up:
Astroproject

Manolia_Ghouli_Astroproject.jpg

Oil Portrait of Astrocytes

Included in creative cover design by Manolia Ghouli – Graduate Student
University of California, Riverside
–Binder lab, Biomedical Sciences

Ultimate Biomed Retreat (UBR) "Vision, Mission, and Purpose Statement"

Participants: All Faculty, Fellows, Staff and Students in the Division of Biomedical Sciences and the Graduate Program for Biomedical Sciences

UCR Vision: This forum will engage the diversity of individuals, perspectives and expertise in activities focused on enrichment, evaluation and creative exploration of synergies to facilitate the Division in attaining its aspirational goals to be a campus, school and national leader in the practice of innovative high-impact Biomedical Sciences research, teaching and service.

UBR Mission: To provide an annual forum for the Division to:

- Feature and celebrate our achievements and progress
- Foster community amongst all in the Division and its administered programs
- Provide opportunities for leadership and impact for trainees, staff and those not traditionally in leadership positions
- Involve, engage and enrich the entire Division community
- Identify opportunities & challenges in its 3 part research, teaching and service missions
- Identify aspirational, strategic and pragmatic goals with metrics for the upcoming year
- Ensure that the Division's goals and activities embody the values of the School of Medicine
- Foster and evaluate the Division's commitment to pursuing an anti-racist agenda in its 3 part mission

UBR Purpose: To foster community and high-impact research involving all cohorts and ranks in the Division and Division-sponsored programs; reveal and examine our community strengths, challenges and opportunities; deconstruct institutional racism present within academia; and provide a safe interactive forum for team building, introspection and professional development.

Thank-you all for your active participation in this retreat and we hope to see you again next year for our 4th Annual Ultimate Biomed Retreat which will be held in the fall quarter of 2021!

Lukasz Jaroszewski, Patricia Pirbhoy, Rebecca Ruggiero
Nicholas DiPatrizio, and Anandasankar Ray
2020-2021 Steering Committee - BMSC – Ultimate Biomed Retreat

Ultimate Biomed Retreat Agenda

Welcome

8:45am - 8:55am	**Welcome Address** Dr. Monica Carson
8:55am - 9:15am	**"Anti-Racism Through Storytelling"** Dr. Adwoa Osei, Keynote speaker
9:15am - 9:40am	**The Division of Biomedical Sciences "Call for Action" Taskforce** Isaac Owusu-Frimpong **A Call for Volunteers for Inland Empire Community Outreach** UCR Planning Committee Co-Chairs
9:40am - 9:50am	**Break**

Morning Faculty Presentations

9:50am - 10:10am	**"Understanding COVID-19 through the SARS-CoV-2 evolution"** Dr. Adam Godzik
10:10am - 10:30am	**"COVID-19 Vaccine and Treatment Development Landscape"** Dr. Juliet Morrison
10:30am - 10:40am	**Break**

Morning Breakout Sessions

10:40am - 11:20am	**COVID-19 Pandemic Breakout Sessions** Pica Preston *Participants breakout into their respective sessions (based on selection during registration)*
11:20am - 11:25am	**Break**

11:25am - 11:35am	**Breakout Session Debriefs** **"What made SARS-Cov2 a causative agent for a pandemic? and COVID-19 Diagnostics"** Dr. David Lo
11:35am - 11:45am	**"Racial disparities in COVID-19 pandemic"** Dr. Ann Cheney
11:45am - 11:55am	**"Impact of COVID-19 on CNS and other systems"** Dr. Byron Ford
11:55am - 12:05pm	**"Nutrition and Exercise during COVID-19 pandemic and beyond"** Dr. Mitra Hooshmand
12:05pm - 12:15pm	**"Work/life Balance during COVID-19 pandemic and beyond"** Amanda Smith
12:15pm - 12:25pm	**"Stress management and rest during COVID-19 pandemic and beyond"** Anacary Ramirez

Slack Poster Presentations

12:25 pm - 1:10 pm	**Poster Presentations via Slack** *Participants are encouraged to grab lunch during the poster session*

Afternoon Presentations

1:10pm - 1:25pm	**Afternoon Session Welcome Address** SOM Dean Dr. Deborah Deas
1:25pm - 1:45pm	**Lightning Talks: Group I** **"Discover SUMOylation as a critical host factor for influenza virus replication"**

	Dr. Jiayu Liao **"Elucidating the mechanisms of differential gonadotropin hormone gene expression and its role in female reproductive physiology"** Rebecca Ruggiero **"Epigenetic mechanisms of safeguarding mixed lineage states during hematopoiesis"** Yiming Livelo **"Analysis of Single Cell Expression Data from Sepsis Patients"** Xinru Qiu
1:45pm - 2:05pm	**Group I: Q/A** Jeff Koury
2:05pm - 2:30pm	"**Everyday Mindfulness and Meditation"** **Mediation break** Amanda Smith
2:30pm - 2:55pm	**<u>Lightning Talks: Group II</u>** **"Large scale analysis of smoking-induced changes in the tumor immune microenvironment"** Dr. Arghavan Alisoltani-Dehkordi **"Interdisciplinary Collaborations in Neuroscience Research"** Dr. Gerald Maguire **"The role of Interferon Beta in HIV Associated Neurocognitive Disorder (HAND)"** Jeffrey Koury **"Doping the gut: Identifying the role for CB1 in gut-barrier function"** Mark Wiley

	"Development of 3D culture assays to evaluate the anti-cancer properties of experimental XIAP inhibitors" Parima Udompholkul
2:55pm - 3:15pm	**Group II: Q/A** Rebecca Ruggiero
3:15pm - 3:25pm	**Break**

