NATURAL SCIENCES UNDERGRADUATE RESEARCH SYMPOSIUM

THURSDAY, APRIL 11
TUDOR FIELDHOUSE

RICE UNIVERSITY
Wiess School of Natural Sciences

Table of Contents

Welcome to our first annual Natural Sciences Undergraduate Research Symposium (NSURS). We are excited to present the culmination of our students' hard work, creativity and dedication to exploration. Within these pages, you'll find a diverse array of research spanning all disciplines within the School of Natural Sciences, each representing the curiosity and ingenuity of our developing scholars. As you peruse these abstracts, we invite you to embark on a journey of discovery, celebrating the passion and innovation that drives our academic community forward.

At our symposium, posters have been organized into five thematic areas that serve as focal points:

- **Human Development, Health, Performance and Disease**
- **The Earth: Geology, Ecology and Environment**
- **Materials from the Fundamental to the Complex**
- **Patterns and Origins in Nature**
- **Cancer: Biology, Prevention and Therapy**

These allow attendees to navigate through a diverse array of research topics and provide a framework for understanding the breadth and depth of our students' scholarly pursuits. We encourage you to explore these thematic areas, engage with the posters and discover the fascinating insights that our undergraduate researchers have uncovered.

We extend our gratitude to all research mentors, both on campus and off campus, whose guidance, expertise and support have been instrumental in nurturing the academic growth and success of our students. And we thank you for joining us in celebrating the achievements of our talented undergraduate researchers.

NSURS Schedule

Poster Sessions

Session 1: 11:00 a.m. – noon
Session 2: 12:45 – 1:45 p.m.
Session 3: 2:30 – 3:30 p.m.

Closing Celebration and Awards Ceremony

4:00 p.m.

Keynote remarks by Dan Wagner, associate professor of biosciences
Award presentation by Dean Thomas Killian

Reception with cotton candy, popcorn bar and paletas

SESSION 1

Human Development, Health, Performance and Disease

Exploring the Effects of Wild Type Ataxin-1 Dosage in Spinocerebellar Ataxia Type 1

Natalie Byron | Mentor: Xhako Eder

Spinocerebellar ataxia type-1 (SCA1) is an inherited adult-onset neurodegenerative disorder caused by the polyglutamine expansion of ataxin-1 (*ATXN1*). Symptoms include coordination deficits, breathing dysfunction, and early lethality. To model SCA1, the mouse Atxn1 locus was modified to contain one expanded allele. These knockin mice (SCA1) express the mutation endongenously and recapitulate all SCA1 phenotypes. Previous work showed that a selective decrease of the expanded allele rescues SCA1 phenotypes, while decreasing both expanded and wild-type (WT) alleles equally does not lead to rescue. This led us to hypothesize WT ATXN1 has a protective effect in SCA1. To test this, we used embryonic stem cell recombination to make a mouse model that overexpresses (OE) WT ATXN1 by 60%. We characterized the OE and SCA1-OE animals and found cerebellar-specific resuce in SCA1-OE mice. To ensure that overexpression of ATXN1 in non-CNS tissue does not lead to negative phenotypes, we selectively OE WT ATXN1 just in the CNS. The OE of WT ATXN1 in the CNS did not have adverse phenotypes. Next, we aim to characterize homozygous OE mice to observe dosage dependent phenotypes of WT ATXN1.

Elucidating the Differentiation Potential of Mef2c-AHF Cre+ Cells

Rommel Caballero and Ashley Chen | Mentor: Miao-Hsueh Chen

Obesity and related metabolic disorders present significant health challenges globally, necessitating a deeper understanding of brown adipose tissue and its therapeutic applications. Brown adipose tissue (BAT) plays a crucial role in metabolism by utilizing nutrients through non-shivering thermogenesis to generate heat, thus aiding in the regulation of energy balance. A crucial aspect of this field involves elucidating the differentiation potential of specific progenitor cells contributing to supraclavicular BAT (scBAT) development, a tissue vital for regulating energy metabolism. This study aims to address this knowledge gap by exploring the differentiation potential of Mef2c-AHF Cre+ cells, identified as progenitors for scBAT development, beyond adipogenesis.
Our approach involves a comprehensive series of differentiation assays encompassing various lineages beyond adipogenesis. Leveraging lineage tracing

analyses, we isolate Mef2c-AHF+ cells from scBAT and assess their differentiation capacity into brown adipocytes, myocytes, and potentially other lineages.
Through this, we seek to identify the role of Mef2c-AHF+ cells as versatile progenitors contributing to scBAT development.

Transduction of Genetic Rescue in Brain Cell Populations of STXBP1 Related Developmental and Epileptic Encephalopathy Mouse Models in Adulthood

Jose Paulo Carneiro | Mentor: Mingshan Xue

Function of Nephronectin during Early Ocular Development in Mice

Evelyn Chiu | Mentor: Peter Lwigale

The extracellular matrix (ECM) provides a crucial environment for embryonic development, contributing to key processes such as cell adhesion, migration, and differentiation. Nephronectin (Npnt), an ECM protein reported to regulate these processes, was recently found to be expressed in murine ocular development, but its role in the mouse cornea remains largely unknown. Building upon previous work on avian corneas, we hypothesized that Npnt positively regulates cellular migration and/or cell proliferation. To test this hypothesis, mouse corneas were collected at embryonic stages E12, E13, and E14, and histological techniques were used to analyze differences in cell proliferation between wild type and mutant embryos. No statistically significant differences were found in cell proliferation and cell density, both in the epithelium and neural crest derivatives. These results will contribute to a larger investigation on the function of Npnt during murine corneal development, and future research may apply this knowledge toward a broader examination of the interplay involved in matrix signaling.

Neuroanatomical Features of *EBF3*-related Neurodevelopmental Disorders

Ashira Edelheit-Rice | Mentor: Hsiao-Tuan Chao

Telomerase as a Potential Agent to Reduce DNA Damage and Reverse Cellular Senescence

Angela Hu | Mentor: Anahita Mojiri

Cellular senescence, a permanent state of cell cycle arrest, is a driving mechanism behind aging and age-related disease. Persistent DNA damage and telomere attrition, in particular, are notable hallmarks of cellular aging. For instance, Hutchinson-Gilford Progeria Syndrome is a premature aging disorder where accelerated telomere shortening is associated with severe endothelial dysfunction

and vascular senescence. This study examines how the transient expression of human telomerase (hTERT) mRNA in human aortic endothelial cells (HAEC) can repair irradiation or bleomycin-induced DNA damage and reverse cellular senescence. Through Western Blot, qPCR, and immunofluorescent staining analyses, I found that the DNA damage marker and inflammatory markers showed increased expression levels in damaged HAEC; the concentration of these damage markers was then significantly reduced in cells transfected with telomerase mRNA. Thus, hTERT mRNA transfection is a promising approach to repair DNA damaged cells and damage phenotypes associated with aging.

An Evaluation of HIV Knowledge, HIV Stigma, and Telehealth Use in Lactation Consultants in the U.S. and Canada

Andrew Kim | Mentor: Emily Barr

Breastfeeding/Chestfeeding (BF/CF) is beneficial for parents and infants however, due to the potential for HIV transmission, people with HIV (PWH) in high-income countries were previously advised to use formula. Recent updates (2023) to the U.S. Health and Human Services Infant Feeding Guidelines for PWH include recommendations for BF/CF in PWH on antiretroviral therapy with a suppressed HIV viral load. Specialized support, accessible via telehealth, is needed to ensure safe breastfeeding practices. Lactation consultants are a key resource for successful BF/CF, yet they may not know the new guidelines. We developed a cross-sectional mixed-methods survey study enrolling (N=150) certified lactation consultants in North America. The survey assesses knowledge of HIV and BF/CF, standard HIV knowledge, HIV stigma, and experience and opinions on telehealth use to support BF/CF. Preliminary findings include a need for specialized HIV education and telehealth use for PWH. Results will inform interventions supporting PWH making infant feeding decisions in higher-income countries, preventing perinatal HIV transmission, and improving HIV health outcomes of those impacted by HIV.

Optimization of In Vivo Atovaquone Dosing with Differing Treatment Backbones

Lana Kim | Mentor: Alexandra Stevens

Pediatric acute myeloid leukemia (pAML) survival is poor, requiring novel therapeutics to improve outcomes. The FDA-approved antimicrobial drug atovaquone (AQ) suppresses oxidative phosphorylation, induces apoptosis in pAML cells, and prolongs survival in pAML xenografts. Adults with AML receiving AQ for *Pneumocystis jiroveci pneumonia* prophylaxis have lower relapse rates. However, AQ levels are lower than expected when AQ is administered with concomitant chemotherapy in pAML patients (NCT03568994, target 40-80μM) and as a single agent in pAML xenografts once mice are moribund. We hypothesize

standard doses of AQ are sufficient in achieving target levels when given with azacytidine but higher doses are required with cytarabine and CPX-351 due to greater cytotoxicity and injury to mucosal membranes. We expect that AQ levels will be lower as mice become symptomatic from pAML due to impaired absorption and enterohepatic recirculation. We tested modified AQ dosage regimens in non-conditioned immunodeficient NSGS (NOD-scid IL2Rgnull-3/GM/SF) mice. High-Performance Liquid Chromatography quantified AQ concentration. Our results will guide future experiments with AQ for pAML.

Using Microfluidics in New Pathogen Wastewater Surveillance

Marga Lee | Mentor: Yousif Shamoo

COVID 19 has spotlighted the threat that emergent pathogens represent to all populations. In order to address these novel infectious agents, communities must be aware of their circulating pathogens. Wastewater surveillance is a cost effective technique for identifying which infectious agents are present in a population. Its effectiveness has been shown in the city of Houston's COVID-19 wastewater surveillance system which has been recognized as a "National Wastewater Surveillance System Center of Excellence" by the CDC. This project aims to expand the scope of Houston's COVID-19 wastewater surveillance system to include other potentially pathogenic bacteria present in the city's wastewater. To do this, we plan to combine the established system with our microfluidic technology to provide strains with segregated environments, removing competition between strains and preserving the biodiversity of the sample. This research project will identify how many of the isolated strains are resistant to common and last resort antibiotics. This paper outlines the phenotypic assays used on the strains as well as the results derived from them.

The Effects of Low-intensity Shockwave Therapy on Spermatogenesis & Testosterone Levels in an Aged Rat Model

Nelson Mills | Mentor: Mohit Khera

Low-intensity shockwave therapy (LIST) non-invasively promotes angiogenesis. Previous research determined that LIST does not affect testosterone (T) production or spermatogenesis in rats aged 6 to 9 months. No research has been conducted on LIST's effect on late-onset hypogonadism (LOH) in older males. This study sought to determine the effect of LIST on T levels and sperm quality in an aged rat model. 16 Sprague-Dawley rats aged 11 to 17 months were evenly divided into control and treatment arms. Treatment group received 600 shocks on the testes 3 times a week for 4 weeks. Control group received 0 shocks. 1 month after treatment, rats were euthanized, and epididymal sperm was analyzed via microscopy. Blood was collected at 4 points before and after treatment; T levels were calculated via enzyme-linked immunosorbent assay. Non-parametric

Wilcoxon statistical analysis was performed. No statistically significant differences were noted between control and treatment groups, except in sperm curvilinear velocity. Age did not affect LIST response. T levels declined linearly with age. LIST may not serve as an effective treatment for LOH; further testing with new LIST parameters is needed.

Recruitment Strategies for the Teaching Kitchen Multisite Trial Studying the Effects of Nutrition Education on Behavior Retention and Metabolic Markers

Samiha Momin | Mentor: Natalia Heredia

Behavioral based nutrition and cooking lessons have proven effective in addressing chronic diseases. The Teaching Kitchen Multisite Trial, a year-long program implemented at five U.S. institutions, including UT Houston School of Public Health, aim to help adults with overweight/obesity by integrating culinary skills, nutrition education, and health coaching strategies to facilitate sustainable behavior change. The Houston site had trouble recruiting, leading to strategic adaptations. The goal was to enroll 80 participants in two cohorts with a BMI 25 -40 and an abnormal cardiometabolic marker. Recruiting involved pre screeners, anthropometrics, and lab work. Many methods were used, such as a website, flyers, provider recommendations, digital postings, and the news. Local news advertising was the most successful strategy, with 22% of participants citing it, and provider recommendation the least success (1.9%). Out of 337 individuals completing the pre-screener, 58 were eligible, 49 consented, and 31 passed the lab work and anthropometrics to enroll. This dynamic approach underscores the complexity of recruitment and the need for tailored strategies to foster participant engagement.

Grooming microstructures in a mouse model of a monogenic autism spectrum and neurodevelopmental disorder

Rija Naqvi | Mentor: Tuan Chao

The Effect of RyR1 (T4706M)™ Mutation on the Muscular Strength and Endurance of Mice.

Lauren Nguyen | Mentor: Susan Hamilton

The Ryanodine receptor type 1 (RyR1) is pivotal for calcium regulation and muscle contraction. Mutations in the RyR1 gene cause myopathies which are the most prevalent childhood-onset non-dystrophic muscle disorders. The absence of an accurate animal model has hindered therapeutic development. The impact of the (T4706M) mutation on both alleles (TM/TM) of the RyR1 gene remains unexplored. We hypothesized that the TM/TM mutation mice would display increased exercise intolerance, reduced muscle mass, and decreased muscle strength. On wildtype

(WT) mice and homozygous TM/TM mice at 13 weeks of age, body composition analysis and muscle function tests including the grip strength assessment, wire-hang test, and forced running assessment were conducted. The TM/TM mice displayed statistical differences with an increased exercise intolerance on the treadmill and a decreased muscle strength on the wire-hang test (total number of times the mice fell off the wire). The comparative analysis between WT and TM/TM mice on grip strength assessment, reaching times, and holding impulse on the wire-hang test did not demonstrate statistical significance due to lack of sample size.

Garden Education for Future Medical Doctors: Programmatic Results from HOUSTON Academy 2.0's Cohort 1 and 2

Gecy Obambo | Mentor: Daphne Hernandez

This poster presents outcomes from HOUSTON Academy 2.0's first two cohorts, integrating a 10-week garden education into future health professionals' training. Supported by a USDA grant and partnerships, the program aimed to boost participants' gardening self-efficacy and emphasize garden-based nutrition in medical training. The method involved a 10-week gardening curriculum within a 12-month nutrition program, with pre and post-intervention surveys measuring changes in gardening confidence. Results indicate significant improvements in trainees' self-efficacy, underscoring the seed-to-plate approach's effectiveness in enhancing practical nutrition and disease prevention skills among medical students.

Determining Socs3a Expression in Asxl1TG and M. avium treated Mice

Temitope Olarinde | Mentor: Apoorva Thatavarty

IL-6 mediated STAT3 drives arrhythmogenic CaMKII in postoperative atrial fibrillation

Isabelle Ong | Mentor: Josh Keefe

Postoperative atrial fibrillation (POAF) occurs in 1/3 of patients and increases the risk of future AF by 8-fold. The risk of POAF correlates with the degree of post-surgical inflammation, in particular interleukin-6 (IL-6). Prior studies have demonstrated that IL-6 is sufficient to induce Ca^{2+} mishandling in cardiomyocytes of isolated rat hearts. We hypothesize that IL-6 mediated STAT3 activation leads to Ca^{2+} mishandling through CaMKII-mediated hyperphosphorylation of RyR2, a key Ca^{2+} channel, as STAT3 was found to upregulate *CAMK2D*. To test whether IL-6 upregulates *Camk2d* in the heart, WT mice were administered IL-6 for 3 days. To

assess the arrhythmogenic consequences of IL-6, atrial cardiomyocytes (ACMs) were incubated with IL-6 for 30 mins prior to imaging of RyR2 Ca^{2+} leak. In IL-6 exhibited a 2.2-fold (P=0.04) increase in *Camk2d* expression. IL-6 led to 10.0-fold (P<0.001) and 3.0-fold (P=0.047) increases in Ca^{2+} spark and wave frequency, respectively, compared to vehicle, without changes in Ca^{2+} transient amplitude and sarcoplasmic reticulum Ca^{2+} load. Altogether, these findings provide evidence that treatments targeting the IL-6-CaMKII axis can prevent POAF.

Identifying Effect of PAX3 Gene on Micropatterning of Human Embryonic Stem Cells in Neurulation

Ana Park | Mentor: Ye Zhu

Neurulation is the formation of the vertebrate brain and spinal cord, involving the folding up of cells into a neural tube (Smith and Schoenwolf, 1997). Observing the signaling patterns in neurulation provides the key for understanding the molecular basis of various neural tube defects (Colas and Schoenwolf, 2001). The process is sensitive to varying expressions of signals; in particular, PAX3 is a transcription factor necessary for the migration of neural crest cells in the neural tube, neural crest, and presomitic mesoderm (Mansouri, 2001). Furthermore, PAX3's role continues beyond migration and affects maintenance of cells and survival (Moase and Trassler, 1991). Therefore, identifying the effect of PAX3 by comparing the micropatterning signals of WT and PAX3 knockout colonies will be crucial in deepening the understanding of neurulation. Eventually, the goal is to recreate human neurulation in a 3D model to observe direct pathologies of neural tube defects. By focusing on a 2D model using micropatterned plates to confine cell growth, the role of PAX3 in neurulation will be further explored.