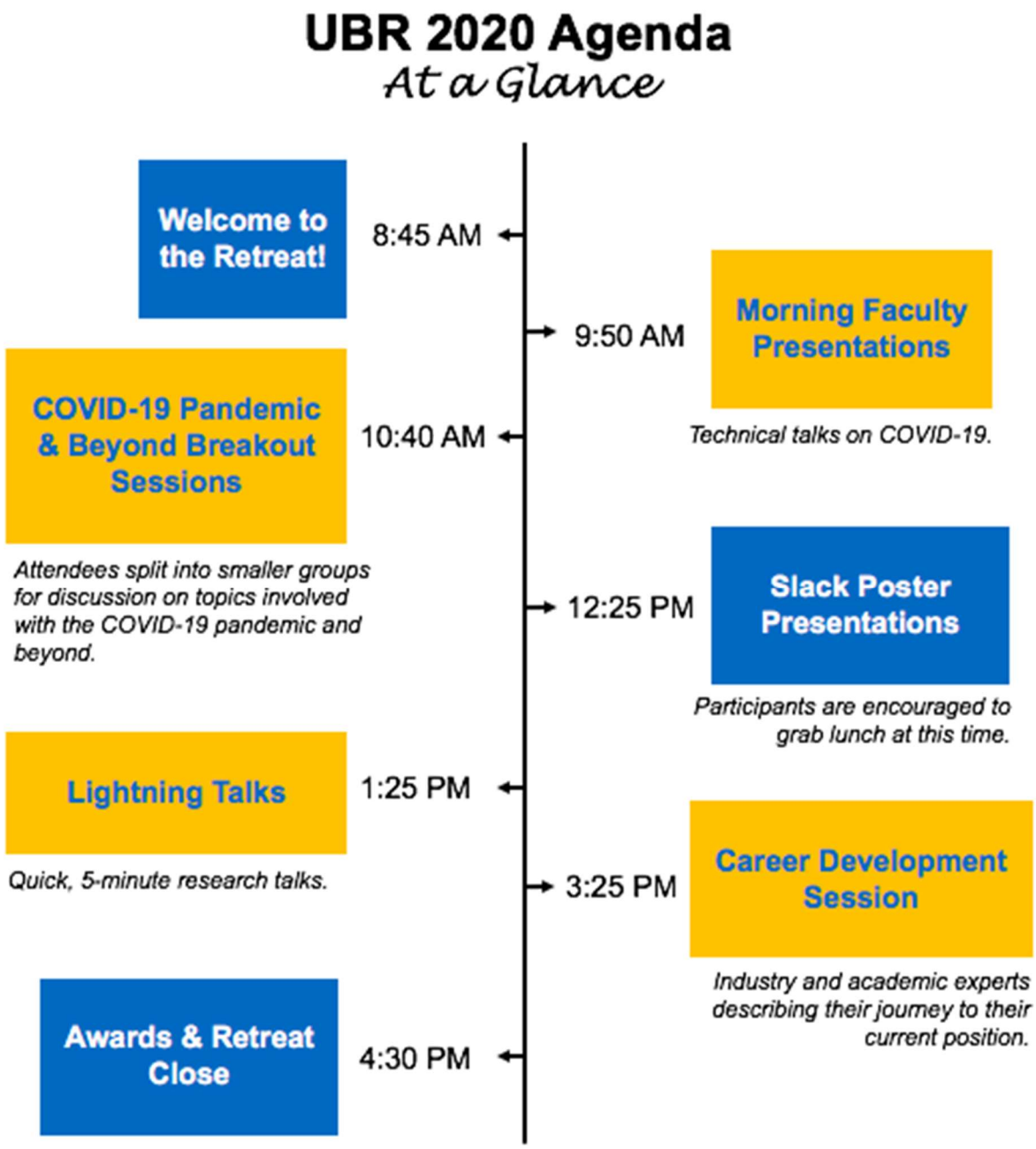
Afternoon Career Development Session

3:25pm - 3:30pm	**Introduction to Career Development Session** Dr. Nicholas Dipatrizio
3:30pm - 3:40pm	**"Careers in Medical Writing and Medical Affairs"** Dr. Andrea Menicucci Industry Speaker, Medical Writing
3:40pm - 3:50pm	**"Balancing Research and Teaching: exploring academic careers in a teaching institution"** Dr. Deborah Fraser Academia Speaker, Teaching Based Institutions
3:50pm - 4:00pm	**"The (Long) Road to an Academic Career"** Dr. Nicholas Dipatrizio Academia Speaker, Research Based Institutions
4:00pm - 4:10pm	**"The Biotech Launch: Successfully Transitioning from Academia to Industry"** Dr. Sean Boyle Industry Speaker, R&D Operations
4:10pm - 4:20pm	**"Transitioning to Health Policy at the State Level"** Dr. Shannon Muir Policy Speaker
4:20pm - 4:30pm	**Career Development Session Q/A**

	Dr. Nicholas Dipatrizio

Retreat Close

4:30pm - 4:35pm	**Awards**
4:35pm - 4:45pm	**Closing Remarks** Dr. Monica Carson



Program Speakers and Guests

Morning Faculty Presentations

Adwoa Osei, MD, PhD
Assistant Clinical Professor, Health Sciences, School of Medicine
University of California, Riverside
Keynote Speaker

Adwoa Osei, MD specializes in pediatrics. She received her education from The University of Ghana Medical School and her board certification from The American Board of Pediatrics. Dr. Osei is an active member of the American Board of Pediatrics. Dr. Osei received the Berton Mathias Award in 2008 for clinical excellence and compassion in patient care, Academy Award for Excellence in Compassion in 2017, and Teaching Excellence Award in 2020 from UCR SOM Alumni.

Adam Godzik, PhD
Professor, Biomedical Sciences Research Division, School of Medicine
University of California, Riverside

The Godzik lab research is focused on proteins. We try to combine insights from physics and biology to answer basic questions about the relation between the protein sequence and its structure and function. From physics we know that proteins are ruled by universal laws - at equilibrium they are at the free energy minimum. From biology we know that proteins come in families and studying relations in such families we can learn more about how changes in protein sequences influence their structures and functions. You may find more in our publications and bioinformatics servers at the Godzik lab website. http://godziklab.org/pages/

Juliet Morrison, PhD
Assistant Professor, Microbiology and Plant Pathology, College of Natural & Agricultural Sciences
University of California, Riverside

My research combines immunological and virological methods with computational analysis to address questions at the host-pathogen interface. A major interest of my lab is understanding how emerging and re-emerging viruses antagonize innate immune pathways to promote their replication. We also use virus-encoded interferon antagonists as tools to define previously unknown aspects of interferon signaling regulation. Another interest of my lab is using tissue deconvolution algorithms and immunological tools to study the dynamics of lung immune cell populations during influenza virus infections, and spleen and liver immune cell populations during dengue virus infections. Our goal is to translate our findings into host-targeted influenza and flavivirus therapeutics.

Morning Breakout Sessions: COVID-19 Pandemic and Beyond

David Lo, MD, PhD
Professor, Biomedical Sciences Research Division, School of Medicine
University of California, Riverside

David D. Lo, M.D., Ph.D., is the senior associate dean for research at the University of California, Riverside School of Medicine and a distinguished professor in the Division of Biomedical Sciences.Lo is Director of the BREATHE center (Bridging Regional Ecology, Aerosolized Toxins, and Health Effects; breathe.ucr.edu), and Director of the NIH-supported U54 Center for Health Disparities Research (healthdisparities.ucr.edu). In brief, the Lo laboratory has been studying the development of M cells and the mechanisms used by M cells in their surveillance of the mucosal tissues.

Ann Cheney, PhD
Assistant Professor, Department of Social Medicine Population and Public Health, School of Medicine
University of California, Riverside

Ann Cheney, PhD, is faculty in the Department of Social Medicine Population and Public Health at the University Of California Riverside School Of Medicine. She is a medical anthropologist with research expertise in in health services research and community based participatory research. She has conducted research with disadvantaged populations in rural communities, including African Americans, Latino immigrants, and indigenous Mexicans. Her work addresses structural inequality in health and she uses community based participatory methods to empower grassroots leaders to use research as a vehicle to activate communities and change narratives of health and wellbeing. Dr. Cheney's current work focuses on the impact of structure in health with a focus on Latino immigrant farmworkers in rural southern California. She is the director of HABLAMoS (Hispanic and Bilingual Longitudinal Ambulatory Medical Studies), a 4-year program for medical students that focuses on Spanish language acquisition and studies in cultural and structural competence. Dr. Cheney is faculty supervisor of the Global Health at Home group and oversees the Coachella Valley Free Clinics.

Byron Ford, PhD
Professor, Biomedical Sciences Research Division, School of Medicine
University of California, Riverside

My laboratory studies the cellular and molecular mechanisms involved in the pathophysiology of stroke and acute brain injuries. We investigate the neuroprotective roles of neuregulin-1 (NRG-1) and other compounds in stroke and other acute neuroinflammatory disorders. My group utilizes in vivo and in vitro models as well as high-throughput tools to scan the genome, transcriptome, proteome and metabolome to understand mechanisms associated with neuronal pathology and neuroinflammation following acute brain injuries. I have published extensively on the neuroprotective roles of NRG-1 in acute brain injury models, including rodent and non-human primate cerebral ischemia models and a novel model of nerve agent exposure. We are specifically interested in the role of NRG-1 in regulating the immune response and the activity of glial cells following brain injury. NRG-1 is currently in human clinical trials and showed significant efficacy in a phase II study of heart failure patients. My work has yielded nine full U.S. patents, two Canadian patents and one each from China and Australia. The results of these studies have therapeutic implications for other acute neuroinflammatory disorders include traumatic brain injury, nerve agent toxicity, cerebral malaria and sepsis.

Mitra Hooshmand, PhD
Adjunct Faculty, University of California Los Angeles
Director of Scientific Programs, Campaign behind Prop 14

Dr. Mitra Hooshmand received her PhD at UC Irvine where she studied the therapeutic effects of stem cells after spinal cord injuries. She completed 2 years of post-doctoral fellowship at the same institution before transitioning to her role as the director of scientific programs at Americans for Cures where she educated the public about the importance of stem cell research. From there, Dr. Hooshmand took on her present position as the Director of Scientific Programs at the Campaign behind Prop 14. She is also an adjunct faculty at UCLA where she teaches multiple courses on stem cell biology, policy, and ethics. Mitra has also started 2 businesses: a yoga studio (Mixx Yoga) which recently permanently closed due to financial duress, but led to a spin-off company, Be Fit Biz, which provides evidence-based wellness programs to corporations.

Amanda Smith, MS, LCSW
Director of Medical Student Support & Wellness, School of Medicine
University of California, Riverside

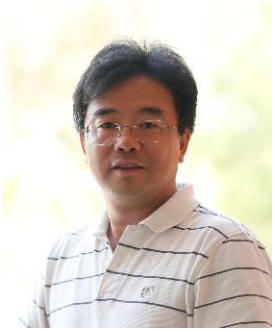
Amanda Smith is a UCR alumni. She has a Masters in Social Work from CSUSB and is a Licensed Clinical Social Worker as well as Mindfulness Facilitator. She is an expert in mental health services and crisis intervention for over 14 years. She previously worked for Veterans Affairs in various departments including Veterans Treatment Courts, In Home Nonskilled services, and finally Supervisor for clinical staff in the ED and Inpatient Psychiatric Units. She was also actively involved in creating an employee wellness program. She is always looking for ways to build connection and community with clients and student populations to assist individuals with improving their overall wellbeing.

Anacary Ramirez, **MA**
School of Psychology

Anacary is a doctoral student in school psychology and her research interests focus on parent-school-community collaboration/consultation as well as behavioral and mental health interventions with diverse populations. Her current research involves teleconsultation services with Spanish-speaking families and focuses on student behavior change using applied behavior analysis. Anacary is a also co-leader of the non-clinical R'Grad Peer Support Group for graduate students which covers topics such as anxiety, depression, nutrition, work-life balance, and self-care.

Lightning Talks

GROUP I



Jiayu Liao, PhD

Associate Professor
Bioengineering, University of California, Riverside
Research Focus: Studies on quantitative FRET assay, quantitative system biology, high-throughput screening assay development and drug discovery, SUMOylation and Ubiquitin-like pathways, Bioconjugation on solid surface.

Rebecca Ruggiero, BS

3rd year PhD student, Djurdjica Coss' laboratory
Biomedical Sciences Research Division
University of California Riverside, School of Medicine
Research Focus: Investigation of epigenetic mechanisms governing gonadotropin hormone transcriptional regulation in female reproduction.

Yiming Livelo, MS

3rd year PhD student, Sihem Cheloufi's Laboratory
Biochemistry and Molecular Biology Department
University of California Riverside
Research Focus: Role of CAF-1 Histone Chaperon in Cellular Plasticity.

Xinru Qiu, MS

3rd year PhD candidate, Adam Godzik's Laboratory
Genetics, Genomics, and Bioinformatics Program
Research Focus: Studying Immune Cell Heterogeneity by Using Single-Cell RNA Sequencing Analysis

GROUP II

Arghavan Alisoltani-Dehkordi, PhD

Senior postdoctoral fellow, Adam Godzik's Laboratory
Biomedical Sciences Research Division
University of California Riverside, School of Medicine
Research Focus: Comprehensive study of smoking-induced changes in tumor-immune microenvironment

Gerald A Maguire, MD, DFAPA

Professor and Chair, Psychiatry and Neuroscience
University of California, Riverside School of Medicine
Research focus: Elucidating the causes of stuttering and developing novel treatments for this disorder.

Jeffrey Koury, MS

3rd year PhD student, Marcus Kaul's Laboratory
Biomedical Sciences Research Division
University of California Riverside, School of Medicine
Research Focus: Neuroinflammation and Neurodegeneration.

Mark Wiley, BS

5th year PhD candidate, Nicholas V. DiPatrizo's Laboratory
Biomedical Sciences Research Division
University of California Riverside, School of Medicine
Research Focus: Endocannabinoids in Gut-Barrier Function.