Investigating the Role of Transcription Factor NFIX in Mature Astrocytes of the Adult Brain

Priyanka Patel | Mentor: Sanjana Murali

As the most abundant glial cell in the central nervous system, astrocytes regulate synapse formation, metabolic support, the blood-brain barrier, and various other crucial functions. Recent advances show that astrocytes regulate neuronal circuits. The overarching goal of the lab is to elucidate novel transcriptional networks that regulate mature astrocytes in the adult brain. NFI family of transcription factors which includes NFIA, NFIB and NFIX play critical roles in gliogenesis, astrocyte differentiation and maturation throughout development. Transcriptomic studies have revealed that their expression is maintained in mature astrocytes in the adult brain, but the functional role remains to be studied. Preliminary studies with astrocytic NFIX loss of function suggest specific roles regulating cortico-thalamic circuits. To understand whether NFIX deficient astrocytes affect other glial cells,

specifically in the thalamus, I sectioned brain tissue from control and NFIX deficient mice, stained for oligodendrocytes, microglia, and neuronal markers. I used a confocal microscope to take images and quantified the intensity and number of glial and neuronal cells using FIJI software.

Estrogen-related Receptor Alpha Promotes Angiogenesis and Skeletal Muscle Vascularization

Addison Saley | Mentor: Vihang Narkar

Measuring TCRVβ21.3 Expression to Investigate Clonal Expansion following SARS-CoV-2 Vaccination in Children with a History of MIS-C

Esha Shenoy | Mentor: Tiphanie Vogel

Following COVID-19 infection, some children develop an acute hyperinflammatory response known as multisystem inflammatory syndrome in children (MIS-C). Manifestations include fever, abdominal pain and rash. The illness can be severe including hypotension or shock, all making MIS-C clinically similar to Toxic Shock Syndrome which is triggered by superantigens (SAgs). SAgs have high affinity for T-cell receptors (TCR) complexed with their ligands and stimulate T-cells to create an intense inflammatory response. The etiology of MIS-C is still unknown, but research has shown that during acute illness patients with MIS-C display an expansion of T-cells expressing TCRVβ21.3, which is consistent with a SAg-triggered response. Vaccination can protect against severe COVID-19 re-infection. Families of children with a history of MIS-C may be hesitant to vaccinate against SARS-CoV-2, fearing a recurrence of hyperinflammation. We aim to determine if the immune response following SARS-CoV-2 vaccination of patients with a history of MIS-C differs from control children by comparing immune parameters, including TCRVβ21.3 expressing T-cells, at baseline, and 2 and 6 months post vaccination.

Analyzing the relationship between polyparasitism and Chagas Disease

Lindsey Vongthavaravat | Mentor: Rojelio Mejia

Chagas disease, caused by the protozoan parasite *Trypanosoma cruzi*, is one of the neglected tropical diseases in the Western Hemisphere, including the USA. Endemic to 21 countries, this disease is primarily associated with areas of poverty due to exposure to the vector Triatomine bug. Polyparasitism is an infection of two or more parasitic species within a host. Studies have shown high levels of polyparasitism with *Blastocystis* in Chagas-positive patients. Our lab aims to determine the association of Helminth infection with Chagas Disease. We conducted stool-based real-time quantitative PCR on a cohort of children living in

Colombia. Preliminary results revealed 57.9% of patients tested positive for *Blastocystis* DNA, 20.3% *Cryptosporidium*, 20.3% *Giardia lambia*, 9.41% *Necator americanus*,1.98% *Trichuris trichiura*,1.98% *Entamoeba histolytica*, and 1.49% *Ascaris lumbricoides*. No positive samples were found for *Ancylostoma duodenal* and *Strongyloides stercoralis*. *Blastocystis* contained the highest parasitic prevalence. Future work involves determining the parasitic prevalence and burden of Chagas disease within the patient sample.

The Earth: Geology, Ecology and Environment

Bacterial Development in Drinking Water Sources Over Time: Experimental Observations of the Jones Drinking Station at the North Servery at Rice University

Elena Alvarado | Mentor: Carrie McNeil

Bacterial colonies have been found in bottled water and local sources of drinking water. Most soda dispensers didn't meet standards for heterotrophic bacteria. This study focuses on the change in bacterial quantity and diversity in water over a 24-hour period at an AquaHealth station and a soda fountain. We hypothesized that the quantity of bacteria in the water samples would increase over the day, and the counts and variety of bacteria would consistently be higher for the soda fountain's water. We plated water samples on R2A agar and then counted the resulting colonies. Select colonies were screened for gram-negative on differentiating media. Both stations had the highest counts of bacteria before meals, followed by a drastic drop at breakfast, and an increase at lunch and dinner. The AquaHealth station contained gram-negative bacteria; all other samples were gram-positive. Gram-negative bacteria has previously been in samples of water from dental devices, seeming consistent with the Aquahealth station being used for personal water bottles. This work has implications for the impact of flushing as a cleaning mechanism, personal water bottle use, and possible presence of biofilms.

Endophyte Prevalence in Agrostis hyemalis Throughout Varying Climates in the Southern U.S

Dumari De Leon | Mentor: Tom Miller

Due to rapidly changing climates throughout the United States, grass populations are beginning to rely on mutualistic symbionts to adapt to the severe shift in temperature and habitat suitability. Specifically, Epichloë is a heritable, filamentous fungal endophyte and a biotrophic organism. They occur symbiotically in grass populations worldwide, including winter-bent grass Agrostis hymealis. We are

observing five regions across the Southern United States and comparing them with others in the database. Through the breakdown of mature seeds attached to the plant using sodium hydroxide, endophytes can be identified by using aniline blue on the aleurone cells to distinguish the hyphae. In our analysis, Agrostis hymealis is endophyte positive for more than half of the seeds, indicating that it is consistent with current hypotheses on microbes responding to environmental stress in drier conditions. We intend to correlate the percentages of positive endophytes for each region with the climates. These findings may form an understanding of how species interact with their hosts in varying climate zones and further understand the context-dependent fluctuations among them.

Recording von Willebrand factor interactions with platelet receptor glycoprotein Ib via APEX2

Michael Dong | Mentor: Andrew Yee

Interaction between von Willebrand factor (VWF) and its platelet receptor, glycoprotein Ibα (GPIbα), underlie hemostatic responses to vascular injury. Dysregulation of this interaction due to pathogenic variants or pathological environments can lead to coagulopathies or thrombosis. Investigating the interaction between VWF and GPIbα can be challenging due to its transient nature. To capture binding events, we fused GPIbα to an engineered variant of soybean ascorbate peroxidase (APEX2) for proximity labeling of proteins with biotin-phenoxy-radicals. Feasibility studies demonstrated enriched recovery of phage displayed VWF fragments of its platelet binding domain when in competition against a VWF, non-platelet binding domain. Introduction of a gain-of-function VWF variant resulted in a greater enrichment over wild-type (wt) fragments. These results suggest that this approach may be useful for functional characterizations of VWF variants in environments where GPIb-VWF interactions are transiently induced.

Chemically-Induced Dimerization of CRISPR-Cas9 Gene Activation Systems on Synergistically Activated Mediator Sites

Rohan Palavali and Catherine Stidham | Mentor: Tyler Daniel

CRISPR systems provide bacteria and archaea with adaptive immunity. A guide RNA (gRNA) can be programmed to guide a CRISPR-associated enzyme (Cas) to any genomic region, where it cuts DNA so other fragments can be inserted. TadA deaminases can be added to these DNA-binding proteins to selectively convert nucleotides. However, these systems are currently not spatiotemporally controllable, which reduces their utility in therapeutic applications.

To solve this problem, we present a chemically-induced dimerization (CID) system to better control an adenine base editor (ABE), creating a split adenine base

editor (sABE). The system exists in two parts, and upon addition of rapamycin, the parts dimerize and begin editing nucleotides. Our results show that nucleotide editing efficiency is high upon induction of rapamycin when compared to ABE8e, and unintended editing is low in the absence of rapamycin. When delivered in vivo to murine models via dual adeno-associated virus vectors, sABE can effectively convert an A-T base pair to a G-C base pair in the PCSK9 gene. Thus, we demonstrate precise in vivo control of the base-editing system, opening the door for safer therapeutic applications.

Investigating the Link between Aggression and Social Preference in *Drosophila melanogaster*

Elim Taffere | Mentor: Julia Saltz

How an individual interacts with the world is affected by a variety of factors, ranging from their perception of it to physical differences. In some cases, the differences in interactions can even stem from being of different genotypes. This concept of different genotypes of the same species reacting differently to the same environment is called "genotype by environment (GxE)." Many experiments have identified GxE, then focused on identifying the genetic differences between their individuals. We do the opposite, using known genetic differences in *Drosophila melanogaster* that correspond to different traits (social group size preference) to create GxE interactions. We have male flies interact with different-sized social groups, then observe the frequency of aggressive behaviors in one-on-one situations. It is important to know how organisms will react to their environment, especially in light of climate-change induced destruction of many ecosystems today.

The Effect of Group Size on Aggression in *Drosophila melanogaster*

Ellery Underhill and Jayna Yoon | Mentor: Julia Saltz

What is the Effect of Different Feedback Selection Regimes on Aggressive Behavioral Patterns of *D. melanogaster*?

Maggie Xia | Mentor: Marina Hutchins

Evolutionary feedback allows behavioral changes in one generation to impact selection pressures for future generations, resulting in the evolution of broad social dynamics. The existing literature lacks full contextualization of how feedback impacts behavioral evolution, particularly in empirical studies. We investigated the impact of evolutionary feedback on aggression, an important social behavior that impacts mating and resource-gathering. Male fruit flies were subject to 25 generations of selection designed to increase or decrease aggression. Our

approach consists of watching videos of interactions between evolved males to describe their behavioral repertoire. We will document aggressive behaviors (lunging, chasing, fencing, boxing, wing threat) between individuals. It is important to characterize these dynamics to illustrate: 1) what behaviors are most frequently observed, 2) whether behavior patterns like retaliation or bullying occur, and 3) the emergence of high-aggression behaviors like boxing. This research has relevant applications in improving behavioral models, contributing to cultural evolution theories, and increasing capabilities to predict behavioral evolution.

Materials from the Fundamental to the Complex

Metal-to-Insulator Transition in the Mott Insulator Sr2Mn3As2O2

Emma Codianne | Mentor: Emilia Morosan

In condensed matter physics, the compound Sr2Mn3As2O2 is a Mott insulator, which is a material that demonstrates insulating behavior when measured, contradictory to band structure calculations that find no band gap and suggest it is conducting. Chemical tuning can be used to drive Mott insulators into a critical regime straddling the local-to-itinerant magnetic moment, in which emergent states like unconventional superconductivity or correlated topology are predicted to occur. Our approach to reaching this crossover region with Sr2Mn3As2O2 single crystals includes tuning the oxygen content of the compound, using both time-dependent and temperature-dependent annealing in reducing atmospheres. We have successfully observed this crossover manifesting in resistivity measurements going from insulating to metallic behavior, and we have seen a faster decrease in resistivity at higher temperatures. In further experiments, we will increase the oxygen deficiency of Sr2Mn3As2O2 in hopes of observing superconductivity.

Optimizing Wet-Spun Carbon Nanotube Fibers

Kathryn Dale | Mentor: Michelle Durán-Chaves

Carbon nanotubes display exceptional physical properties and promise as an alternative to environmentally-taxing materials commonly used across various disciplines. For industrial use, carbon nanotubes are wet spun into macroscopic fibers. However, carbon nanotube fibers currently fail to meet their theoretical properties. This project aims to improve the quality of carbon nanotube fibers by exploring optimal production parameters from purification to collection. This is accomplished by experimenting with the thermal oxidation of raw carbon nanotube samples at various parameters, the preparation and spinning of dopes at various concentrations, and alteration in the geometries and speeds of fiber extrusion and collection. We found that the thermal oxidation of samples

approaches its limit within 20 hours; we hope to identify the ideal temperature and the effect of increasing sample surface area on the extent of oxidation. Lower-concentration dopes produce fibers of satisfactory quality while higher-concentration dopes fail to produce decent properties. The use of different extrusion geometries has the potential to improve the quality of fiber spun from higher-concentration dopes.

Solid-state Electrolyte Reactor Design for Hydrogen Peroxide Electrosynthesis

Alexander Hwang | Mentor: Haotian Wang

Synthetic Phosphorylation Signaling Protein Domains of Predefined Specificities

Mustafa Latif | Mentor: Caleb Bashor

Synthetic signaling pathways that rely on rapid, protein-protein interaction can be incredibly useful for engineering synthetic cell behaviors. Phosphorylation signaling in native pathways rely on protein-protein interactions to dynamically regulate function; these networks rely on kinase proteins that phosphorylate substrate proteins to be recognized by SH2 reader proteins. This recognition reaction can conditionally activate other proteins that will execute downstream functions. Our study analyzes in vitro peptide array screening data to understand biochemical trends in human kinase-substrate-SH2 interactions. By comparing those trends to the results of a kinase-substrate-SH2 screening assay done in mammalian cells, we identify key determinants of interaction specificity that will drive future engineering. Finally, we trained a machine learning model to assist in engineering synthetic protein variants. This integrative approach not only validates a novel assay for future engineering but also paves the way for the rational design of synthetic pathways with implications for therapeutic development and synthetic biology.

Competitive Binding of ssDNA and SDS on Structurally Sorted Single-Wall Carbon Nanotubes

Luke Moore | Mentor: Bruce Weisman

Single-wall carbon nanotubes (SWCNTs) are a diverse group of nanomaterials with varied properties that originate from their distinct structures. One SWCNT property is near-infrared fluorescence, which occurs at specific excitation and emission wavelengths and can be used to selectively study structure-dependent SWCNT processes. Sodium dodecyl sulfate (SDS) and single-stranded DNA (ssDNA) can noncovalently adsorb to the surfaces of SWCNTs. Previous experiments have shown that when SWCNTs coated by SDS are exposed to

ssDNA, coating displacement occurs and can be monitored spectroscopically through red-shifts and intensity decreases in emission spectra. However, to date this has only been observed in samples containing many SWCNT structural forms and multiple simultaneous equilibria that prevent detailed thermodynamic analysis of the data. In this project, I will apply the previous method using structurally sorted SWCNT samples. As a result, I will be able to deduce coating exchange equilibrium constants for individual species of SWCNTs. This will give important insights into the interactions of carbon nanotubes with their adsorbed coatings.

The Effect of Shortening the Lamin B2 Replicon and dCas Episomal Tethering Protein on Persistence of a Non-Integrating Episomal Tethering Construct

Ana Naqvi | Mentor: Daniel Brenner

Unlike integrating vectors, non-integrating vectors allow for expression of an episome without insertion of the episomal DNA into the host cell genome. While this avoids the insertional mutagenesis that integrating vectors cause, non-integrating vectors only allow for temporary expression of an episome because they do not integrate into and replicate with the host cell genome. To allow for episomal persistence using non-integrating vectors, our team has created a self-replicating construct that replicates via lamin b2 and attaches the episome to the genome via two dCas9 tether proteins connected by a linker sequence. Although this 14-kb construct has proven to persist, a shorter construct is needed for use with adenoviral non-integrating vectors that have a 10-kb storage capacity. To examine the most optimal way to shorten the construct, we use flow cytometry to analyze percent fluorescence–a positively-correlated indicator of episomal persistence–of different constructs in proliferating HEK293T cells over a 3-month period.These constructs vary by replacement of the spdCas9 tether protein with a more compact dCas12f mutant– denOs or dCasMini–and truncation of the lamin b2 replicon.

Environmental Modulation of Living Material Mechanical and Structural Properties

Carlson Nguyen | Mentor: Esther Jimenez

Our lab has reported the first bottom-up de novo engineered living material (BUD-ELM) using the bacterium *Caulobacter crescentus*. Its matrix is composed of a secreted surface layer protein, with an elastin-like polypeptide (ELP) biopolymer region that defines the material mechanical and physical properties. However, it remains unclear how altering growth conditions affect matrix properties. Prior research shows that growing *C. crescentus* in low Ca2+ conditions results in decreased surface layer protein display, and we predict a similar trend in our material. Here, we show that BUD-ELM strains, grown under depleted Ca2+ concentrations, form macroscopic ropes. To test the rope's mechanical properties,

we measured the material's strength using uniaxial tensile testing. Preliminary results indicate the ropes are stretchy and when knotted, can undergo maximum length without failure. Structural properties of the ropes were studied using microscopy. Structural analysis reveals that growth in decreasing Ca2+ concentrations causes increasing separation between cells and matrix. We show that altering environmental growth conditions creatematerials with high elasticity and strength.