Parima Udompholkul, MS

5th year PhD candidate, Maurizio Pellecchia's Laboratory
Biomedical Sciences Research Division
University of California Riverside, School of Medicine
Research Focus: Targeting ML-IAP for the design of cancer therapeutics

Career Development Session

Andrea Menicucci, PhD
Medical Writer, Agendia, Irvine

Dr. Andrea Menicucci obtained her Ph.D. in Biomedical Sciences at UC-Riverside. Dr. Menicucci completed her dissertation research, which focused on viral immunology, in Dr. Ilhem Messaoudi's laboratory. During her training she gained extensive experience in scientific writing, including grant proposals and peer-reviewed manuscripts. Along with her experience in genomics and bioinformatics, she leveraged her training to become a Medical Writer at a biotech company called Agendia, which utilizes genomic signatures to inform treatment decisions for breast cancer patients. In this role, she is involved in significant aspects of translational and clinical research, and collaborates with medical oncologists, surgeons and scientists to generate innovative evidence that will ultimately improve treatment strategies for breast cancer patients.

Deborah Fraser, PhD
Associate Professor, Department of Biological Sciences
California State University, Long Beach

Dr. Deborah Fraser teaches a wide range of classes from freshman and sophomore introductory courses, to upper division and graduate classes in molecular cell biology and cancer biology. Her lab studies the molecular mechanisms of innate immune responses in autoimmune and inflammatory diseases. She is currently funded by NIH to study the role of complement in atherosclerosis. Alongside her teaching and research, she is involved in running the NIH RISE program at CSULB, which is an undergraduate training program aimed at increasing the number of underrepresented students who go on to graduate programs and successful STEM careers.

Nicholas Dipatrizio, PhD
Associate Professor, Biomedical Sciences Research Division, School of Medicine
University of California, Riverside

The DiPatrizio laboratory is dedicated to elucidating the integrative neurobiology and physiology that controls food reward, sensory processing, and energy homeostasis, and dysregulation of these pathways in metabolic disorders. A combination of state-of-the-art analytical chemistry (i.e., ultra-performance liquid chromatography/tandem mass spectrometry), genetic (i.e., first-of kind genetic mutant mice with conditional organ-selective knockout of endocannabinoid system components), surgical, biochemical, molecular, pharmacological, and behavioral tools are employed to achieve these goals.Our research program investigates the molecular and neural underpinnings of obesity and hedonic eating, which are suggested to share characteristics with addictive and compulsive behaviors. Moreover, the DiPatrizio lab investigates the impact of cannabis exposure on endocannabinoid system function in health and disease. Collectively, our work supports the discovery and development of novel therapeutic strategies to safely treat metabolic and related disorders.

Sean Boyle, PhD
Senior Director, Bioinformatics Applications
Personalis, Menlo Park

Sean is Senior Director of Bioinformatics Applications at Personalis, with broad experience across analysis and interpretation of cancer genomics data. At Personalis, Sean leads development of neoantigen prediction, cell free applications, tumor microenvironment analysis, and biomarker discovery. His team also applies these technologies through external scientific collaborations with both academic and industry partners. Prior to Personalis, Sean received his PhD from UCR in the laboratory of Dr. Anandasankar Ray, identifying naturally occurring repellent compounds which affect the behavior of disease vector species. Most recently, Sean worked on advancing genomics and personalized genomic medicine, notably with the Dr. Mike Snyder lab at Stanford University, where he developed novel methods for analyzing and interpreting patient samples from both cancer and inherited disease.

Shannon Muir, PhD
Co-Director of the California Initiative to Advance Precision Medicine, Governor's Office of Planning and Research, Sacramento

Dr. Shannon Muir is Co-Director of Precision Medicine within the California Governor's Office of Planning and Research. She manages the California Initiative to Advance Precision Medicine, the first state-funded initiative for precision medicine in the United States. Prior to OPR, Shannon was Director of the Research Proposal Development Service at UC San Diego where she supported the development of large, interdisciplinary research proposals led by UCSD faculty. She was formerly a Senior Program Associate with the California Council on Science and Technology (CCST), where she worked closely with the Department of Energy and NASA Laboratories located in California. In 2015 Shannon was as a CCST Science Policy Fellow and served as a consultant for the California Senate Committee on Health. Shannon earned her Ph.D. in Biomedical Sciences from UCSD where she studied pediatric cancer genetics, and holds a M.S. in Pharmacology from Tulane University and a B.S. in Psychobiology from UCLA.

Student/Trainee Lightning Talk Abstracts
(In order of occurrence on agenda)

GROUP I

1. **Discover SUMOylation as a critical host factor for influenza virus replication**

Jiayu Liao
University of California, Riverside Bioengineering/Biomedical Science

Substantial studies indicate that SUMOylation play a key role in anti-pathogen infections. The secretion and signalings of several key cytokines in innate immunity, such as Type I IFN, IL2, TNF and IL4, are suppressed by the SUMOylation and disruptions of SUMOylation genes can confer the mice more resistance to lethal doses of viruses. Several viruses, such as SARS-CoV-2, SARS, influenza, MERS, Ebola, hijack SUMOylation for their replication benefits. The biological impact of SUMOylation for SARS-CoV-2 is not fully understood. We will leverage our recent breakthroughs on full SUMOylation assay to identify novel essential SUMOylation sites for influenza virus replication to determine the roles of SUMOylation for influenza and future SARS-CoV-2 replication and potential as therapeutics.

2. **Elucidating the mechanisms of differential gonadotropin hormone gene expression and its role in female reproductive physiology**

Rebecca E. Ruggiero and Djurdjica Coss
Division of Biomedical Sciences, School of Medicine, UC Riverside, CA, USA

Mammalian reproduction is controlled by the hypothalamic-pituitary-gonadal (HPG) axis. GnRH from the hypothalamus regulates the synthesis and secretion of gonadotropin hormones, LH and FSH. In females, LH regulates steroidogenesis and ovulation, while FSH regulates folliculogenesis. LH and FSH are differentially regulated throughout the menstrual cycle via changes in GnRH pulse frequency. The imbalance in LH and FSH synthesis and secretion leads to infertility or amenorrhea, where an increase in LH correlates with Polycystic Ovarian Syndrome (PCOS) and an increase in FSH leads to Premature Ovarian Failure (POF) in women. Gaps exist in our understanding of how GnRH can differentially activate gonadotropin genes in the same cell. Significant progress has been made in elucidating transcriptional regulation, which however failed to provide answers for understanding the mechanisms of differential regulation. We postulate that epigenetic mechanisms may be at play. Using a discovery proteomics-based approach, we will identify novel transcriptional cofactors and chromatin-modifying enzymes that play a role in tightly regulating differential gonadotropin hormone synthesis in response to hormonal stimuli. Understanding the mechanism whereby GnRH differentially regulates gonadotropin hormone levels will provide insight into the physiology and pathophysiology of the reproductive system.

3. Epigenetic mechanisms of safeguarding mixed lineage states during hematopoiesis

Yiming Guo[1], Fei Ji[2], Jernej Murn[1], David Frankhouser[3], M Andres Blanco[4], Carmen Chiem[1], MiHyun Jang[5], Ruslan Sadreyev[2], Russel C. Rockne[5], David B. Sykes[6], Konrad Hochedlinger[2, 6-9], Sihem Cheloufi[1]

[1] Department of Biochemistry, Stem Cell Center, University of California, Riverside, 900 University Ave. Boyce Hall 4411, Riverside, CA 92521-0129

[2] Department of Molecular Biology, Massachusetts General Hospital, 185 Cambridge Street, Boston, MA 02114, USA

[3] Department of Population Sciences and Department of Diabetes Complications & Metabolism, City of Hope, National Medical Center, Duarte, CA, United States

[4] Department of Biomedical Sciences, School of Veterinary Medicine, University of Pennsylvania, Philadelphia, PA, United States.

[5] Department of Computational and Quantitative Medicine, Division of Mathematical Oncology, City of Hope National Medical Center, Duarte, CA, United States

[6] Center for Regenerative Medicine, Massachusetts General Hospital, 185 Cambridge Street, Boston, MA 02114, USA

[7] Department of Stem Cell and Regenerative Biology, Harvard University, Cambridge, MA 02138, USA

[8] Harvard Stem Cell Institute, 1350 Massachusetts Avenue, Cambridge, MA 02138, USA

[9] Cancer Center, Massachusetts General Hospital, 185 Cambridge Street, Boston, MA 02114, USA

Cell fate commitment during hematopoiesis is driven by lineage-specific transcription factors and accompanied by dynamic changes in chromatin structure and chromatin modifications. How chromatin accessibility regulates maintenance of somatic cell identity during normal homeostasis is poorly understood. To address this question, we investigated the consequences of the histone chaperone CAF-1 depletion in a granulocyte-macrophage progenitor (GMP) myeloid differentiation system. Single cell RNA-seq analysis of CAF-1 depleted myeloid progenitors revealed concomitant activation of megakaryocyte and erythrocyte progenitor markers resulting in a mixed cellular state. We further identified distinct transcription factors that control canonical and alternate differentiation pathways upon CAF-1 inhibition. Manipulating chromatin accessibility potentiates the activity of lineage specific transcription factors and may provide a strategy for improving the generation of different blood cell types.

4. Analysis of Single Cell Expression Data from Sepsis Patients

Xinru Qiu[1], Jiang Li[2], Meera Nair[2] and Adam Godzik[2]
[1] Graduate Program in Genetics, Genomics and Bioinformatics, University of California Riverside, Riverside, CA 92521
[2] Division of Biomedical Sciences, University of California Riverside School of Medicine, Riverside, CA 92521.

The human immune system is able to respond to a broad range of threats, but occasionally it fails and may start acting against its host. With a better understanding of how the immune system works, we would be better equipped to intervene in such cases to set it back on track. Tackling infections requires the cooperation of different types of immune cells, with the type of cells and their interactions evolving during the course of the infection. In the early stages of the immune response, the most important of these are innate immune system cells, neutrophils, and macrophages. Infections that were not destroyed by this attack attract the attention of lymphocytes, which are cells using the functions of adaptation and memory, allowing the immune system to respond more and more specifically and remember the various types of infections, thus responding to reinfections with a faster and more effective counterattack. Furthermore, the interactions between these cell populations establish the check and balance mechanisms that are essential to prevent autoimmunity or immunodeficiency. However, most of our knowledge about the immune system came from bulk, large scale measurements, which provide average values that blend or mask the functions of individual cells, especially when their behavior is highly heterogeneous or driven by rare cell types. Also, for individual patients, these may be different, and understanding the details would be important for the application of personalized medicine. It is essential to study how in different diseases, individual cells and their populations change their interactions within metabolic, signaling, and transcriptional networks. Understanding how individual immune cells process information, how they respond to infections, perturbations, and perform differently under various threats has been a challenge in immunology.
Sepsis is a life-threatening organ dysfunction syndrome, which is caused by the host's dysregulated response to infection, resulting in uncontrolled inflammation and subsequent immunosuppression, leading later to a complete shutdown of the immune system (immunoparalysis). Sepsis remains one of the major causes of death in the intensive care unit (ICU) patients. Each year more than one in four deaths in the world are caused by sepsis. However, despite the high case fatality rate, there has been no specific treatment or drugs with good efficacy to treat sepsis. Sepsis is known for its very complex immune pathogenesis; some patients may die from inflammatory response, while most patients die later in sepsis with immunosuppression and simple anti-inflammatory therapy does not reduce the mortality. The biggest challenge in sepsis research is to understand the interplay between pro-inflammatory and anti-inflammatory responses that do not form a linear progression of events but are mixed together. Thus, therapeutic interventions targeting any specific mechanism may alter the balance between the mechanisms of death, but not the final outcome. One of the reasons for this confounding is the abnormal behavior of the immune cells. These mechanisms are difficult to study using traditional techniques such as cell sorting or mass transcriptome analysis. Emerging single-cell transcriptomics techniques allow researchers to study population heterogeneity of immune cells, unique in its ability to identify abnormal values and subpopulations of abnormal cells. As part of the collaboration between the UCR SOM Nair laboratory and the Riverside University Health System (RUHS) Intensive Care Unit, a series of single-cell transcriptomics studies on PBMC from survivors and non-survivors of sepsis using a

standard pipeline was carried out. The hypothesis evaluated in these studies is that there are certain cell types that are responsible for the failure of immunosuppressive-directed sepsis treatment.

GROUP II

1. Large scale analysis of smoking-induced changes in the tumor immune microenvironment

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Tobacco smoke contains many carcinogenic components that damage DNA and increase the overall rate of mutation, affect methylation patterns, and modify gene expression profiles, all of which affect the risk of cancer initiation and progression. At the same time, tobacco smoking has a well-recognized impact on both innate and adaptive immunity, which may affect the host ability to fight cancer. Since 24% of cancer patients in The Cancer Genomic Atlas (TCGA) cohort studied here continued to smoke after cancer diagnosis, a trend that was independently shown on large cohorts of cancer patients in the USA and other countries, it is essential to understand such indirect effect of smoking on cancer. In this contribution, we expanded upon the recent knowledge on the immune landscape of cancer by performing a comparative analysis of tobacco smoking-induced changes in the populations of major immune cell types between smokers and never smokers. To investigate the immune response of smokers (former/current) and never-smokers, abundance of immune cell types were calculated by both CIBERSORT and xCell tools based on TCGA RNAseq data. We further validated the findings using other cohorts of cancer patients. We revealed statistically significant changes in the population of immune cell types in all studied cancers, with increased plasma cell populations and the changes in the ratio of activated to resting immune cell types being the most consistent features distinguishing smokers and never-smokers across different cancers, with both being correlated with survival outcomes. Even though the tobacco-induced changes in the population of immune cells in cancer of tissues not directly exposed to smoke are not as marked as in lung and head and neck cancers (LUAD, LUSC, and HNSC), the significant differences in the survival of patients with various cancer types suggest that even a small shift in the frequency of immune cell types might result in adverse outcomes. We also noticed that smoking-induced changes in the immune cell populations and their correlations to survival outcomes are more striking in female smokers. In general, the findings of this study suggest the potential of some immune cell types as common prognostic and therapeutic targets for active smoker patients.