Strategies to Optimize the Secretion of Diagnostic Biomolecules from E. coli to Treat Gut Inflammation

Vedha Penmetcha | Mentor: Jeffrey Tabor

Inflammatory Bowel Disease (IBD) is an incurable disorder characterized by painful inflammatory episodes. The leading symptom is diarrhea, but because it is nonspecific various detection methods are needed. Existing screening measures rely on invasive approaches like colonoscopies. Localized delivery of detection biomolecules could significantly improve outcomes and minimize the discomfort of existing diagnostic methods. We employ synthetic biology tools to genetically engineer bacteria as living theranostics which have the potential to circumvent current challenges by directly targeting the site of inflammation. We engineer E. coli to secrete biomolecules of diagnostic interest, such as the bacterial FMO gene (bfmo) in order to secrete an indigo dye. We improve bioactive dye production by improving sensor sensitivity by varying media and promoter levels. For future in vivo delivery to the animal gut, the bacteria are optimized to ensure staining of the patient's stool indicating the presence of gut inflammation without the use of invasive procedures. The secretion modes and diagnostic techniques developed can be applied to other inflammatory illnesses.

Predicting Genotype-by-Environment Interactions

Tania Reyes | Mentor: Julia Saltz

Genotype-by-Environment interactions occur when different genotypes respond differently to the exact same environment. Currently, the predictability of gene-environment interactions is limited because many studies have focused on GxE interactions resulting from environmental impacts. Yet, recent research suggests genetic variation can impact the evolution of GxE. This is known as gene-environment correlation (GEC), when genetic variation influences exposure to different environments. The correlation is not well understood, but by studying GxE variation in fruit flies, a method to understand and predict future variability can be developed. The common fruit fly, *Drosophila melanogaster*, has well-studied genomes and social behaviors. Their short life cycle and small size also allow for the control of their environment. A male fly will be placed in a specially designed arena composed of four quadrants of varying group size. The groups made up of half

males and half females will be separated by a cage barrier allowing the experimental male to select a preferred group size and therefore allowing for the quantification of variability.

Complex Magnetic Order and Magnetotransport in EuAu2Sn2 Single Crystals

Kexin Shen | Mentor: Emilia Morosan

Rare earth intermetallics often display complex magnetic and transport properties, owing to the interplay between different energy scales such as Rudeman-Kittel-Kashuya-Yoshida (RKKY) interactions and crystal electric field effects (CEF). However, Europium ions have a half-full 4f electronic shell, which means that the CEF should be absent in such compounds, and therefore the magnetic order is expected to be a simple collinear antiferro- or ferro-magnetic ground state. Our group has recently shown that a series of Eu-based intermetallics with square net crystal structure, Eu(Ga,Al)4, have complex magnetic and topological properties, even in the absence of CEF effects, prompting the need for finding the origin of the competing interactions other than CEF anisotropy. In this talk, I will discuss our recent synthesis of new high-quality single crystals of a Eu-based square net compound. This material is a candidate for magnetic topological systems. The temperature- and field-dependent magnetization and resistivity measurements reveal at least three magnetic phase transitions below 10 K, and relatively large magnetoresistance MR ~ 20% up to 9 T.

The Usage and Biosynthesis of Non-Canonical Amino Acids to Develop an Evolved Halogenase

Jaime Tellez | Mentor: Jaime Tellez

Currently, there are hundreds of non-canonical amino acids (ncAAs) that have been synthesized. Via genetic code expansion, these ncAAs have been synthesized and integrated into proteins. With their expanded chemical diversity, these ncAAs introduce new groups like azides and alkynes into proteins and can introduce new activity like fluorophore functionality. With the specific incorporation of the ncAAs into proteins, there is a broadened range of applications for the functional groups within these proteins. While ncAAs hold great potential for things like new medicines and exploring biological systems, there exist few biosynthetic pathways to generate cells with ncAAs. As such, there exist great limitations to introducing these ncAAs. A system is being established to biosynthesize ncAAs with an evolved halogenase and incorporate them directly into proteins. If successful, potential applications of this evolved halogenase are the production of chlorotyrosine (ClY) and a biosynthetic pH response fluorescence probe. While the evolution of the halogenase able to perform this is incomplete, we hope the incorporation of chaperones will increase the halogenase activity.

Production of Carbon Nanotubes and H2 From Plastic Waste Using Flash-Joule Heating

Carolyn Teng | Mentor: James Tour

Plastic pollution has become an increasingly pressing issue over the past two decades. Approximately 400 million tons of plastic are produced per year, a rate that has doubled since the beginning of the century. To address this problem, researchers have investigated different methods of plastic upcycling to transform waste into valuable materials. A previous study demonstrated the use of flash Joule heating to convert plastic waste into carbon nanotubes with greater efficiency than traditional synthesis methods. However, past work has yet to capture and quantify hydrogen gas during carbon nanotube synthesis. This study seeks to quantify the concurrent production of carbon nanotubes and hydrogen gas using the flash Joule heating method, employing various metal catalysts, catalyst loadings, and waste plastic precursors. Hydrogen gas is measured using a gas chromatography-thermal conductivity detector. Scanning electron microscopy and Raman spectroscopy are used to verify the presence of carbon nanotubes in the sample post-reaction. Carbon nanotube and hydrogen gas yield are compared for different catalyst loadings and precursors to determine the optimal production parameters.

Engineering Electrically-Driven Quantum Dot Single-Photon Emitters with Tunable Polarization via Ligand Chirality

Clara Ursic | Mentor: Mohite Aditya

Colloidal quantum dots (QDs), dubbed “artificial atoms,” are nanocrystal semiconductors that can act as single-photon emitters (SPEs): non-classical light sources that emit one photon at a time. Properties of QD emission are highly tunable. Tunability of emission frequency has been thoroughly demonstrated in literature, but tunability of polarization less so, which was the focus of this project. We investigated how formation chemistry influenced the optical properties of PbI4 perovskite QDs embedded in a bulk FAPbBr3 perovskite host matrix. In particular, we studied the chirality transfer from chiral surface ligands to the QD core and the chiroptical absorption and emission that is induced. More work is needed to improve optical setups, verify single-photon emission, and ultimately, design an efficient QD-in-matrix electrically driven device for quantum and optoelectronics applications.

Patterns and Origins in Nature

Engineering P300 for potent epigenetic gene activation?

Samrithaa Balakrishnan | Mentor: Daniel Reed

Epigenetics is a vast and quickly growing field that explores the regulation of gene expression in eukaryotes. Epigenome editing using the deactivated Cas9 protein as a DNA binding and recruitment modality is a powerful tool to modulate gene expression. P300 is an epigenetic writer that deposits acetyl groups onto the tails of histones, thus promoting open chromatin for gene expression. One limitation of recruiting P300 to a locus is cell toxicity from off-target acetylation. To address this, our lab has identified single mutations from the deep mutagenesis screen of P300 that result in more stable and functional versions. Gibson Assembly cloning method was utilized for fusing the P300 variants with dCas9. To validate that point mutations within P300 are present and correctly fused to dCas9, I performed a test restriction enzyme digest. I absorbed two distinct DNA bands after gel electrophoresis indicating DNA recombination adject. To ensure functionality and stability, quantitative PCR and flow cytometry were done, respectively. This has many therapeutic applications, including the activation of tumor suppressor genes to fight cancer.

Alkyl Arylation of Alkenes via Decarboxylative Smiles-Truce Rearrangement

Xiaowei Chen | Mentor: Xiaowei Chen

Rearrangement reactions enable the controlled cleavage and reconstruction of chemical bonds, facilitating the incorporation of valuable functional groups into targeted molecules. While radical-mediated rearrangements have shown great promise in difunctionalizing activated olefins, the scope has been limited to olefins with proximal substituents that stabilize radical
intermediates. Recently, a docking-migration strategy has been disclosed for radical functionalization of unactivated olefins. By using a dual-function reagent tethered to a traceless linker, this strategy enables the intramolecular migration of a radical acceptor. Notably, sulfone-based dual-function reagents inverts the polarity-match reaction mode between alkene substrates and nucleophilic radicals. In the docking-migration reactions, the polarity of sulfonyl-decorated alkyl radical is inverted to electrophilic, thus allowing its addition to aliphatic alkenes. Leveraging the docking-migration strategy and iron's LMCT reactivity towards carboxylate group, we proposed an iron-catalyzed radical Smiles-Truce rearrangement mechanism.

Expression of a m-Calpain Sensitive FRET Pair in *Escherichia coli*

Zoe Folarin | Mentor: Matthew Carpenter

Non-Structural Protein Characterization of an RNA Virus that Infects a Key Coral Symbiont

Mitchell Han | Mentor: Yizhi Tao

Symbiodiniaceae is a family of dinoflagellates that form a symbiotic relationship with coral that is required for coral survival. Symbiodiniaceae are negatively affected when subjected to heat stress, but the underlying mechanisms are not fully understood. It is hypothesized that dinoRNAVs, a group of Symbiodiniaceae-infecting positive-sense single-stranded RNA viruses, play a role in this phenomena by replicating during heat stress. Because viral non-structural proteins can have a profound impact on host cells, our focus is on analyzing a non-structural protein of dinoRNAV. Due to the protein's aberrant nature in previous purifications, my project's goal was to clone more stable constructs and purify samples adequate for crystallization. To accomplish this, I employed PCR and Gibson Assembly protocols to isolate the C terminal polymerase domain of the protein. Additionally, I used purification techniques like Ni-NTA chromatography and size exclusion chromatography to purify the protein for crystallization. In conclusion, I successfully created a new construct of the dinoRNAV that improved purification and helped collect a pure sample for future structural analysis.

Symmetries of the N-Body Problem

Evan Huang | Mentor: Jeff Xia

We give a new proof of the non-integrability of the planar 3-body problem using a theorem of Poincare on the eigenvalues of the monodromy matrix of a periodic system. In addition, we develop an equivariant Floquet theory applicable to quasi-periodic systems.

Whole Mount In Situ Hybridization in *Biomphalaria glabrata*

Kushal Kandel | Mentor: Daniel Wagner

This paper investigates the spatial distribution of expressed RNAs in Biomphalaria glabrata embryos through whole-mount in situ hybridization (WISH) using sense and antisense labeled probes. The research builds upon the importance of in situ hybridization in exploring gene expression networks during development and its implications in developmental biology, regenerative medicine, and disease research. Some recent literature suggests that long non-coding RNAs (lncRNAs)

may influence the spatial distribution of mRNAs during embryonic development, impacting the accuracy of in situ hybridization results. This paper aims to address the gap by optimizing probe binding specificity through systematic experiments, including testing different pretreatment conditions, probe dilutions, and wash lengths. Results and discussion focus on gel electrophoresis outcomes and representative WISH images. Challenges and future steps include refining experimental variables and expanding the sample size for better insights into developmental gene expression in Biomphalaria glabrata.

Neurobehavioral implications of Ebf3 loss of function mouse models

Ellen Kang | Mentor: Hsiao-Tuan Chao

Characterizing Protein and RNA Interactions with the C-terminal Domain of Influenza D Virus Non-structural Protein 1 (NS1D)

Andrew Kim | Mentor: Jane Tao

Influenza D virus (IDV) is a member of the family Orthomyxoviridae, and as a part of bovine respiratory disease complex, it mainly infects cattle and small ruminants, costing the US feedlot industry about $1 billion annually. It is known that influenza A virus (IAV), a relative of IDV, uses its NTD (N-terminal dsRNA binding domain) and its CTD (C-terminal effector domain) to modulate host innate immunity. I aimed to determine if that is the case for IDV, and investigated how the CTD of influenza virus D nonstructural protein 1 (NS1D) forms complexes. Protein purification, gel shift assays, fluorescence anisotropy binding assays, and crystal screening characterize CTD complexes with Importin α (Impα) and RNA, suggesting that it has an affinity for Impα and RNA like its relative, NS1A. I plan to

further delineate the molecular basis of this interaction by solving the structure of NS1D and its various complexes using X-ray crystallography. For now, my findings form a strong foundation for further inquiries concerning IDV's host interactions mediated by NS1D.

Multi-Omics Single-Cell Atlas of the Human Optic Nerve and Optic Nerve Head

Atulya Mandyam | Mentor: Cristal Villalba Silva

The optic nerve is a crucial part of many visual disorders that afflict the population, including glaucoma, toxic amblyopia, blindness, and optic nerve atrophy. Our overall goal is to develop a single-cell atlas of the human optic nerve and optic nerve head. Through single nucleus ATAC sequencing and single nucleus RNA sequencing technology, we aim to compile a comprehensive list of cell types in these tissues and to investigate differential gene expression as well as regulatory mechanisms across different genders, ages, and races. A total of 588,824 and 691,671 nuclei from 63 donors of diverse ancestry, including 34.43% White, 31.15% Black, 26.23% Hispanic, and 8.20% Asian, were profiled with sc-ATAC-seq and sn-RNA-seq, respectively. Integrative multi-omics analysis identified key transcription factors and gene regulatory networks that are important for defining each cell type and their functions. In the current study, we have successfully developed a multi-omics single-cell atlas of the optic nerve and the optic nerve head. This atlas can be used as a foundational resource for a deeper understanding of the cellular and genetic landscape of these regions.

Expressing and Purifying Stable *Colletotrichum camelliae* Filamentous Virus 1 (CcFV-1) Replisome for Structural Analysis

Pranav Mandyam | Mentor: Yizhi Jane Tao

The vast majority of double-stranded RNA (dsRNA) viruses have icosahedral capsids that remain intact during infection to allow efficient viral genome transcription without triggering host innate immune response. However, the discovery of a filamentous dsRNA virus, *Colletotrichum camelliae* Filamentous Virus 1 (CcFV-1), challenges this evolutionary trend. Studying the structure and function of the CcFV-1 replisome would address how the transcription and replication of CcFV-1 may differ from typical dsRNA viruses. The CcFV-1 P1, or RNA-dependent RNA Polymerase (RdRP), has been purified individually and found to be active. However, Alphafold2 predicted that other CcFV-1 proteins may interact with P1, indicating they could affect P1 activity. These include putative methyltransferases P2 and P3 and unknown proteins P6 and P7. Pulldown of P1 during purification with a tagged P3 demonstrated that P1 and P3 interact strongly. Thus, we designed purification studies with truncated versions of P3 to determine the interaction interface between P1 and P3. Understanding the interactions

between P1 and these CcFV-1 proteins will help elucidate the mechanism of the CcFV-1 replisome.

Optical Simulation in the Deep Underground Neutrino Experiment

Huijun Mao | Mentor: Aaron Higuera

The Deep Underground Neutrino Experiment (DUNE) represents an international endeavor to study neutrino, the universe's most elusive and second most abundant particles. This research focuses on a critical component of the experimental apparatus in DUNE called the photon detection system (PDS), designed to measure the number of photons. Our goal centers on employing machine learning (ML) methods to simulate the detection of photons by optical sensors within ProtoDUNE VD, a small-scaled prototype. While traditional simulation methods are computationally demanding, ML offers a promising avenue with its potential for speed and memory efficiency. We aim to develop ML models to predict the number of photons for each optical sensor using event spatial coordinates. We started with constructing a baseline multilayer perceptron neural network (MLP) using TensorFlow. Subsequently, we plan to explore more sophisticated ML methods, including generative models. The research allows to evaluate the performance of the current testing on the PDS in ProtoDUNE VD, and, ultimately, the full-scale DUNE experiment, as part of an effort to uncover new insights into the fundamental nature of the universe.

Examining Biodiversity of Microbial Communities in Flask and Microdroplet Environments

Lily Remington | Mentor: Yousif Shamoo

Antimicrobial resistance (AMR) is on the rise, with resultant infections becoming one of the leading causes of death worldwide. Emergent phenotypes, which occur in microbial communities from collective interactions, may provide solutions to AMR by unlocking new biosynthetic pathways for drug discovery. However, the lack of high-throughput methodologies to observe community interactions has limited their study. This study investigates how microdroplets may overcome the limitations of communities of cells in well-mixed batch reactors or flasks, which are unlikely to facilitate the formation of stable communities. Using Streptomyces spp. as model organisms, biological replicates of 10-strain communities were grown, with a 1% dilution of each culture every 48 hours for 10 iterations. The first and last iterations were sequenced using next-generation sequencing (NGS) and computational analysis assessed the frequency of strains. Ultimately, increasing homogeneity was observed in the microbial communities grown in flask culture. As such, different methods, like microdroplets, are necessary to observe emergent phenotypes due to their ability to maintain biodiverse communities better.

PROJECT-J: JWST Observations of the HH46 IRS Outflows and Protostar

Megan Schultze | Mentor: Patrick Hartigan

PROtostellar JEt's Cradle Tested with JWST (PROJECT-J, P.I. B. Nisini) is a JWST-Cycle 1 project aimed at investigating the environment of the Class I protostar HH46 IRS and its outflow through NIRSpec and MIRI Integral Field Spectroscopy from 1.6 to 28 microns. The new observations detect both the jet and counter-jet close to the protostar for the first time, and the spectral-images of the atomic lines trace the densities, temperatures and ionization conditions throughout the region. Images of several H2 lines outline a complex molecular flow, where a bright cavity, molecular shells, and a jet-driven red-shifted bow-shock are shaped by the ambient conditions encountered by the outflow as it travels away from the source. The protostar displays a rich spectrum of ice and dust features as well as several molecular absorption lines. These observations demonstrate the power of JWST to investigate the properties of embedded regions around young class I protostars that remain hidden even at near-IR wavelengths.