2. **Interdisciplinary Collaborations in Neuroscience Research**

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UCR School of Medicine has provided an excellent incubator for translational research and we have many opportunities ahead. As the first, permanent clinical chair appointed at UCR SOM, I will share my perspective as to how our clinical and education growth can greatly enhance our school's research efforts. As we grow our clinical practice, we in psychiatry, have done so in a manner that supports our school's primary missions of education and research. Avenues of communication and incentives have been outlined to foster collaborative, translational research. Our collaborative approach in stuttering research will be presented as a model for the school to consider in enhancing translational research moving forward.

3. **The role of Interferon Beta in HIV Associated Neurocognitive Disorder (HAND)**

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HIV Associated Neurocognitive Disorder (HAND) is characterized by cognitive, motor and memory impairments in about 20-30% of people living with HIV. Combination Antiretroviral Therapy has improved the lifespan of people living with HIV, but does little to ameliorate the prevalence of HAND. IFNb has been shown to transiently increase early on in a mouse model of HAND, prior to any neuropathological signs suggesting a role in neuroprotection. Here we identify IFNb to act directly on human microglia resulting in a dose dependent increase in expression of neuroprotective beta chemokines CCL4 and CCL5. These factors have been shown to bind to chemokine co-receptor CCR5, located on all cell types of the CNS, and confer neuroprotection.

4. **Doping the gut: Identifying the role for CB1 in gut-barrier function**

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Over-active inflammatory processes in the gut contribute to the development of Inflammatory Bowel Disease (IBD), an ailment which has doubled in prevalence in the US over the last 20 years. Development of IBD is associated with an over-active immune response which compromises the barrier function of the intestinal tissue with idiopathic etiology. Recent evidence implicates a role for the endocannabinoid (eCB) system in improving gut-barrier function in models of IBD. The eCB system consists of the lipid signaling molecules 2-arachidonoyl-sn-glycerol (2-AG) and anandamide (AEA) which bind and activate cannabinoid receptor subtype-1 (CB1R) and -2 (CB2R). We report that mice on a high-fat, high-sucrose western diet (WD) gain significant weight after 60 days which disrupts in vivo gut-barrier function and is coupled to a reduction in 2-AG production in the

large intestine mucosa. Furthermore, transgenic mice lacking CB1R in the intestinal epithelial cells only display exacerbated gut-barrier dysfunction after 60 days on WD. Future studies will identify the mechanism by which intestinal epithelial CB1 alters gut-barrier function in diet induced obesity.

5. **Development of 3D culture assays to evaluate the anti-cancer properties of experimental XIAP inhibitors**

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Inhibitor of apoptosis proteins (IAPs) are a family of proteins with anti-apoptotic activity and are highly expressed in various types of human cancers. Among the IAP protein family, X-linked IAP (XIAP) is the only member that can directly bind to and inhibit caspases-3/7 and caspase-9, thereby suppressing apoptosis. IAPs are inhibited by endogenous IAP-antagonist proteins such as SMAC/Diablo. Thus, SMAC mimetics have been developed as possible IAP inhibitors to either induce apoptosis in cancer cells or render them more sensitive to chemotherapeutics. Recently, our laboratory has derived innovative, potent Lys-covalent XIAP inhibitor 142D6. When tested in 2-dimensional (2D) culture assays, 142D6 induces apoptosis in MDA-MB-231 breast cancer cells with effective concentrations (nM) that were comparable to those of the clinical pan-IAP candidate LCL161 (Novartis). To better assess the efficacy of 142D6 in tumors, we have developed 3-dimensional (3D) culture assays based on a multicellular tumor spheroid (MCTS) model. Our 3D culture system could be an invaluable and reliable tool for high-throughput evaluations of experimental therapeutics from our laboratory. We found that 142D6 is very effective in inducing tumor regression in 3D culture. In addition, we have recently demonstrated that the agents are orally active and present a favorable pharmacokinetic profile, despite the presence of the Lys-reactive electrophile. Hence, the combination of 3D culture and in vivo pharmacokinetic studies can be used to more rationally select agents to be tested in more clinically relevant orthotopic and/or patient-derived orthotopic models of cancer growth and metastasis.

Slack Poster Session Abstracts

(Alphabetical order by first name of presenter)

1. **Targeted Overexpression of Glutamate Transporter-1 Reduces Seizures and Attenuates Pathological Changes in a Mouse Model of Epilepsy**

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Temporal lobe epilepsy (TLE) is the most common form of epilepsy with focal seizures. Unfortunately, TLE is also frequently associated with refractory epilepsy. Approximately 25% of patients will develop refractory epilepsy that is resistant to currently available antiepileptic drugs (AEDs). Current AEDs work primarily by targeting neurons through

modulation of neurotransmission by inhibition of glutamatergic excitatory neurotransmission or enhancement of GABAergic inhibitory neurotransmission. Targeting neurons can adversely affect cognitive function and can even lead to neurotoxicity. Therefore, non-neuronal targets are an attractive alternative approach to treat epilepsy with potentially fewer deleterious side effects. To date, there are no AEDs available that target non-neuronal cell types. Neuronal hyperexcitability is a major contributor to epilepsy but increasing evidence suggests that changes in astrocytic glutamate transporters can contribute to the development of epilepsy. Glutamate transporters have been shown to be reduced at epileptic foci in preclinical models and patients with TLE. In addition, de novo mutations in glutamate transporters, particularly GLT-1, have been identified in patients and families with early-onset epilepsy. Epilepsy is associated with hippocampal abnormalities including neuronal cell loss, dentate cell dispersion and gliosis. Here we demonstrate that using an AAV8-gfa2-GLT1 viral vector to promote cell-type specific GLT-1 transcription under the glial fibrillary acid protein (GFAP) promoter in the intrahippocampal kainic acid (IHKA) model of epilepsy delays neuronal cell loss, decreases dentate cell dispersion and suppresses seizure activity at early time points in epileptogenesis. Previous studies have also shown that Neuregulin-1 (NRG-1), a growth factor with various functions in the central nervous system, increases glutamate uptake and is neuroprotective in various animal models of brain injury. We also demonstrate that daily treatment with high dose NRG-1 (25 µg/kg) is neuroprotective at early time points in epileptogenesis. We hypothesize that astrocytic glutamate transporter dysregulation contributes to the development of epilepsy; thus, targeting glial glutamate transporters could lead to novel therapeutics for the treatment of refractory epilepsies..