How Oxidation Affects the Function of a Mitochondrial Protein Disaggregase

Claire Shi | Mentor: Francis Tsai

To protect against stress, cells have evolved sophisticated stress response mechanisms. One such mechanism involves specialized proteins called disaggregases that recover functional protein from aggregates. SKD3 is a mitochondrial disaggregase that is important for protein quality control. Importantly, SKD3 interacts with and maintains the solubility of HAX1, a protein associated with severe congenital neutropenia. Mutations in SKD3 have also been directly linked to human disease. In particular, mutations within the ankyrin-repeat domain (ANK domain), which is essential to SKD3's function, cause 3-methylglutaconic aciduria type 7, a metabolic disorder characterized by increased levels of 3-methylglutaconic acid. This disease is associated with variable neurologic deficits and severe neutropenia that can result in early death in infants. Consistently, disease-associated ANK domain mutations were shown to impair the protein disaggregating activity of SKD3 in vitro. However, the structural basis of disease pathomechanism remains poorly understood. My research aims to further investigate how oxidative stress conditions affect SKD3 protein structure and its interaction with substrate.

Effect of SPO1 Genes 55-53 and 45/46 on *Bacillus subtilis*

Amy Son and Ishita Mahajan | Mentor: Charles Stewart

During infection of *B. subtilis* by phage SPO1, at least 6 SPO1 genes appear focused on inhibiting cell-division, a surprising result. We are investigating the role of genes

45/46 and 55-53 in this inhibition, by expressing specific genes in uninfected *B. subtilis*. Both gp45/46 and gp55-53 have shown a substantial decrease in cell viability while turbidity increased, consistent with cell growth taking place while cell division was inhibited. The expression vector uses chloramphenicol resistance as its selective marker, and complications have arisen from the appearance of large numbers of chloramphenicol-sensitive cells. These might be explained by contamination or by massive loss of plasmids, but tests of those possibilities have been inconclusive. Once this issue has been resolved, we will continue research on the effect of these genes on inhibition of cell division. We will observe cell lengths microscopically and expect to see the lengths increase with time after induction, while viable cell concentration decreases.

Spectral Differences between Quantum and Stochastic Systems

Ziyin Xiong | Mentor: Evelyn Tang

Stochastic topological systems draw from topological invariants first developed for quantum systems. While stochastic and quantum systems can share the same invariant in the bulk, their spectra differ under open boundary conditions, leading to new properties. We systematically investigate how spectra in both systems differ. Solving the spectrum analytically using Chebyshev polynomials, we find that in a 1D uniform chain and SSH model with even sites, the stochastic spectrum is given by a one-site smaller quantum system. The spectral differences are most prominent in small system sizes and large non-reciprocity, where quantum states converge while the gap increases between the steady-state and the slowest decaying state in stochastic systems. In the 2D SSH model, we find that exceptional points emerge in different areas of the spectrum in the topological phase. More broadly, this work characterizes unique physical properties that emerge from identical networks described by Laplacian and adjacency matrices respectively.

Understanding the Intermediary Role of Lsm12 in NAADP-Evoked Calcium Mobilization from Endolysosomes

Angel Xu | Mentor: Jiusheng Yan

NAADP is a secondary messenger which mobilizes Ca2+ from mammalian endolysosomes via the two-pore channel TPC2. Although disorders in NAADP signaling are implicated in lysosomal storage diseases, the mechanism of NAADP-mediated Ca2+ release remains poorly understood. Previously, our lab identified the Lsm domain of the RNA-binding protein Lsm12 as a high-affinity NAADP receptor and found that Lsm12 appears to mediate the association of NAADP to TPC2. To gain a better understanding of Lsm12's role as an intermediate accessory protein in NAADP-evoked Ca2+ release, we purified the fusion protein TPC2-Lsm12 and later reconstituted it with a lipid nanodisc encircled by membrane scaffold proteins (MSPs): this purified complex can then be analyzed in functional and structural

assays such as Cryo-EM. In addition, we quantitatively analyzed the binding of Lsm12 to fluorescently marked NAADP using fluorescence polarization (FP) assays.

Cancer: Biology, Prevention and Therapy

Analysis of the Role of Different Photoreceptors in Light-Driven Optic Gliomagenesis and Potential Mediator Signaling Molecules

Nathan Bui | Mentor: Khushboo Irshad

Optic nerve gliomas are low-grade central nervous system (CNS) tumors that predominantly affect children. These gliomas represent a significant subset of brain tumors originating from the optic pathway, accounting for 5% of childhood brain tumors worldwide. Although slow-growing, optic nerve gliomas could induce severe early vision impairment and hypothalamic dysfunction. This study aimed to identify the photoreceptors and mediators responsible for light-driven optic gliomagenesis via series of optic nerve collection, tissue immunohistochemistry, Western blotting, and software analysis. Further validation studies with larger cohorts and follow-ups are warranted to translate these findings and their relevance into clinical practice.

Synthesis of Substituted Tetrahydroquinolines via Prins-Ritter Cyclization

Afton Fults and Adara Toran | Mentor: Chamakuri Srinivas

Tetrahydroquinolines (THQs) represent a crucial class of compounds in medicinal chemistry and drug discovery due to their diverse pharmacological properties and structural versatility. These heterocyclic molecules show a wide range of biological activities, making them attractive candidates for the development of therapeutic agents against cancer, neurodegenerative disorders, and infectious diseases. The unique structural features of THQs allow for fine-tuning of pharmacokinetic and pharmacodynamic properties, enabling researchers to design compounds with improved drug-like characteristics. The potential power of THQs has not been fully explored but can be inferred as extremely valuable. Before being able to explore their full biological importance, the development of an effective synthetic method of substituted THQ derivatives was needed. Based on prior research, a synthetic method using a triflic acid-promoted Aza Prins-Ritter cyclization reaction was developed. We hypothesized this method would be effective for producing substituted THQs from 2-alkenyl substituted N-tosyl aniline and carbonyls, which was proven successful using chemically diverse aldehydes and ketones.

The Role of Neurotransmitters in Glioblastoma Pathogenesis

Aishani Gargapati | Mentor: Dr. Yuan Pan

Characterizing Extracellular Vesicles From HEK 293 Cells as Delivery Vehicles for Ovarian Cancer Treatment

Samah Haidar | Mentor: Samah Haidar

Extracellular Vesicles (EVs) have been considered as a vehicle for drug delivery for cancer and other indications, but they have not been fully characterized for such indications. Therefore, we examined extracellular vesicles derived from HEK 293 cells for potential applications in ovarian cancer; we isolated EVs using ultracentrifugation and determined cellular uptake and in-vivo distribution of EVs. Nanosight analysis of isolated samples found EVs were present at a concentration of 1.44 x 10^9 particles/mL. Results of in-vitro cellular uptake experiments identified that 68.7% of treated ID8 ovarian cancer cells contained EVs. Finally, super resolution microscopy images of tumor tissue collected from an in-vivo mice model experiment showed sufficient tumor distribution. These findings suggest that EVs derived from HEK 293 cells may be useful as drug carriers for cancer treatment.

Novel Regulatory Role of TRAF7 in HIPPO Signaling Pathway within Meningiomas

Abhinav Kona | Mentor: Tiemo Klisch

Meningiomas, making up nearly 30% of primary brain tumors, often recur aggressively and are resistant to chemotherapy and radiation, leaving surgery as the sole option. Molecular analyses identified three subgroups (MenG A, B, C), with over 50% of MenG A tumors having TRAF7 mutations, notably N520S. We hypothesize that TRAF7 is a novel regulator of the HIPPO pathway, a key kinase signaling cascade from MST1-LATS1-YAP1, and its mutations function in a dominant-negative manner, resulting in the inhibition of the pathway.

To explore TRAF7's role in the HIPPO pathway, we engineered C-terminal tagged mutant-N520S & wild-type (WT) TRAF7 proteins. We assessed cellular localization via GFP fluorescence in overexpressed 293T cells & HIPPO pathway activation using a novel luciferase biosensor fused to 14-3-3 and YAP phosphorylation sites.

Our results suggest that WT TRAF7, but not mutant TRAF7 activates HIPPO signaling. Moreover, mutant TRAF7 appears to cluster, while wild-type TRAF7 is ubiquitously expressed. Together, this suggests that TRAF7 plays a role in the HIPPO pathway and its mutations increase cell proliferation by shutting off HIPPO, allowing cell cycle gene transcription.

Hedgehog signaling

Ilyas Kose | Mentor: Ilyas Kose

A Semi-Supervised Approach to Classify Atypical BRAF Mutations to Identify Effective Targeted Therapies in Colorectal Cancer

Abhinav Madduri | Mentor: John Paul Shen

Due to a minority of atypical BRAF alleles being classified as either activating and RAS-independent (class 2) or kinase-impaired and RAS-dependent (class 3), few pre-clinical models of these atypical BRAF mutations exist, limiting efforts to discover effective targeted therapies for these tumors. Here, we evaluated the activity of 100 different mutant BRAF alleles (84 unclassified) using Reverse Phase Protein Array (RPPA) profiles and then used principal component analysis (PCA) and semi-supervised clustering learning methods to classify the 84 unclassified mutations.

Our analysis of RPPA profiles across each BRAF class, using several markers utilized by Yao and colleagues, showed similar patterns in protein expression levels between the putative and Yao classification systems. In conclusion, our research has extended the previous BRAF-mutant Yao classification system to create the Yao Classification System Plus, incorporating 84 more atypical BRAF mutations. This significant expansion allows for developing a wider range of therapeutic options to target tumors carrying these newly characterized mutations, thereby expanding care options for many CRC patients.

Analyzing the Genomic Alteration Landscape of SPOP Mutant Prostate Cancer using Next Generation Sequencing Data from a Safety Net Hospital

Sai Prasada Rao Manikonda | Mentor: Salma Kaochar

Investigation of STAT5/GLDC Interaction on Breast Cancer Risk

Tiffany Nguyen | Mentor: Amy Ku

Breast cancer is the most prevalent cancer and the second leading cause of cancer-related fatalities among women globally and in the US. Given the universal susceptibility of women to breast cancer risk, this study seeks to understand how the physiological states of pregnancy and lactation may influence breast cancer risk. In ER+ breast cancer cells, STAT5 has been identified as a key player in fostering proliferation, survival, and metastasis. However, during the late stages of pregnancy and lactation, STAT5 emerges as a critical factor in mammary gland

differentiation. By investigating STAT5-induced GLDC expression, this study aims to determine whether the GLDC enhancer region serves as a direct downstream effector of STAT5-mediated activation during breast cancer tumorigenesis. Understanding the molecular mechanism is vital due to GLDC's significant role in cancer metabolism, particularly in providing an alternative energy source for cancer cells via glycine breakdown. Preliminary efforts involve utilizing luciferase reporter assays and RT-qPCR techniques to validate STAT5 activation of GLDC expression in HC11 cells optimized for mammary gland differentiation.

Analyzing the Role of Donor Cells in the Leukemic Patients Responsive to Donor Lymphocyte Infusions

Rishi Pasumarthi | Mentor: Pavan Bachireddy

Donor lymphocyte infusions are a common treatment option for patients experiencing relapses in a variety of leukemic conditions. In the event of a leukemic relapse, a regular-course DLI patient will receive T cells from a donor from whom they have prior received stem cells from in the hopes of bolstering patient immunity. Despite DLI being an oft-successful treatment, little is known about the cellular mechanisms that drive its success. In order to explicate the mechanism of Donor Lymphocyte Infusions, we analyzed donor T cells along with native bone marrow cells at multiple infusion time points to define the cellular pathways requisite for the success of DLI. We utilize a number of novel bioinformatics methods on single-cell RNA sequencing data we collected from 4 different CML patients to determine involved cellular interactions as well as enriched cell states. Through cell-cell interaction inference analysis, we find that monocyte cells are crucial in the resulting T cell states of patients responsive to DLI. Additionally, we establish a bioinformatic workflow to compare cell states at different infusion time points using a mix of methods from the R packages Seurat and Scriabin.

Intracellular Localization Patterns of Common NF2 Mutants in Meningiomas and Role in Hippo Signaling Pathway

Ansh Rai | Mentor: Tiemo Klisch

Meningiomas make up nearly 30% of all primary intracranial brain tumors with roughly one fifth recurring. Our lab has used molecular analyses, such as methylation profiling and RNA-seq, to identify three distinct subgroups: MenG A, B, and C. MenG B and C tumors are characterized by mutations in just one gene: neurofibromatosis 2 (NF2). We hypothesize that NF2 is a true regulator of the HIPPO pathway and its mutations function in a dominant-negative manner, resulting in the inhibition of the pathway.

To model and understand the role of NF2 in HIPPO pathway regulation, we engineered five N-terminal tagged NF2 proteins. We determined localization by

overexpression in 293T cells and analyzing GFP fluorescence. HIPPO pathway activation was measured by co-transfection of a HIPPO biosensor, which merges the two luciferase halves upon activation that can then be quantitatively detected by using a dual-reporter assay.

Our results suggest that there are differences in HIPPO activation using different wildtype NF2 variants, and that NF2 plays a role in the HIPPO pathway and its mutations increase cell proliferation through shutting off the pathway, allowing cell cycle gene transcription.

Using Machine Learning for the Assessment of Pathogenic Inframe Indels in Inherited Retinal Diseases

David Rauch | Mentor: Meng Wang

Generating Tooth Agenesis-Associated Mutations in hESC H1 Cells Using CRISPR/Cas9

Taylor Rosen | Mentor: Lee Dung-Fang

Tooth agenesis, or the congenital deficiency of one or more teeth, is one of the most frequent deformities during cranial and facial growth. This condition is caused by mutations in the genes involved in epithelial-mesenchymal activity in the dental lamina, and numerous studies have linked the condition to cancer development. To better understand the mechanisms involved with tooth agenesis, I utilized the CRISPR/Cas9-mediated HDR-based method to create hESC H1 knock-in cells with a mutation in either the DKK1, LAMA3, or LRP6 genes. We selected, genotyped, and sequenced the cell lines to verify the creation of the desired mutation. Mutated clones underwent neomycin resistance cassette removal using FLP-FRT recombination. We isolated the final cell lines selected by puromycin and neomycin. These clones were differentiated into neural crest cells and subsequently validated for their mutation functionality. The differentiated cells can be used to study the pathways involved with tooth formation in the hopes of finding evidence for using tooth agenesis as a screening tool for early signs of cancer risk.

Evaluating the Role of Enzyme X in Sugar Sweetened Beverage Enhanced Colorectal Cancer Metastasis

David Skwarchuk | Mentor: Jihye Yun

Evaluating Changes in Enhancement Pattern Mapping for the Early Detection of Hepatocellular Carcinoma

Shane Smith | Mentor: Eugene Koay

Cancer early detection research aims to improve survival rates of highly lethal cancers such as hepatocellular carcinoma (HCC). We aimed to use novel image processing called Enhancement pattern mapping (EPM) to test the hypothesis that EPM can predict risk of HCC prior to clinical diagnosis. We collected Magnetic Resonance Imaging (MRI) scans from patients undergoing liver surveillance due to high HCC risk from cirrhosis, identified cases (developed HCC), controls (no HCC), and analyzed at least two MRIs for each patient. Preliminary results from log rank and cox proportional hazard models indicate that cases with high absolute changes in lesion EPM mean per day have shorter times-to-disease compared to those with low absolute changes per day (p=0.004). Similarly, cases with shorter time-to-disease displayed high absolute changes in lesion EPM skewness (p=0.009) and standard deviation (p<0.001), indicating potential changes in tumor morphology. Ongoing work will incorporate clinical factors, such as cirrhosis etiology, into a multivariable model to predict HCC risk. With proper validation, our work may help identify those at the highest risk of HCC at earlier, curable stages.

Evaluating the Functional Impact of SNPs in the Enhancer Region of IKZF1 Associated with Leukemia Susceptibility

Kai-Yuan (Kalina) Tsung | Mentor: Karen Rabin

Children with Down Syndrome (DS) exhibit a 20-fold increased risk of developing B-cell acute lymphoblastic leukemia (B-ALL). Genome-wide association studies identified single nucleotide polymorphisms (SNPs) near IKZF1 enhancer regions associated with an increased risk of B-ALL in DS children. We hypothesize these SNPs decrease enhancer activity, IKZF1 expression, and binding of transcription factors. Prior experiments indicated the rs1110701 and rs17133807 risk alleles reduce IKZF1 activity. To perform functional characterization of these risk alleles, we used CRISPR Cas9 to generate risk and non-risk alleles at these SNP loci in DS lymphoblastoid cell lines (LCLs). We annealed gRNAs and cloned them into Cas9-expressing vectors with restriction enzyme digestion and ligation. We confirmed the gRNA-containing Cas9 plasmids express GFP by transfecting them into 293T cells, and we are optimizing DS LCL transfection. After cells are mutated, we will measure IKZF1 mRNA expression, the binding of transcription factors associated with B-cell differentiation, and cell proliferation in risk vs non-risk allele LCLs, to assess for characteristics mediating increased susceptibility to DS-ALL.

Optimization of T cell Isolation from Neuroblastoma Tumors to Investigate Mechanisms of T Cell Dysfunction

Giancarlo Valenzuela | Mentor: Eveline Barbieri

Neuroblastoma (NB) is a commonly diagnosed cancer in children under the age of 5, with a median diagnoses of 18 months. The cancer arises from neural crest elements in the developing embryonic sympathetic nervous system which leads to tumors in the adrenal glands and/or the sympathetic ganglia (Matthway et al. 2016). A main contributor to the development of NB is the amplification of MYCN, a proto-oncogene involved in many signaling pathways that contribute to cell growth and proliferation of progenitor cells (Kohl et al., 1983; Ruiz-Pérez et al., 2017). Previous research has discovered that MYCN recruits immune suppressive cells (tumor-associated macrophages and myeloid-derived suppressor cells), contributing to T cell dysfunction in the tumor microenvironment (TME) (Carlson & Kogner, 2013; Xia et al., 2019). Nevertheless, these dysfunctional T cells have not been molecularly characterized. With our main objective to characterize NB tumor-infiltrating T cells to understand the mechanisms through which MYCN induces T cell dysfunction, we have optimized the method of isolating T cells from MYCN-driven immunocompetent TH-MYCN +/+ NB genetically engineered mouse models (GEMM).

Upregulation of Histone Demethylase KDM5D Leads to Sex Difference in Colorectal Cancer

William Wu | Mentor: Jiexi Li

Why do females have longer average life expectancy than males? One of the reasons comes down to males having a worse prognosis in lethal disease, such as colorectal cancer(CRC). CRC is one of the most common malignant cancers and the second leading cause of cancer death in the US. Males typically experience higher metastases and mortality, which is often attributed to males having a worse life style, such as consuming more red meat. With the lack of an explanation on the genetic level, we performed cross-species molecular and transcriptomic analysis to identify the Y chromosome gene *KDM5D* as a contributor to sex differences in CRC. KDM5D is a histone demethylase upregulated by KRAS*, one of the most common mutations in CRC. Deletion of *kdm5d* leads to decreased cancer cell invasiveness and enhanced immune response. More specifically, upregulation of KDM5D impairs tight junction integrity, thereby increasing metastasis, and represses antigen presentation by MHC-I, thus reducing T cell response. Our work shows *KDM5D* is a major contributor to sex differences in CRC and provides a novel therapeutic strategy for treating men afflicted with KRAS* CRC.

SESSION 2

Human Development, Health, Performance and Disease

Streamlining Development Efforts for "In Vitro" Culture and Genetic Manipulation of "Biomphalaria glabrata": A Novel Approach

Seryna Ayala | Mentor: Daniel Wagner

Biomphalaria glabrata is a species of snail widely studied as an intermediate host and holds promise as a model organism for developmental biology. Building upon previous success in embryo culture, this study focuses on refining culture chambers to optimize embryo survival rate and efficiency.
Successful and efficient in vitro culture will allow for diverse embryo manipulation method application.The project addresses limitations in prior methodology. Previously used pulled capillary tubes as culture vessels allowed only one embryo at a time to be cultured per tube, and the curved surface of the tubes obscured observation, resulting in inefficient timelines. To overcome these challenges, a culture suspension model is proposed. This model utilizes 3D-printed microslides, allowing accommodations of 1 to 5 embryos per drop and facilitating uniform visualization.
As this project reaches a reliable benchmark, future directions include microinjections followed by in vitro culture, with a focus on lineage tracing. This approach has implications for understanding cell fates and resolving phylogenetic relationships within the lophotrochozoan clade, particularly within the phylum Mollusca.

Measuring the Success of RAPTR Splicing Various mRNA Target Sites

Nafisa Azizi | Mentor: Maria Claudia Villegas Kcam

The utility of natural antimicrobials is increasingly limited due to the rise of antimicrobial resistance and lack of specificity in most antimicrobial compounds. Therefore, it is important to expand research focusing on creating synthetic antimicrobial systems. This project focuses on characterizing the activity of a newly developed antimicrobial system called RNA-Activated Protein by Trans-Splicing Ribozyme (RAPTR). RAPTR is a ~1 kb catalytic RNA sequence that can be programmed to encode a protein output of choice, which is spliced into a target mRNA sequence to express a chimeric protein output. Thus, a protein output inducing cell death can be chosen to target antimicrobial resistant pathogens. Our study explores the success of using RAPTR to target different sites within an mRNA in comparison to the activity from a direct-fusion version of the chimeric product.

Moreover, we evaluate additional factors possibly contributing to difference in activity, such as the free energy of the spliced mRNA and fusion products. We use GFP as a reporter for our chimeric protein output and clone the spliced and direct fusion plasmids using Golden Gate and Gibson assembly, respectively.

The loss of striated muscle preferentially expressed gene (SPEG) kinase, leads to decreased contractility and increased hypertrophy in the heart leading to heart failure.

Dean Barazi | Mentor: Yuriana Aguilar-Torres

Heart Failure (HF) affects 6.5 million people in the US. HF is characterized by decreased contractility and increased cardiac hypertrophy. The ryanodine receptor type 2 (RyR2) regulates calcium dynamics and contractility. SPEG is a kinase that regulates intracellular calcium dynamics by phosphorylating the RyR2 at S2367. However, the role of phosphorylation at S2367 in HF progression has not been assessed. We hypothesize that SPEG knockout mice (SPEGcKO) will develop increased lung edema, heart hypertrophy, and decreased contractility, all indicative of HF. We injected SPEGfl/fl mice with AAV9-TNT-cre-mCherry to induce SPEG knockout and analyzed the phenotypic differences. Cardiac function was assessed from echocardiograms recorded at baseline and 4, 8, and 12w post-injections. Our data reveal that reduced RYR2 phosphorylation at SPEG site is critical in HF progression. Importantly, cardiac function was protected in SPEGcKO mice by mimicking the RyR2 site-specific phosphorylation at S2367 (SPEGcKO-S67D mice). In conclusion, we found that SPEG is critical for RyR2 phosphorylation at S2367 and its loss leads to HF.

Elucidating the effect of CRISPR-Cas9 mediated *fgf13a* knockdown on auditory development and cochlear neuron apoptosis in *Danio rerio*

Pamela Duarte | Mentor: Rosa Uribe

Congenital hearing loss, one of the most common sensory disorders, stems from genetic or environmental factors. Despite over 400 syndromes linked to hearing impairment, the molecular intricacies of syndromic deafness are unknown. Examining patients with syndromes characterized by loss-of-function mutations in the fibroblast growth factor (FGF13) gene, such as Wildervanck syndrome, reveals consistent sensorineural deafness. FGF13 is a potent regulator of cell proliferation and differentiation, however its role in the pathogenesis of deafness is unclear. Prior studies using mice suggest it is a novel candidate for further research. This project sought to extend earlier findings using zebrafish, a model organism with similar auditory function, and regenerative capabilities, which mammals lack. To elucidate the role of FGF13 in auditory development, I established zebrafish lines with a CRISPR/Cas9 mediated knockdown of fgf13a to utilize the larvae for analysis of possible changes in the morphology and density of cochlear neurons. My aim was

to provide insights into the molecular mechanisms of FGF13-related deafness and contribute to potential therapeutic targets for hearing disorders.

Identification & Characterization of Allergen-Specific T helper Cells in SA

A'Zhariya Ellis | Mentor: Carla Davis

Shellfish allergy is a complex immune reaction that arises when the body's immune system comes into contact with any variation of shellfish. Shrimp allergy (SA) is the most frequent severe case associated with shellfish-based allergies. To understand the pathologic interactions between T and B cell populations that lead to the antibody production against major shellfish allergens, subpopulations of T helper (Th) cells were examined. While there have been many alterations described within these Th cell subpopulations in SA, there is still uncertainty regarding the cells that are allergen-specific in contrast to bystander activated Th cells. The overall goal of this project was to identify and characterize pathogenic Th cells. Proliferation assays, and flow cytometry as well as marker activation analyses were used to determine which of the Th cell subsets are shrimp allergen-specific. It was hypothesized that gdT and Tph cells would be identified as pathogenic T cells in SA. Based on preliminary results, there were strong expressions of common T cell activation and proliferation markers observed within the Tph subpopulation, supporting its allergen-specific T cell candidacy.

Investigating MicroRNA Regulation of Dnmt3a for Development of ASO Therapeutics

Madeleine Garrity | Mentor: Laura Lavery

Proper neural function and development are facilitated by epigenetic mechanisms, including DNA methylation. Dnmt3a is a DNA methyltransferase crucial in neurodevelopment as the sole writer for non-CpG methylation in the postnatal brain. Its dysregulation is linked to neurodevelopmental disorders (NDDs), including Tatton-Brown-Rahman Syndrome (TBRS) and Autism Spectrum Disorder (ASD). My research investigates microRNA as a regulatory factor of Dnmt3a to identify potential therapeutic targets. Using qPCR to profile miRNA expression in the cortex across developmental stages, I have identified miRNAs with expression patterns complementary to Dnmt3a; validating known candidates and confirming new ones. I am comparing wild-type and Dnmt3a-deficient neurons in culture to characterize cellular and molecular changes due to Dnmt3a loss of function mutations. I aim to develop and test antisense oligonucleotides (ASO) designed to impact miRNAs regulating Dnmt3a mRNA, restoring function and rescuing TBRS-like symptoms in vitro. Future experiments will leverage these results to evaluate the efficacy of ASO therapeutics in vivo in rescuing molecular and behavioral phenotypes of TBRS mouse models.

Evaluating the effectiveness of neutrophil phenotyping on delayed neurological deficits after an aneurysmal subarachnoid hemorrhage

Harveen Kaur | Mentor: Devin McBride

Considered one of the most frequent causes of admission in neurocritical care with high rates of morbidity/mortality, aneurysmal subarachnoid hemorrhage (SAH) is a neurological emergency where blood vessels rupture and blood invades subarachnoid spaces in the brain. In spite of advancements in treatment, many who survive develop delayed neurological deficits and cerebral ischemia, which is the primary reason for poor outcomes in SAH survivors. These defects have vaguely been known to have multifactorial mechanisms of attacking the brain, which signals the need for diving into specific biomarkers and therapeutic targets that prevent such cognitive decline. One cell type that is exacerbated after ischemic injury is neutrophils, which normally provide an immune response but can lead to stroke pathogenesis when stressed. Understanding the role that neutrophils play in neuromodulation can connect their activity to deficits after SAH, especially since they already serve as a peripheral biomarker for inflammatory burden. This study focuses on evaluating neutrophil activity alongside several antibodies via flow cytometry to track their presence and intensity for delayed deficits after SAH.

Developing a noninvasive RMA approach for retinal monitoring

Jocelyn Lee | Mentor: Jiaxiong Lu

Continuous monitoring of retinal health is crucial for assessing degeneration and functionality. Existing noninvasive methods have limitations, requiring the development of improved approaches. In this study, we introduce Released Markers of Activity (RMAs) as a novel method for monitoring gene expression through a simple blood draw without the need for animal sacrifice. RMAs consist of secretion, translocation, and detection domains, making them a promising technology for observing retinal function. Our findings demonstrate that RMAs can be expressed in photoreceptor and retinal ganglion cells, effectively crossing the blood-retina barrier and exhibiting sensitive expression. Leveraging cell type-specific promoters, such as the Müller-glia-specific GFAP promoter and the photoreceptor-specific GRK promoter, this new technology enables dynamic monitoring of specific cell populations in vivo. RMAs prove effective in monitoring the activation of Müller-glia cells and assessing the survival, integration, and functionality of transplanted photoreceptor cells. This innovative approach holds notable potential for advancing our understanding of retinal health and therapeutic interventions.

Enhancing Osteoarthritis Cell Therapy with Biomedical Engineering: Evaluating Fat Pad-Derived Mesenchymal Stem Cells in 3D Spheroid Culture and on Collagen-Based Scaffold

Jaesang Lim | Mentor: Banche-Nicolt Federica

The current cell therapy clinical standard for osteoarthritis (OA) uses bone marrow-derived mesenchymal stem cells (MSC). However, an alternate source is the infrapatellar fat pad (FP), offering a less invasive harvesting approach. As OA is an inflammatory-based disease, the immunosuppressive potential of MSC plays a crucial role in successful cartilage regeneration. 3D spheroid cell culture shows superior mimicry of the in vivo tissue architecture and cell-cell interactions, garnering attention. We optimized spheroid creation with 3000 FP-MSC cultured for 24 hours on a polymeric-coated plate. The simulation of inflammatory condition was also tuned, setting 40 ng/mL as the optimal concentration of combination IFN-γ and TNF-α. Then, we demonstrated that 3D spheroids have greater immunosuppressive potential characterized by superior PTGES, PTGS2, and IDO1 expression compared to traditional 2D cultures. Finally, we enhanced the biomimicry using freeze-dried collagen scaffolds as a substrate for 3D spheroid culturing. A seeding titration approach was employed to determine the optimal spheroid density, and CellTiter Glo® and Live/Dead assays were utilized for scaffold viability.

Developing a Physical Activity Intervention for Adolescent and Young Adult Central Nervous System Tumor Survivors

Elizabeth Pan | Mentor: Maria Swartz

Up to 45% of adolescent and young adult (AYA; 15-39 years old at diagnosis) central nervous system (CNS) tumor survivors experience cognitive impairment (CI). Physical activity (PA) is a promising approach to mitigate CI. The purpose of this study is to design a feasible and engaging PA intervention using active video games (AVG) to improve survivorship outcomes for the AYA CNS population. Guided by the Adaptome framework, we aimed to adapt the behavioral coaching materials and PA components of an existing virtual PA intervention using AVG for AYA CNS tumor survivors. We recruited 16 AYA CNS tumor survivors and 16 clinical providers to participate in online semi-structured focus groups. Preliminary thematic analysis resulted in 12 subthemes under 5 levels of adaptation based on the Adaptome framework. Top themes included tailoring the PA intervention to physical limitations and abilities, promoting inclusivity, building community, and carefully selecting key survivorship topics. Preliminary findings indicate that the adaptation needs to occur at all 5 levels of the Adaptome framework. Key suggestions included program flexibility, inclusivity, and autonomy in exercise selection.

Assessing Mean Transverse Momentum of Ultracentral Collisions as a Tool for Extracting the Speed of Sound in Quark-Gluon Plasma

Derick Pascual | Mentor: Wei Li

In high-energy nuclear collisions, a new state of hot and dense matter, called quark-gluon plasma (QGP), is predicted to form. Experimentally constraining the equation of state (EoS) of QGP remains a key challenge. In steps towards quantifying the EoS, recent measurements by the Compact Muon Solenoid (CMS) experiment at CERN's Large Hadron Collider have spurred precise estimations of the speed of sound in QGP. These estimates assume that, in ultracentral collisions, the slope of the average transverse momentum (<pT>) over the number of charged particles (Nch), corresponds to the speed of sound. However, the extent that the speed of sound is quantitatively connected to this experimental observable has not been systematically tested.

In this work, we use the relativistic hydrodynamic model, MUSIC, to study this assumption. By varying the input EoS which governs the speed of sound (e.g., switching from Lattice QCD to ideal gas calculations), we will demonstrate how the slope of <pT> vs Nch responds to EoS variations in the MUSIC model and compare with CMS data. Our findings will reveal the strengths and limitations of extracting the speed of sound via <pT> in ultracentral collisions.

Determining the Relationship Between Enteric Neuron Differentiation and Expression of the Retinoic Acid Signaling Pathway

Victoria Payne | Mentor: Rosa Uribe

The retinoic acid (RA) pathway aids stem cell proliferation to differentiation transitions, activating gene transcription to induce stem cells to neural type cells in various tissues. It has been shown that enteric nervous system (ENS) development, a bodily system of neurons and glia modulating secretion and homeostasis intrinsically found along the gut, relates to the RA pathway. However, if ENS neurons require RA for their neurogenesis is unknown. This study examines if ENS neurons and/or their gut microenvironment express RA pathway components. To analyze if RA candidate markers co-localize with ENS neuron markers, we used whole-mount immuno-coupled hybridization chain reaction (WICHCR) on zebrafish embryos across various time points to assay expression of the RA markers aldh1a2, cyp26a1, and raraa along with ENS markers phox2bb, sox10, and Elavl3/4. We will compare markers by analyzing data from confocal microscope images along the ENS, discerning if RA pathway members co-localize with ENS differentiated neurons in addition to RA's role in ENS formation. These findings will give an understanding as to if the RA pathway may regulate enteric neuron differentiation and migration.