2. Acute western diet preference in mice is controlled by cannabinoid CB1 receptors in the intestinal epithelium.

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The endocannabinoid system serves an important role in the intake of palatable food. We reported that endocannabinoid signaling in the upper small-intestinal epithelium is increased (i) in rats after tasting dietary fats, and this signaling controls fat intake, and (ii) in a mouse model of diet-induced obesity, which promotes overeating through a mechanism that includes blocking nutrient-induced release of gut-derived satiation peptides. We now utilized a combination of pharmacological, genetic, and behavioral tools to identify roles for cannabinoid CB1Rs in the upper small-intestinal epithelium in preferences for western diet (WD; i.e., high fat and sucrose) versus a standard rodent diet (SD; i.e., low-fat, no sucrose) in mice. Mice were maintained on ad-lib SD in automated two-hopper feeding chambers. At the time of testing, mice were given access to the WD hopper for the first time and intakes of SD and WD were recorded for the testing period. Mice displayed large preferences for WD, an effect inhibited by systemic pretreatment with the cannabinoid CB1R antagonist/inverse agonist, AM251, for up to 12-h after initiation of the preference test. We next used our conditional intestinal epithelium-specific cannabinoid CB1R-deficient mouse model (IntCB1-/-) to investigate the necessity for CB1Rs in the gut in preferences for WD. Similar to systemic inhibition of CB1Rs with

AM251, preferences for WD were largely absent in IntCB1-/- mice when compared to control mice for up to 12-h. Together, these data suggest that CB1Rs in the intestinal epithelium are required for acute WD preferences
in mice.

3. **Mechanisms of astrocyte swelling in elevated potassium conditions and potential effects on neuronal excitability**

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Increased excitability of neurons has been linked to both cellular swelling and elevated extracellular potassium ($[K^+]_o$). However, the amount of neuron vs. astrocyte swelling in elevated $[K^+]_o$ conditions and the effects of cell swelling in these conditions on neuronal excitability are poorly understood. Astrocytes regulate $[K^+]_o$ by uptake through astrocyte-specific K^+ channels, transporters and/or pumps, and are thus likely candidates for high $[K^+]_o$ induced cell swelling and subsequent reduction of the extracellular space (ECS). Our work suggests that $[K^+]_o$ in the range of 6.5 - 26 mM produces selective swelling of astrocytes in stratum radiatum, with little to no swelling of CA1 pyramidal cells. Astrocyte swelling increases proportionally with increasing $[K^+]_o$ concentration. Ongoing pharmacological experiments suggest that astrocyte swelling is regulated mainly by the Na^+/K^+ ATPase, with little contribution from inwardly rectifying potassium channels, the NKCC cotransporter or the sodium-bicarbonate cotransporter (NBC). Experiments performed using $AQP4^{-/-}$ mice indicate that astrocyte swelling in 10.5 mM $[K^+]_o$ is also independent of AQP4, and furthermore, data suggest that AQP4 may be more important for water efflux in these conditions. Overall, our experiments suggest a prominent role for the Na^+/K^+ ATPase as a primary K^+ influx pathway in elevated K^+ conditions. Additional experiments are ongoing to isolate the effects of elevated $[K^+]_o$-induced astrocytic swelling on excitability of CA1 pyramidal neurons. In summary, our work sheds light onto the mechanisms underlying selective astrocyte swelling in elevated $[K^+]_o$, and the possible impact of elevated $[K^+]_o$-induced astrocyte swelling on neuronal excitability.

4. **The Role of the Gut Microbiome in Shaping Immune Responses against Vibrio cholerae**

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Despite improvements in treatment, the diarrheal disease cholera caused by *Vibrio cholerae* remains a significant global health burden. Several studies show that oral cholera vaccines elicit a reduced antibody response in populations from developing versus industrialized regions. We hypothesize that one source of variation in vaccine responses is differences in gut microbiome structure. Our studies examine the role of commensal microbes on vaccination, with a view to develop effective microbial interventions that can boost immune responses to vaccines. To examine the role of different human microbiomes, we assembled a susceptible community comprised of Streptococcus

species, and a resistant consortium of Bacteroidetes and Firmicutes. These groups represent respectively an unhealthy community, similar to the post-diarrhea gut microbiome, and a normal adult microbiome. We used adult CD-1 mice treated with an antibiotic cocktail to deplete the murine microbiome, and then introduced our defined communities along with *V. cholerae*. We characterized changes in antibody response after Vibrio infection by ELISA and quantified the antibody efficacy by using an in vitro vibriocidal assay. Another measure of protection is the ability of antibodies from each of our microbiome contexts to limit infection of naive animals. Suckling mice were gavaged with *V. cholerae* that had been incubated with purified antibody from feces of adult mice infected with either microbiomes. Our data suggest that serum and fecal antibody from mice bearing the susceptible community confer less protection than the resistant community. Further, heat killed commensal bacteria mitigate this observed phenotype suggesting that live bacteria from the susceptible community suppress antibody responses. Additionally, when mice were depleted of CD4 T cells, the suppression was mitigated, suggesting that it is a T-cell dependent process. These data provide insights into how gut microbiome configurations contribute to variable mucosal vaccine responses.

5. Acute high-altitude exposure upregulates inflammatory gene expression and impacts TLR4 signaling

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Transcriptional responses to hypoxia and inflammatory stimuli are linked via hypoxia inducible factor (HIF) and NF-kB crosstalk. Tissues experience hypoxia during infection or inflammatory states due to increased metabolic demand of immune cells, or impaired oxygen delivery by occluded blood supply or fluid buildup. However, while the evolutionarily conserved inflammatory responses to oxygen limitation are necessary for modulating the physiological responses to hypoxic stress, during chronic and/or systemic hypoxia, the crosstalk between these two pathways can become maladaptive. For example, hypoxia-induced inflammation may contribute to the development of Acute and Chronic Mountain Sickness. We hypothesize that pro-inflammatory gene expression will increase upon acute high-altitude exposure. We compared the inflammatory profiles in whole blood collected in the morning during fasting at sea level and after one night at high altitude (3800 m elevation) in 14 healthy sojourners (4 women, 10 men). Expression of 255 inflammation-related genes was determined via the nanoString Inflammation panel. 18 genes showed significant differential expression at altitude. These include upregulation of *LY96*, *DDIT3*, *HMGB1*, and *TGFBR1* (adj. $p<0.0003$ for all). Gene ontology analysis revealed that differentially expressed genes were enriched for positive regulation of toll-like receptor signaling ($p<0.00001$) and positive regulation of interleukin-6 production ($p=0.00471$). Additionally, *HIF1A* expression was significantly correlated with the expression of multiple genes including *HMGB1* ($R = -0.54$, $p=0.038$), *TLR8* ($R = 0.59$, $p=0.0076$), and *NFE2L2* ($R = 0.57$, $p<0.0001$). Furthermore, *LY96* encodes MD2, a coreceptor with toll-like receptor 4, which is upregulated in macrophages via HIF and involved in modulating the inflammatory response to bacterial endotoxin. Therefore, this data suggests that at high altitude, hypoxic stress may sensitize the TLR4 signaling pathway and exacerbates subsequent responses to inflammatory stimuli.