Network Analysis Identifies Endolysosomal Gene Alterations that Modulate Synucleinopathy Pathology

Leo Rao | Mentor: Justin Moore

Synucleinopathies, a type of neurodegenerative disease characterized by the accumulation of alpha-Synuclein (aSyn) protein in neurons, cause movement difficulties and cognitive decline, affecting over a million people in the U.S. Researchers have identified the endolysosomal pathway (ELP), a cellular degradation system, as frequently dysfunctional in synucleinopathies such as Parkinson's disease (PD). To identify specific ELP mechanisms that could harbor risk factors or therapeutic targets for PD, multi-omic network analyses were done to find 3 gene clusters: Syntaxin, PIP and ESCRT. Genes from these clusters were experimentally validated *in vivo* to identify ELP gene alterations that can modulate aSyn-induced deficits. Using a *Drosophila* model of aSyn, ELP alterations were validated using behavioral screening, immunoblotting, and histopathology. Results show that dCHMP3 gene knockdown ameliorates behavioral deficits and neurodegeneration induced by aSyn, indicative of the therapeutic potential of dCHMP3 alterations for PD. Further research must be done to validate remaining genes, and dopaminergic neuron degeneration should be analyzed through tyrosine hydroxylase staining.

Processes of Mullerian Duct Regression During Male Sex Development

Ariah Richards | Mentor: Rachel Mullen

The Mullerian Ducts (MD) serve as the precursor to female reproductive tract organs. In males, the development of testes prompts the release of Anti-Mullerian Hormone (AMH), leading to MD elimination. Conversely, in females, lacking AMH or testosterone, the MD persists. Investigating MD regression sheds light on Differences in Sex Development origins.

Using whole mount immunofluorescence, researchers examined Pax 2 (an epithelial tissue marker) alongside Cleaved Caspase 3 or Phospho-Histone H3 (apoptotic and proliferating cell markers, respectively). Imaris software aids in segmentation and quantification of cells. Wnt7aCre mice crossed with mTmg mice enabled visualization of MD regression via fluorescent markers, facilitating time-lapse imaging.

MD regression in males occurs post-E14.5 in three stages: thinning, breaking, and contracting, with apoptosis initiating at E14.5. Male MDs exhibit more apoptosis than females at this stage. Additionally, males display lower cell proliferation than females at E13.5. Observations through static and time-lapse imaging suggest biomechanical processes contribute to MD fusion and regression.

Investigating Common Modifiers in the Shared Pathogenesis of Alzheimer's and Parkinson's Disesase

Alexandra Serrato | Mentor: Juan Botas

Alzheimer's (AD) and Parkinson's disease (PD) stand as the top two most prevalent neurodegenerative diseases affecting elderly people worldwide. Both disorders have distinct pathophysiological hallmarks that can be used to diagnose patients. AD is characterized by beta-amyloid peptide and tau protein accumulation, while PD exhibits alpha-synuclein (aSyn) aggregates. Mixed pathologies of aSyn and tau/beta-amyloid aggregation are common in the brains of patients with dementia. Extensive molecular and genetic investigations have been conducted in each disease through large-scale human genome-wide association studies and transcriptomic analyses, revealing shared dysfunctional traits. However, there is a lack of studies comparing these disorders and their potential shared risk loci and genetic modifiers. At the moment, there are no effective treatments for either of these disorders. We hypothesize that these disorders share genetic modifiers that can serve as potential targets for treatment of AD and PD. Here we investigate genes previously identified through bioinformatics analysis in tau and aSyn *Drosophila* disease models in our lab, using behavioral and molecular assays.

Comparing "Exercise Snacks" to Current ACSM Guidelines

Darsh Shah and Darren Wang| Mentor: Nadia Agha

Sedentary behavior is a known risk factor for several diseases. Despite this knowledge, many individuals find it difficult to adhere to fitness recommendations. We sought to address this health challenge by comparing "exercise snacks," which consist of brief periods of activity performed repeatedly throughout the day, to the American College of Sports Medicine's (ACSM) standard recommendation for exercise. We recruited 7 individuals (4 males, >50 years of age) and randomized them to the ACSM or Snacks group. All participants completed exercise tests to measure muscular strength, and cardiorespiratory fitness before and after (12-weeks) of their prescribed intervention. We found that both groups exceeded the minimal exercise requirements prescribed. Both groups performed similarly with respect to average distance walked, steps per day, stairs per day, sedentary minutes, and calories burned. This finding suggests that individuals have flexibility in choosing an exercise protocol that fits with their lifestyle. We hope to employ this exercise program in populations who may struggle with longer duration exercise prescriptions, specifically patients with neuromuscular disorders.

Investigating the Role of Public Assistance in Managing Cardiovascular Emergencies in Rural Areas

Claire Shi | Mentor: Lisa Basgall

While public assistance (PA) has been shown to increase access to EMS care for underserved rural populations, few studies document the effect of PA on the outcome of cardiac emergencies. This study aims to investigate the association between cardiac emergency outcomes and PA usage in rural areas. An analysis of cardiac patient encounters was performed utilizing the 2021 NEMSIS database. Patient encounters were separated based on acuity level into Green, Yellow, and Red. Statistical tests were run to determine if PA and 911 respond to significantly different acuity calls and whether significant variations in acuity exist as a result of PA and 911-response differences. The two-sample Z-test of proportions indicated a statistically significant difference in the proportion of acuity levels between PA and 911-response (p<0.01). The χ^2 test of independence (χ^2=0.797,p=0.6713) suggested that there is no significant association between change in acuity and the presence of PA. The proportion of Red acuity cardiac encounters is higher amongst 911-responses, while Green acuity calls are more common in PA-responses. The presence of PA has no significant relationship with change in acuity.

Immunofluorescence studies on the role of macrophages in Epithelial to Mesenchymal Transition in Lupus Nephritis and renal fibrosis.

Julie Trinh | Mentor: Chandra Mohan

Systemic Lupus Erythematosus (SLE) is an autoimmune disease marked by harmful autoantibodies and organ deposition, notably prominent in lupus nephritis (LN) affecting the kidneys. Our focus is on the role of overexpressed M2 macrophages in LN kidneys and their significant contribution to organ inflammation, aiming to deepen our understanding of their modulation. This research is structured in two distinct phases. In the first phase, we investigate triggers inducing the transition of M2 macrophages from human monocytes THP1 and U937 where flow cytometry (FACS), immunofluorescence (IF), and RT-qPCR is performed. The second phase involves an *in vivo* study exploring the effects of CRISPR Cas9-edited genome on a mouse group. This particular project focuses on using IF protocol to examine markers of Epithelial to Mesenchymal Transition (EMT) induced by Transforming Growth Factor beta (TGF-β) in THP1 and U937 cells. Our observations reveal a significant increase in Vimentin (VIM) from both cell groups, indicating EMT occurrence. This discovery of increased Vimentin could become a potential target for therapeutic interventions in LN to modulate its expression.

Perinatal Nutrition in Women Recently Pregnant and Homeless: Barriers and Facilitators

Crystal Unegbu | Mentor: Annalynn Galvin

Women experiencing homelessness (WEH) are at increased risk for reduced perinatal care and access to nutrition. This narrative review summarizes what we know about preconception, prenatal, and postpartum nutrition for WEH. A systematic search of articles published before 2023 on PubMed and Ovid/Medline identified full-text, peer-reviewed studies (n=21) assessing perinatal nutrition needs for WEH. Findings suggested providing targeted care for WEH; emphasizing the connection between diet and birth weight; and accounting for food scarcity, environmental factors, shelter limitations, social support, and trauma processing. Fewer studies focused on specific nutrient-based needs (i.e., pregnancy weight, calorie needs, folic acid/multivitamin intake). Researchers and clinicians should address nutrition-specific behaviors while accounting for the unique shelter-based and trauma-informed barriers that WEH encounter in the perinatal period. Certain structural factors less amenable to individual-level supportive nutrition behavioral change may require larger healthcare and social service policy reform.

The (Anti)synergistic Effect of Methionine Restriction and Taxanes on Tumor Growth

Cayla Xue | Mentor: Julia Salamat

Majority of cancer cells are more dependent on essential amino acid methionine than normal cells. Dietary methionine restriction (MR) shows antitumor effect in a variety of models; in limited studies, MR also improves response to chemotherapeutics. It is unknown whether MR synergizes with all chemotherapies, so we tested the effect of MR when combined with 119 FDA-approved chemotherapies through a high-throughput drug screen in vitro. MR increased the efficacy of most drugs tested with the exception of taxanes: paclitaxel (PTX) and docetaxel (DTX). To validate our drug screen in vivo, we studied the effect of MR, PTX, DTX, MR+PTX, and MR+DTX in two syngeneic breast cancer mouse models, A7C11 or E0771, confirming that MR antagonizes the effect of taxanes. We then conducted metabolomics analysis of tumor samples to explore the mechanism of anti-synergy between MR and taxanes. Preliminary analysis showed that taxanes reduced acylcarnitines, indicators of fatty acid oxidation, which was largely reversed by MR. Overall, MR shows synergistic effect with most chemotherapy drugs tested except for taxanes, and the mechanism behind this anti-synergistic effect remains to be further explored.

The Earth: Geology, Ecology and Environment

The Effects of High Concentrations of CO2 on Marine Dinoflagellate *Karenia brevis* in Exponential and Stationary Growth Phases

Radhiya Bharmal and Maia Figueroa | Mentor: Sven Kranz

The anthropogenic release of carbon dioxide (CO2) not only causes global warming but also
leads to ocean acidification in the marine ecosystem. Understanding the impact of elevated CO2 levels and altered carbonate chemistry on marine dinoflagellates like *Karenia brevis* is crucial due to their significant role in marine ecosystems. These organisms are key to primary productivity and nutrient cycling- impacting fisheries, biodiversity, and the overall health of marine ecosystems. Previous research has provided valuable insights into the physiological responses of *K. brevis* to elevated CO2, however, the specific mechanisms driving these responses are not yet fully understood. To address some gaps in knowledge, we employed a comprehensive approach combining physiological measurements, analysis of cell counts through flow cytometry, and fluorescence monitoring. Specifically, we aimed to monitor the response of *K. brevis* to elevated CO2 during the exponential phase (when cells are rapidly dividing) and compare this data to cells in stationary phase (when cells reach their maximum achievable biomass) to determine how these responses are modulated by other environmental factors

CAX1 Function in Repeated Anoxic Stress: A New Perspective

Sebastian Cubilla | Mentor: Kendal Hirschi

This study examines CAX1's role in anoxic stress tolerance in Arabidopsis thaliana, focusing on its function in ion homeostasis and stress response. Previous research indicates that plants with CAX1 gene knockouts exhibit enhanced tolerance to single, severe anoxic stress events compared to wild-type (WT) counterparts. This project aims to explore this phenomenon under multiple, less severe anoxic stress conditions, mimicking natural environmental stressors. Both wt and cax1 plant types will be exposed to different anoxic stress levels to evaluate their responses. Results could highlight CAX1's importance in stress adaptation and its potential in improving crop resilience to environmental changes.

Unearthing the Impact: The Effects of Prescribed Fires on the Bacterial and Mineral Concentration on a Prairie Over One Year

Annie Nguyen, Kathryn Petree, Tin Vu, Trinity Porter and Manny Ponce | Mentor: Carrie McNeil

Controlled burning is a technique utilized to control the vegetation of a prairie. By purging the environment of organic material, controlled burns can prevent wildfires but also influence organism populations and mineral concentrations. The project addresses the impact of fire on soil bacteria population and soil mineral composition and describes how this, in turn, can influence how controlled burns are utilized. The project analyzes soil samples collected 6 months and 10 months after a controlled burn at a prairie plot adjacent to the Booth Centennial Pavilion at Rice University. RapiTest Soil Test Kit will be used to analyze nitrogen, phosphorus, potash, and pH. Utilization of MacConkey agar will differentiate gram-positive and gram-negative bacteria. Spectrophotometric analysis will examine the diversity and concentration of bacteria. Preliminary results suggest that there is less of an observable difference between the burned and control soil collected 10 months after the controlled burn compared to the burned and control soil collected 6 months after the burn. This work could aid local researchers in understanding the impacts of prescribed burns.

Utilizing Acoustic Monitoring to Understand Differences in Primary vs. Secondary Tropical Rainforest

Meghan Paral | Mentor: Annie Finneran

Primary, or Old Growth, forest may provide different resources for species compared to Secondary, or Regenerating, forests. New approaches, such as acoustic monitoring, in conjuction with methods such as camera trapping, can help us see which areas of a forest species use. We deployed acoustic monitors in 28 locations of either primary or secondary forest to identify bird species across a tropical rainforest in Costa Rica. We used the open source software Arbimon and its Pattern Matching program to identify species in these recordings. We ran a linear regression using habitat variables and camera trap occurrences to see if bird species differed across forest types. We hypothesized that there would be a statistically significant difference between secondary sites with more degraded habitat and primary forest sites with less species found in secondary forests. Preliminary results from camera traps support these hypotheses with less species found in secondary forest sites. A greater knowledge of the difference in species habitat use may help us better format conservation plans as human disturbance of environments continues.

Vikings, Volcanoes, and Satellites: An Analysis of Icelandic NDVI Trends and the Issue of Scale in Vegetation Remote Sensing

Marlo Wilcox | Mentor: Kirsten Siebach

The devil is in the details, especially for remote sensing where the scale of the imagery does not always match the scale of interpretation. Iceland, a subarctic volcanic island in the north Atlantic, has a long history of dynamic vegetation changes. However, the scale at which these changes occur may be smaller than the resolution of datasets most commonly used to study arctic vegetation trends. In this study, I used MODIS Aqua 250m satellite imagery to evaluate nationwide trends in Normalized Difference Vegetation Index (NDVI) over the past twenty years. Then, for a handful of sites representing land cover classifications of interest, I used 30 meter Harmonized Landsat and Sentinel-2 (HLS-2) imagery to quantify information loss between the 30m trend map and several synthetically upscaled trend maps. Over Iceland as a whole, the trend in NDVI was found to be minimal. However, the higher resolution imagery revealed dynamic trends which are lost at lower resolutions. The greatest information loss occurred in highly heterogeneous land cover classes, with a maximum information loss of 63% from 30m to 240m and 90% from 30m to 1000m.

Predicting Fall Bird Migration over Rice Using Nocturnal Flight Calls

Annie Xu | Mentor: Cin-Ty Lee

Migratory bird population sizes have fallen drastically over the past five decades. Understanding bird migration is critical for informing conservation efforts, but the timing of migration, particularly for the fall, is still not fully understood. Existing studies primarily rely on data sources like mist net capture data, visual observation, and radar detection. Nocturnal flight call data has the potential to augment existing data sources by providing a large volume of species-specific bird counts. This project studies three autumns of bird counts derived from nocturnal flight calls recorded at the Rice University campus in Houston, Texas. Using daily counts, we characterize the days of first and last passage for several species of interest, then model the relationship between daily bird counts and weather variables using logistic, Poisson, and negative binomial regression. Finally, we describe differences in migration timing between the years.

Materials from the Fundamental to the Complex

Conical carbon nanobelts: Exploring new rigid tubularene connectivity

Mohammad Bilal | Mentor: Raúl Hernández Sánchez

The synthesis of bent aromatic molecules has fascinated organic chemists for over a century. Fullerenes, carbon nanotubes (CNTs), and carbon nanocones (CNCs) are some examples that fall in this category of compounds with radially conjugated π systems. Synthetic protocols usually face the challenging uphill battle against strain, which has proven to be the bottleneck for their widespread applications. Our group has developed a method to synthesize a novel family of conjugated molecular tubes, which we have termed tubularenes. This method takes advantage of a resorcin[4]arene macrocycle which is functionalized with four equivalents of dibromo quinoxaline, making up the walls of the resulting nanotube after the top segment is covalently tied up into a cycloparaphenylene-like top segment. Our group has been working with para- and meta connected phenylenes as the connecting units of the tubularene's top rim. My work that I report here centers around the synthesis of nanotubes installing meta-terphenyls forming the nanotube top rim architecture. The aromatic top segment of these new terphenyl tubularenes will be further rigidified by pushing Scholl reactions into nanocone structures.

Multidentate Carbene Group 1 and 2 Complexes for Small Molecule Activation

Kayla Bui | Mentor: Samantha Yruegas

The development of early main group metal complexes has garnered recent interest due to their high abundance, non-toxicity, and ecological sustainability. Specifically, the use of s-block metals for bond activation has been limited due to a lack of well-defined complexes, coupled with unselective formation of aggregate metallic clusters. Select ligand systems with strong σ-donating ability have been shown to encapsulate these group 1 and 2 metals effectively. In comparison, the discovery of N-heterocyclic carbene (NHC) ligands revolutionized transition metal catalysis due to strong σ-donation, resulting in extensive work in many different areas of catalysis. Modified tridentate NHCs, or CNCs, which refer to their carbon-nitrogen-carbon binding sites, can also act as supporting ligands to isolate monomeric group 1 and 2 metals. However, in the case these tridentate complexes are difficult to access, two bidentate analogues can be used: CNs and cyclic(alkyl)(amino)carbenes, which can provide a different binding environment for these group 1 and 2 metals. In this work, group 1 and 2 alkyl precursors were synthesized for metalation with bidentate carbenes and tridentate ligands.

Goldilocks Diol

Samantha Cox | Mentor: Zachary Ball

There's been an increasing interest in boronic acids as small molecule recognition motifs. However, due to their instability using traditional purification methods, boronic acids are often converted to boronic esters through reversible binding with diols. Currently, the two more common boronic esters, formed from 3,4-diethyl-3,4-hexanediol (ethyl pinacol "Epin"), and pinacol, contain reversibility and instability problems, respectively. This led the Ball Lab to explore a hybrid diol that could form an ester containing the stability of Epin and the reversibility of pinacol, the Goldilocks diol. Herein is described the synthesis of this diol, its application in the formation of different boronic esters as well as their stability studies in different matrices. The creation of a hybrid ester, amenable to purification through column chromatography and subsequent hydrolysis to yield its boronic acid form, will enhance the versatility of boronic acids.

Investigating an Unexpected High Energy Bump Produced in the Texas Petawatt Laser and the Possibility of Tritium Production From Generated Photoneutrons

Dylan DuCharme | Mentor: Edison Liang

This study investigates the presence of a High-Energy Gamma Ray Bump (HEB) in experiments conducted at the Texas Petawatt Laser (TPW), and the potential of using neutrons that result from the HEB for laser-driven tritium production. We successfully generated photoneutrons via high-energy electron bombardment of high-Z element targets (Au, Pt, Re, W). An unexpected HEB in the gamma-ray spectrum significantly enhanced photoneutron production due to its energetic alignment with the Giant Dipole Resonance in these target elements. We propose confirming the presence of this gamma ray bump by analyzing the energy spectrum of positrons and comparing it to the energy spectrum of neutrons in simulations of the TPW experiment through Geant4. We also consider leveraging the photoneutrons produced to irradiate Lithium-6 targets for tritium creation, potentially offering a waste-minimized alternative to conventional nuclear reactor methods. Geant4 simulations currently show a peak neutron energy of 0.5 MeV, which is suboptimal for tritium production. We are exploring methods within the simulations to downscatter these neutrons to the ideal energy of 0.3 MeV.

Magnetic Properties of the New Compound Hexagonal ZrFe2

Jonathan Dunbar | Mentor: Emilia Morosan

My research was motivated by studying the effects of flat electronic bands in crystals with specific structural motifs. Such flat bands have been proposed theoretically to occur in crystal structures with corner-sharing tetrahedra, called

pyrochlores. Laves phases are compounds with the formula AB2, where the B atoms form this pyrochlore sublattice. I have attempted to grow several AB2 Laves phases such as ZrFe2. While attempting to synthesize cubic ZrFe2, I grew a hexagonal phase of the same composition, which I will refer to as h-ZrFe2. The physical properties of the hexagonal phase had not been previously characterized, opening a new avenue of research. From here, my participation in the project shifted to characterizing h-ZrFe2, while also continuing my attempts to synthesize the cubic phase in hopes of comparing the properties of the two. While it has since become clear that the cubic phase is very challenging to grow and will require longer experiments, I will present my progress in characterizing the magnetic properties of h-ZrFe2 and compare it to what known about the cubic phase from literature to highlight the importance of structure in determining a crystal's properties.

Engineering Gene Therapy Vector Properties in the Baculovirus

Tanya Jain | Mentor: Gang Bao

Viral vectors such as AAV are commonly used for delivery of gene therapies but have limited packaging capacities, and are unable to deliver complicated gene regulation circuits. This research aims to use baculovirus, an insect-virus with a 100kb carrying capacity, to deliver inducible, targeted gene therapies to mammalian systems. BV was pseudotyped with various proteins to enhance transduction, immune protection, and targeting. Both *in vitro* in HEK293T, C2C12, and HEPA-1,6 cells and *in vivo* in mouse liver and brain, vesicular stomatitis virus protein-G (VSV-G) has been determined to improve transduction efficiency. Decay accelerating factor (DAF) also appears to provide protection from the complement portion of the immune system. *In vivo* in mouse liver and brain, while pseudotyping with VSV-G and DAF independently increased BV transduction, adding both proteins together led to the highest transduction. Ongoing efforts are focused on further engineering of BV with proteins to enhance targeting and transduction in primary T-cells. The level of control afforded by the large BV DNA capacity can be used for nuanced, complex gene expression and editing-based therapeutics.

Oxidative Nitrogen Insertion into Silyl Enol Ethers

Alex Lin | Mentor: Zachary Ball

Nitrogen is one of the most important and common heteroatoms found in complex natural products, as well as pharmaceuticals and agrochemicals. Therefore, selective and mild methods for incorporating nitrogen into organic compounds are of great interest. Previous reports have utilized the combination of an iodine(III) reagent and an ammonia surrogate for the insertion of nitrogens into various aromatic scaffolds, such as indoles, pyrroles, and indenes. However, nitrogen insertion into aliphatic systems still remains a challenge, and the application of iodonitrene conditions to such systems is unprecedented. Herein, we report our recent discovery of a novel oxidative nitrogen insertion into silyl enol ethers. Our

method performs a formal 4-electron oxidation of the silyl enol ether, cleaving the C=C bond in the process, to give an *N*-acyl-*N*,*O*-acetal. These products are simple, bench-stable precursors to *N*-acyl iminium species via treatment with either Lewis or Bronsted acid, which are excellent, versatile synthetic intermediates toward amides and lactams. The mechanism of this transformation will also be discussed.

Expression of Cpf1 genes containing introns in *Cladocopium goreaui*

Emily Liu | Mentor: Mike Gustin

Coral are currently threatened by stressors, largely manmade. Rising ocean temperatures and acidification make extinction an increasingly possible future, potentially affecting the entire aquatic ecosystem. While genome studies in coral in the past have produced negligible results, the idea of intron manipulation has gone largely untouched. This research examines the possibility of introducing introns into *Cladocopium goreaui*'s, a species of *Symbiodiniaceae*, genetic code in order to allow more in-depth genetic manipulation. Greater control would enable us to potentially perform drastic changes to the coral such that it can survive increasingly harsher conditions. To determine if the insertion of introns affects genome editing in *C. goreaui*, we examine bacterial transformations following intron insertion into Cpf1. If successfully transformed, this research might serve as a stepping stone to ensure coral's existence and preserving our ocean ecosystem's health and sustainability.

Leveraging Copper-Mediated Bioorthogonal Coupling to Pyroglutamate-Histidine Dipeptide Handle for Purification of Peptides

Timmy Mansfield | Mentor: Zachary Ball

Site-specific modifications to peptides are important reactions in chemical biology, which can be useful for modification of antibodies, enzymes, or other proteins. Research in the Ball lab has shown that through the naturally occurring dipeptide handle of pyroglutamate-histidine (Glp-His), proteins can be selectively modified with alkenyl boronic acids. Further research resulted in
an alkenyl boronic-acid containing resin which can selectively immobilize peptides containing Glp-His. By identifying a method to release immobilized peptides, this resin could be used to purify peptides through a process of immobilizing Glp-His containing peptides, washing away unbound proteins, then releasing pure Glp-His containing peptides. To this end, a linker containing both an alkenyl boronic acid and a photocleavable coumarin structure was synthesized, as well as a test compound for the future screening of reactions for chemical cleavage of peptides from resins.

Design of a Biopolymer to Modulate Local Inflammation in Skin Wounds

Adam Nelson | Mentor: Crystal Shin

Solving the Hardcore Bose Hubbard Model Using a Variational Quantum Eigensolver

Arielle Sanford | Mentor: Kaden Hazzard

In this work, we develop and test a Variational Quantum Eigensolver (VQE) for solving the Hardcore Bose-Hubbard model, intended for use on a novel hybrid analog-digital quantum computing platform based on ultracold atoms in optical lattices or tweezer arrays. We discuss the construction of an efficient ansatz for this quantum computer, which harnesses multi-qubit Hamiltonian evolution and single-qubit rotation gates to achieve a minimum energy state. Initial results confirm the VQE's effectiveness for the benchmark 1D hardcore Hubbard model, as well as more complex Hamiltonians with nearest and next-nearest neighbor interactions. Despite fast convergence to low error rates for up to five sites, greater numbers of sites demand a deeper ansatz to achieve similar convergence. Finally, we analyze the error scaling with increased ansatz layers for two to seven sites, deriving a formula to predict the required layers for minimizing errors.

Decatungstate as an Efficient Photocatalyst for the Addition of

Paige Sutter | Mentor: Julian West

Decatungstate is a completely inorganic molecule that can be cheaply and easily synthesized. It is also a well-known radical photocatalyst. Recent developments have shown that acetone can be coupled to olefins via a radical photocatalytic mechanism. This work seeks to utilize the radical activity of decatungstate to accomplish this transformation using cheap, earth abundant reagents. Reaction conditions for this transformation were developed and optimized for activated olefin (olefins that are resonance stabilized when in their radical form) substrates. Initial substrate screenings were predominantly styrenes. Initial results have been promising, as desired acteone products have been produced in good yields. Next steps for this project include expanding the activated olefin substrate scope, and developing/optimizing reaction conditions for unactivated olefin substrates.

Investigation of Release Kinetics of Charged Peptide-tethered GMP-SH System for Controlled Delivery of Therapeutic Peptides

Reyhan Umurhan | Mentor: Antonios Mikos

Controlled release of peptides has significant applications in tissue engineering and drug delivery. This study investigates the release kinetics of a novel charged peptide-tethered gelatin microparticle system (GMP-SH) for the controlled

delivery of charged therapeutic peptides. Gelatin microparticles, particularly GMP-SH, have previously demonstrated efficacy as potential carriers due to their charged state and chemically active sites. In this study, positively charged (K4mal) and negatively charged (E4mal) peptides were synthesized and covalently attached to negatively charged GMP-SH, forming a modular delivery platform. To observe the release kinetics, the charged associating peptides were fluorescently tagged and then electrostatically loaded to the carrier system. Four experimental and four control groups (no charged interactions) were designed and subjected to release studies in PBS and enzymatic conditions over 28 days. Results from fluorescent assays are expected to reveal sustained release of the therapeutic peptide in groups where conjugating and associating peptides bear opposite charges, indicating the effectiveness of leveraging attractive electrostatic interactions.

Boronic Acid Dynamic Covalent Chemistry in the Controlled Release of Small Molecules and Biologics from Supramolecular Peptide Hydrogels

Samuel Wu | Mentor: Kevin McHugh

The duration of drug release from supramolecular peptide hydrogels is often limited by rapid diffusion. We overcome this challenge by developing self-assembling peptides with N-terminal modifications to enable dynamic covalent bonding with boronic acids (BAs) to enhance drug retention. We demonstrate a Self-Assembling Boronate Ester Release (SABER) hydrogel platform that significantly delayed the release profile of four clinically relevant BA-containing drugs *in vitro*. We also demonstrate that we can significantly enhance the pharmacokinetics of two of these drugs, bortezomib and GSK656, *in vivo*. A single injection of a SABER hydrogel loaded with GSK656 outperformed the standard of care daily oral dosing schedule over two weeks in a mouse model of tuberculosis. Furthermore, we demonstrate that SABER hydrogels can also delay the release of biologics modified with BAs *in vitro* without disrupting the functionality of the biologic. SABER hydrogels are a versatile drug delivery platform—compatible with a variety of small-molecule drugs and BA-modified biologics—and are promising materials for clinical development.

Tunable Delivery of DNA Using Lipoplex-in-Multidomain Peptide Hydrogels

Claire Yang | Mentor: Jeffrey Hartgerink

MultiDomain Peptides (MDPs) are synthetic peptides that self-assemble into extracellular matrix-mimicking hydrogels in aqueous solution. MDP hydrogels possess remarkable potential as drug delivery systems for being biocompatible, injectable, and able to spatiotemporally control the release of encapsulated small molecules and larger biomolecules. This work studies liposome-loaded MDP hydrogels as a drug delivery system that offers superior localized and sustained

drug delivery. Previous work has shown that liposome-MDP systems significantly delay the release rates of encapsulated small molecules, such as the fluorophore calcein and anticancer drug doxorubicin, regardless of MDP or liposome charge. These therapeutic release studies are now applied to a more complex system: DNA lipoplexes, which are large multilamellar liposome formations created by interactions between cationic lipids and negatively charged DNA. Quantification of DNA release and uptake is achieved using mammalian cell expression of green fluorescent protein, which demonstrates the potential for lipoplex-MDP hydrogels to enhance the biodistribution and transfection efficiency of nucleic acid-based therapies.

Patterns and Origins in Nature

Function of GSTs in (Candida Albicans)

Michelle Abiero | Mentor: Michael Gustin

Candida albicans, a common fungus in the human gut microbiota, can cause infections such as oral thrush, genital thrush, vaginal yeast infections, and systemic candidiasis when it overgrows1. Glutathione-S-Transferases (GSTs), a group of eukaryotic and prokaryotic phase II isozymes, play a vital role in catalyzing the conjugation of reduced glutathione (GSH) with xenobiotic substrates for detoxification.

Although the precise functions of the GST family remain incompletely understood, our study aims to investigate how the absence of GST genes may influence C. albicans' ability to withstand oxidative stresses and low nitrogen environments.. Specifically, we explored the response of various Candida albicans GST mutant strains to low nitrogen environments and blood.

Our findings shed light on the potential impact of GST mutations on C. albicans' susceptibility to oxidative stress and antifungal agents, providing insights into novel avenues for combating C. albicans infections.

Determining the Role of *Arabidopsis* VPS13 in Lipid Droplets and Peroxisomes

Chelsea An | Mentor: Tharp Nathan

Although peroxisomal defects lie at the root of many potentially lethal human disorders, there is still much to be discovered about peroxisome structure, function, and biogenesis. Peroxisomes carry out many functions, including fatty acid β-oxidation and ROS metabolism. VPS13, vacuolar sorting associated protein 13, is a lipid transfer protein family conserved across eukaryotes that has roles in vesicular transport and fusion, organelle biogenesis, and autophagy. In humans, the VPS13

gene family is implicated in Cohen syndrome, chorea acanthocytosis, Parkinson's disease, and spastic ataxia. While VPS13 has been studied in yeast and mammals, its role in *Arabidopsis* peroxisomes is unknown. In *Arabidopsis*, four homologs of VPS13 exist: VPS13S, VPS13M1, VPS13M2, and VPS13X. We are using a CRISPR/Cas9-based approach to mutate the *Arabidopsis* VPS13 homologs in a background expressing a reporter that marks peroxisome membrane and lumen. By isolating combinations of VPS13 mutants in *Arabidopsis* and looking at the resultant phenotypes, we will characterize possible roles for VPS13 in LD-peroxisome lipid transfer for β-oxidation.

Addition of His-tag on C-terminus End of ChiA Gene to Improve Protein Purification

Kumaren Anand, Kaira Seth, Moid Asif, Jackie Ku and Abhishek Tripathi | Mentor: Carrie McNeil

Invasive fire ants, *Solenopsis invicta Buren*, pose an ecological threat to the Houston area. Post-Hurricane Harvey polygyne ants have multiple queens, which represent a higher invasive threat. Whole ant PCR can amplify the genes of an ant to determine whether they are polygyne or monogyne. However, whole ant PCR is hampered by the ant's chitinous exoskeleton. The enzyme chitinase can break down chitin, enabling whole ant PCR where traditional maceration methods have been unsuccessful. Thus, successful whole ant PCR will require the purification of chitinase. Previous attempts to purify chitinase using the encoded His-tag via immobilized metal chelate affinity chromatography (IMAC) have been unsuccessful, a result that is theorized to be due to an ineffective location of the His-tag after protein folding. Thus, the objective of this experiment is to successfully clone and ligate the C-terminus His-tag on *E. coli* chitinase by using the C-terminus His-tag already encoded in the plasmid making the chitinase able to be purified for IMAC and ultimately usable in whole ant PCR.

Investigating the Effect of the Liver *Slc19a1* Gene On the Metabolic Phenotypes of Mice

Madison Barendse | Mentor: Alli Antar

We investigated the effect of the *Slc19a1* gene on the metabolic phenotypes of mice. Initially, we maintained a cohort of male and female transgenic mice with liver-specific *Slc19a1* deficiency, albumin-Cre;*Slc19a1fl/fl* (LS19KO), and litter- and cagemate control mice (*Slc19a1fl/fl*). Over 14 weeks, we fed the mice either a high-fat, high-sucrose "Western" diet or a low-fat, low-sucrose control diet, weighing them weekly. We analyzed body composition and tissue weights of the mice. We also placed female LS19KO mice on a liquid ethanol diet for 11 days (NIAAA protocol) to determine effects of chronic and binge alcohol consumption on

alcoholic liver disease. We found that LS19KO females fed the Western diet showed increased NAFLD severity while LS19KO males did not differ from controls. LS19KO mice fed the ethanol diet showed decreased liver glycogen content and decreased non-fasting glucose levels at the end of the study. We intend to compare levels of liver glycogen content for LS19KO mice fed chow and Western diets. Our results show that liver-specific *Slc19a1* deficiency has a significant sexually dimorphic effect on mouse metabolism and merits further study.