6. **Structures of SARS-Cov-2 proteins and distribution of mutations: implications for diagnostic tests and vaccine development.**

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Fast evolution and extensive sequencing of the SARS-CoV-2 virus provides us with unique information about the patterns of genetic changes in a single pathogen in a timescale of months. We show that the distribution of SARS-CoV-2 virus mutations along its genome is closely linked to the structural features of the coded proteins. Specifically, we show that features such as solvent exposure, protein-protein interaction interfaces and structural disorder, as well as functionally important regions of SARS-CoV-2 proteins are crucial factors driving evolutionary selection in protein coding genes. Insights from the analysis of mutation distribution in the context of the SARS-CoV-2 proteins structure and function have practical implications for evaluating potential antigen epitopes or, surprisingly, even for the selection of primers for PCR-based COVID-19 tests.

7. **Regulation of Astrocytic Volume Regulated Anion Channels in Epilepsy**

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Epilepsy is a chronic, disruptive disease that affects more than 50 million people worldwide. It is characterized by recurrent, unprovoked seizures and is associated with adverse neurobehavioral outcomes and a three-fold increase in mortality. The most common form of epilepsy--temporal lobe epilepsy--is often caused by glutamate overstimulation. Current anti-epileptic medications (AEM) target and inhibit neurons, consequently dimming total cognitive function. It is essential to focus research efforts on finding non-neuronal targets for AEMs to circumvent the deleterious side effects of current treatments.

One potential non-neuronal therapeutic target is astrocytic volume regulated anion channels (VRAC). VRAC is activated by astrocytic swelling and functions by expelling anions and organic osmolytes--including glutamate--into the synapse after a synaptic event. Theoretically, inhibition of VRAC should decrease glutamate efflux into the synapse, thereby inhibiting neuronal re-stimulation and diminishing neurotoxicity. However, before determining whether VRAC inhibition decreases the incidence and duration of seizures in epilepsy, we first aim to determine whether VRAC is regulated in epilepsy.

Intrahippocampal kainic acid injections (IHKA) were performed on C57BL6 mice to precipitate seizures, and the brains were collected at 1, 7, 14, and 30 days post-IHKA.

The tissues were stained for mouse Glial Fibrillary Acidic Protein and VRAC, then compared to saline shams. We observed a quantifiable upregulation of VRAC 14 days post-IHKA in both the ipsilateral and contralateral hippocampi, which suggests that seizures regulate VRAC expression 14 days post-IHKA (after the epileptogenic period). We plan to continue these experiments for the other time points to determine how seizures regulate VRAC expression acutely, during epileptogenesis, and chronically. This data will determine the optimal time points for VRAC inhibitor drug studies, which will enable us to determine if VRACs can regulate seizures.

8. Peripheral blockade of CB1R only results in exacerbated lung eosinophilia and tissue damage in Nippostrongylus brasiliensis infection

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More than 2 billion humans carry infectious parasites leading to chronic co-morbidities and growth retardation in children. Parasitic infections induce a T helper type 2 (Th2) immune response in the host to promote clearance which can cause fibrosis if chronic. We recently showed that infection with the soil-transmitted nematode *Nippostrongylus brasiliensis* (Nb) induces overproduction of endocannabinoids (eCBs) in the host. This increased production of eCBs was observed throughout infection in the infected lung and intestine. Endocannabinoids are endogenous cannabis-like molecules that influence the development of obesity and are anti-inflammatory, however their function in infection is largely unknown. Here, we show that pharmacological inhibition of $CB\text{-}_1R$ with AM6545 throughout Nb infection exacerbated hemorrhaging observed in the BAL fluid of Nb infected mice. This effect was coupled to a decrease in the mean linear intercept of lung histological sections and prolonged lung eosinophilia in AM6545 treated Nb infected mice. No changes were observed in any of the measured parameters when comparing $CB_2R^{-/-}$ and WT Nb infected mice. Strikingly, we also found that Nb produces its own eCBs which vary in concentration based on stage of development, and that the eCB system is present in many parasitic nematodes including those that infect humans. The role of eCBs in Th2 immune responses are not well understood; however, increased production of eCBs in response to infection suggests a potential immunomodulatory role. These findings suggest the eCB system is active in several hookworm species, and that host and helminth eCBs may influence immune and anti-inflammatory functions.

9. Optimization of Patient Door-In-Door-Out Times at a Student-Run Free Clinic

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Background:
Student-Run Free Clinics provide accessibility for underserved populations to receive basic healthcare services - a lack of which is well-known to negatively impact health outcomes[1]. Along with improving health equity, these clinics are avenues that enrich medical and inter-professional education with increased awareness of the community

being served. However, since these clinics often serve as an environment for students to learn, clinic efficiency is often overlooked. Using a variety of interventions, the authors of this study aimed to decrease patient wait times and improve patient and provider satisfaction.

Methods:
Using a Student-Run Free Clinic in Riverside, California, clinic flow was observed by medical students where they recorded in minutes the “door-to-door” patient visit time, interprofessional interactions amongst professional students, number of patients lost during clinic and the physical routes patients transverse throughout clinic. Interviews were also conducted with current staff and patients to gauge satisfaction. Clinic flow was then redesigned to model the flow of traffic at typical doctors’ offices. Using a one-tailed two-sample t-test, pre-intervention and post-intervention mean door-to-door times were analyzed. Pre-intervention wait times are composed from 4 clinic days in March-April 2019, with n=71 patients, and post-intervention wait times are from 21 clinic days in May 2019-February 2020, with n=564.

Results:
A one-tailed two-sample t-test analysis found a statistical significant difference in pre-intervention (M=170.50, SD=12.40) and post-intervention mean door-to-door minutes (M=155.48, SD=13.19); $t = 2.11$, $p = 0.0453$. A post-intervention survey of clinic volunteers and staff found that 85% of those interviewed were satisfied with the interventions. Additionally, the optimization of patient flow achieved an overall decrease in the number of lost patients and reduced the patients’ total time in clinic without affecting time spent with healthcare providers.

Conclusion:
Preliminary data shows that the interventions made at this Student-Run Free Clinic resulted in a statistically significant difference in total patient door-to-door time as well as a decrease in lost patients, ultimately improving clinic efficiency and patient satisfaction, while also optimizing clinic flow. Further research is underway to assess if there is greater benefit with more familiarity of these interventions over time.

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