Simulating the Effect of Magnetic Field Turbulence on Gamma Ray Burst Polarization

Samuel Barton | Mentor: Matthew Baring

Gamma Ray Bursts are some of the most energetic events in the universe, and their origin was mysterious for many decades. We know know these huge bursts of energy in the form of gamma rays to come from colliding shock fronts in relativistic jets that are formed by high energy events like hypernovae and neutron star mergers. A less studied aspect of GRBs is the polarization of their emission, and it is thought that observing this parameter could reveal more about the origin and structure of the relativistic jets. In anticipation of future GRB polarimetry missions, I am simulating electron transport in a GRB plasma with turbulent magnetic fields. The goal is to connect the variance of magnetic field turbulence, a standard parameter in turbulence theory, to the polarization of the GRB emission. By understanding how the magnetic field turbulence affects the observed polarization we can be prepared to interpret results from future GRB polarimeters when they begin operation.

Synthesis of 2-piperidylmethylboronate ester

Jiya Bhatia | Mentor: Srinivas Chamakuri

Fragment based drug-design is an established method of drug discovery, whereby small molecule fragments are screened for their binding to specific targets. Fragments that bind well to desired targets are chosen for further optimization to create more potent compounds. One fragment of interest is piperidine: a core scaffold in drug discovery that is regularly found in many FDA-approved drugs and alkaloids. Hence, various efforts are being made to create new piperidine derivatives. The researcher's current work relates to introducing a boronate ester group to the commercially available starting material 2-piperidylmethanol, as the addition of boronate ester would allow for piperidine to partake in Suzuki reactions, a cross-coupling reaction which allows further explore the chemical diversity around the piperidine core by adding different alkyl or aryl groups. With this aim, the researcher is synthesizing the necessary intermediates to access 2-piperidylmethylboronate ester.

Targeting NDU1: Inhibiting Yeast Dispersion from *Candida albicans* Biofilms

Isabella Bourtin | Mentor: Michael Gustin

Candida albicans, a fungal pathogen, poses severe risks to immunocompromised individuals through the diversity and versatility of its yeast and hyphal forms. My research this semester has focused on the NDU1 gene and its role in the release of *C. albicans* yeast cells from biofilms. The release of such cells into human blood, known as candidemia, results in a 40% mortality rate. Using artificial saliva medium for growing biofilms, my data show that a strain lacking NDU1, compared to a control strain, exhibits a substantial decrease in the release of yeast cells from a mature *C. albicans* biofilm. I am currently extending this analysis to include a variety of conditions, including human blood. The aim of my research is to further investigate the NDU1 gene and identify a potential drug that can prevent candidemia by targeting this gene. Since NDU1 is present in *C. albicans* but not in humans, it represents a viable target for pharmacological intervention, and offers many possibilities for medical treatment.

Integration Driven Adaptive Radiation in Pupfishes

Emma Colaco | Mentor: HoWan Chan

As a mechanism of evolution, integration can drive trait divergence and lead to adaptive radiation. However, this process has not been fully understood with integration as the primary force. One embodiment of this concept is the Cyprinodontidae pupfishes on San Salvador Island in the Bahamas with the four species: Cyprinodon variegatus; Cyprinodon lacianatus; Cyprinodon desquamator; and Cyprinodon brontotheroides. We hypothesize that integration drove this adaptive radiation and speciation. By examining the morphologies of the skulls of each species and a hybrid, we can determine the pattern and mode of evolution in this group. This study involves three-dimensional geometric morphometrics and comparative analyses across the skulls to derive any significant differences. The results of this analysis find that these pupfishes still cannot escape the extremely modular functional 4-module system despite undergoing adaptive radiation, but they demonstrate differences in the magnitude of overall integration. Therefore, these pupfishes reveal the strength of integration models, adding greater understanding to the process of adaptive radiation and the field of evolution as a whole.

Gas Reporter System to Monitor Bacterial DNA Transfer in Soil

Andy Corliss | Mentor: Malyn Selinidis

Bacteria share genes through many methods, collectively known as horizontal gene transfer (HGT). HGT impacts bacterial evolution, metabolism, and the spread of antibiotic resistance. Soil is a primary environment where HGT occurs, but *in situ*

studies have been hindered by a lack of suitable tools for opaque matrices. To streamline soil HGT studies, we developed a robust, real-time reporter using the enzyme methyl halide transferase (MHT). MHT produces CH3Br gas which escapes soil for measurement but is too leaky to study rare HGT events. To tightly control gas production, the MHT transcript is split into halves that splice together as RNA by a ribozyme. The recipient strain produces one half, and the other half is coded on a conjugation plasmid in the donor strain. When both strains occupy the same environment, the donor will give its plasmid to the recipient (an HGT event), and the two halves will combine to produce the gas signal. We implemented this tool in *E. coli* in real soil to successfully monitor HGT and are now testing in soil microbes like *P. putida*. We plan to use our tool to investigate how different soil properties affect HGT rates.

Examining the Role of FGF Signaling Pathway in the Development of the *Danio rerio* Enteric Nervous System

Camila DeAlba | Mentor: Lucia Rivas

The enteric nervous system (ENS) plays a crucial role in gastronomical motility and various gastronomical functions such as secretion, nutrient absorption, immune regulation, and defense. Little is known about the differentiation and development pathways of the ENS, but increased research could lead to a better understanding of how it is affected in diseased states. Data from the Uribe lab's single-cell RNA sequencing of zebrafish neural crest-derived cells has uncovered an active Fibroblast Growth Factor (FGF) signaling pathway in the enteric neuron lineage and shows high expression in enteric neurons. FGF family members play several roles in the cell including assisting in repolarization, microtubule stabilization, and cell proliferation. Previous experiments using SU5402, a broad inhibitor of the FGF pathway, demonstrated severe defects in the ENS of zebrafish. To further characterize the FGF pathway in the development of the ENS, we used SU5402 to inhibit the FGF pathway and examined how it impacted cell migration, proliferation, and differentiation into various neuron subtypes. Phenotypic observations were made using live imaging and immunohistochemistry.

Do Early Life Experiences With Social Isolation or Social Competency Impact Aggression in *Drosophila melanogaster*?

Autumn Hildebrand | Mentor: Julia Saltz

Interacting with others in a social context may allow individuals to learn social competency. Social information production, that is, information that is derived from another individual through observation, can dictate how aggressive the initial individual is. I predict that exposure to other individuals during the early stages of life coupled with a social audience upon maturation plays a significant role in how an individual will behave. In this experiment, I am using 4 genotypes of *Drosophila*

melanogaster that have either been socially isolated or socially exposed for four days and afterward, recording their aggressive behaviors against a standard opponent. Changes in aggression for flies in the presence or absence of an observer varied with socially competent or socially isolated treatments would suggest social learning via social information plays a significant role in dictating an individual's behavior.

Investigating the Role of PEX11 in Peroxisome Function and Morphology

James Hwang and Nayeli Shad | Mentor: Bonnie Bartel

Peroxisomes are critical eukaryotic organelles that sequester fatty acid β-oxidation and other metabolic processes dependent on peroxins, or PEX proteins. One such peroxin is PEX11 implicated in membrane shaping and peroxisome division. However, the mechanisms by which PEX11 isoforms influence peroxisome phenotypes remain largely uncharted. Thus, our objective is to investigate the role of the PEX11 family in peroxisome function and plant physiology. We first designed a CRISPR-Cas9 multi-guideRNA strategy to knock out all five *PEX11* genes in *Arabidopsis thaliana*. We show that *pex11a pex11b* and *pex11c pex11d pex11e* mutants display enlarged peroxisomes nearly void of intralumenal vesicles (ILVs), implicating an unanticipated role for PEX11 in sculpting peroxisome membranes. We also examined the physiology and protein levels of *pex11* mutants throughout development. Finally, we tested the ability of PEX11 isoforms from humans, yeast, and moss to restore peroxisome function to *A. thaliana pex11* mutants. These experiments illuminate the mechanistic role of PEX11 in ILV formation and the evolutionary conservation of PEX11 family members across biological kingdoms.

Mutations in Type V Collagen has varied affects on different aged mice

Barakat Ibrahim | Mentor: Keren Machol

Investigating the function of PEX3 in peroxisomes in *Arabidopsis thaliana*

Mohammad Khuroo | Mentor: Ana Swearingen

Peroxisomes are organelles that have detoxifying functions within the cell and can be studied using *Arabidopsis thaliana* as a model organism. Intralumenal vesicles (ILVs) are spherical structures found within the peroxisome lumen. Proteins localize to these internal membranes, including peroxins (PEX), which are proteins that help with peroxisomal biogenesis. PEX3 helps with early peroxisomal membrane protein insertion. PEX3 has two isoforms: PEX3A and PEX3B. To explore the function of PEX3 in ILVs, we used CRISPR/Cas9 to generate viable PEX3 mutants. We identified mutant lines that are homozygous for loss-of-function mutations in PEX3A and a

null mutation in PEX3B and performed seedling growth assays on these mutants to identify peroxisome-related phenotypes. We isolated one homozygous embryonic lethal mutant line with a 1-bp indel in pex3a and three homozygous lines of viable pex3a pex3b mutants with either a missense or an in-frame mutation. We have crossed these mutants to plant lines expressing difluorescent reporters through which we can visualize peroxisomal ILVs in the mutants. This work will expand our understanding of peroxisomal biogenesis disorders in humans.

Isolating and characterizing Arabidopsis thaliana pex8 double mutants to determine the role of PEX8 and its peroxisome targeting signals in peroxisome protein import

Niamh Ordner and Isabella Bartos | Mentor: Bonnie Bartel

Peroxins (PEX) proteins are involved in the biogenesis of peroxisomes, dynamic organelles that perform critical enzymatic reactions, including β-oxidation. In yeast, Pex8 is necessary for post-translational import of lumenal peroxisome proteins from the cytosol; however, a Pex8 homolog has yet to be found in plants or mammals. Using HHPred structural homology software, we identified a novel PEX8 candidate in the model plant Arabidopsis thaliana that shares predicted structural similarities with fungal Pex8. We hypothesize this candidate is orthologous to yeast Pex8. We are investigating the function of candidate PEX8 and its peroxisome targeting signals in peroxisome biogenesis by exploring peroxisome morphology and import in pex8 mutants and by characterizing the genetic interactions of pex8 mutants with existing peroxin mutants. We will use physiological assays that test pex8 pex double mutants' ability to perform β-oxidation, which requires lumenal enzymes, as proxies for peroxisome import function. This research will clarify the process of peroxisome biogenesis in plant and mammalian cells, which could aid in crop development and treatments of fatal genetic diseases.

Transcriptional Regulation of Dnmt3a2 in Adaptive and Maladaptive Reward Learning

Cameron Osterman | Mentor: Laura Lavery

Changes in DNA methylation in activity-dependent learning and memory are required for memory and are mediated by *de novo* DNA methyltransferase 3 alpha (*DNMT3A*). During adaptive learning (AL), transcription of the DNMT3A isoform *Dnmt3a2* is induced by Ca2+ influx through N-methyl-D-aspartate (NMDA) receptors. *Dnmt3a2* is also upregulated by cocaine-induced maladaptive reward learning (MAL), though dopamine receptor (DR) activation is required. Since *Dnmt3a2* transcription is mediated by different receptors in AL vs. MAL, I hypothesize the mechanism of *Dnmt3a2* transcription in AL vs. MAL will differ. To test, I am modeling AL/MAL in primary striatal neurons in conditions that induce

Dnmt3a2 transcription and screening candidate transcription factors (TFs) by comparing *Dnmt3a2* expression following NMDA/DR activation with or without candidate TF knockdown. TFs that show decreased Dnmt3a2 transcription will be validated for direct binding to cis-regulatory elements by CUT&RUN in matched conditions *in vitro* and *in vivo*. Results from this study will impact understanding of the epigenetic mechanism underlying AL/MAL and highlight therapeutic targets.

Expression of *fgf13b* Crispants in *Danio rerio* During ENS Development

Alexander Suh | Mentor: Lucia Rivas

The gut is regulated by a system of coordinated neurons and glial cells, forming the Enteric Nervous System (ENS). Through the ENS, the gut is able to perform essential functions such as peristalsis and blood flow. The ENS originates from neural crest cells (NCC) migrating towards the gut, becoming progenitor cells that eventually undergo differentiation into enteric neurons. Data from the Uribe's Lab single cell RNA sequencing revealed subtypes of zebrafish NCC derivatives, including enteric neurons. This analysis produced an atlas of NCC-derived cells and their gene expression in zebrafish. Components of the Fibroblast Growth Factor (FGF) pathway were seen to be expressed during the differentiation of enteric NCCs to enteric neurons. To understand the effects of the FGF pathway on the ENS, we performed CRISPR/cas9 mediated mutagenesis on zebrafish using a designed fgf13b guide RNA. With the addition of whole mount immuno-coupled hybridization chain reaction (WICHCR) and confocal imaging, the expression of fgf13b and other FGF related probes in transitioning NCCs can be visualized. These results will help better understand the function of fgf13b in the development of the ENS.

Determining the Binding Constant Between Collagen Mimetic Peptides and the α2-I Domain

Maria Telesforo | Mentor: Tracy Yu

Surfactant Protein A (SP-A), is a critical immune protein that is part of the "defense" collagen family. When SP-A binds to the α2β1 integrin it mediates immune complex formation, facilitating phagocytosis. Exploration of the amino acid sequences responsible for this communication is critical in developing artificial immune proteins. Our lab has used collagen mimetic peptides (CMPs) to model rat SP-A and to discover this amino acid sequence. After creating an extensive library, three design peptides were used to confirm the amino acid sequence responsible for binding. To ensure the correct folding, covalent capture was used to hold the trimer together and increase the stability and folding kinetics. Cell binding assays using HT1080 cells confirmed the new α2β1 binding motif in SP-A, but did not provide a binding constant. This project focuses on a proof of concept to determine the

binding constants between our CMPs and the α2-I domain. A fluorophore was attached to a covalently captured "GFOGER" trimer via a succinimidyl-ester amine reaction. Then, the binding constant between this peptide and the expressed α2-I domain protein was determined via fluorescent polarization titration.

Peptide Macrocyclization between Lysine and Introduced Sulfoximine Residue via an ex situ Gaseous Species

Baorui Xiang | Mentor: Zachary Ball

Two-particle Dynamics in the PRBM

Tian Xue | Mentor: Matthew Foster

So far, most theoretical studies of quantum ordered states assume that the system is translationally invariant, but this is not true in real materials. Classical intuition suggests the disorder is bad for forming homogeneous order, but recent work has shown that sometimes disorder can enhance the homogeneous order of the material due to quantum effects. Xinghai Zhang in Prof. Foster's group has found the enhanced amplitude of superconductivity in Aubre-André and a disordered system power-law random-banded matrix model (PRBM). This conclusion surprisingly suggests the homogeneous order of the system is enhanced by the random interactions, but this effect is observed with mean field approximation. How the wave function exactly behaves still remains unclear. Our research aims to solve the two-particle system exactly by exact diagonalization. By this method, we observed delocalization of the wave function and an trend of enhanced superconductivity near the Metal-Insulator-Transition (MIT).

Cancer: Biology, Prevention and Therapy

Early Detection of Cutaneous Melanoma Using Nanoparticle-Assisted Near-Infrared Reflectance Imaging

Kayla Bierman | Mentor: Gabriel Sawakuchi

Skin cancer, with melanoma being the deadliest form, is the most common type of cancer in the United States. The five-year survival rate drops 61% between early-detected melanomas versus when there is advanced metastatic disease, highlighting the need for early detection. Current screening techniques for skin cancer have limitations including lack of efficacy, subjectivity, and extensive cost and training. We propose a novel screening method utilizing a modified commercial photography camera for near-infrared (NIR) light detection, a NIR source, and gold nanoparticles (AuNPs) that reflect NIR. This integrates morphological and molecular information in a large field of view, offering a cost-effective and easily

adaptable solution to skin cancer screening. We hypothesize that melanoma can be detected using NIR reflectance imaging of AuNPs molecularly targeted to melanoma cells. Our preliminary data supports the feasibility of using AuNP's NIR reflectance properties to image melanoma cells, and that commercial photography cameras/lenses have sufficient spatial resolution to observe internalized AuNPs in cells. Our results will improve the early detection of melanoma.

Development and Evaluation of an Imaging Flow Cytometry Panel to Analyze TROP2 Clinical Trial Samples

Sophia Cha | Mentor: Banerjee Pinaki

Real-Time Live Imaging of Osteoclast Activation via Nanoluciferase-based Probe

Josie Feeney | Mentor: Yixian Wang

The bone is the most frequent site for metastasis comprising 70% of all cancer patients. Studying the bone tumor microenvironment is key for detecting bone metastasis. Cathepsin K (CSTK), an osteoclast-secreted protease implicated in bone metastasis, is positively correlated with tumor progression. Understanding the expression pattern of CSTK's expression pattern can inform treatments for different cancers. However, the lack of tools to study in vivo expression impedes new drug development, and current techniques like biopsy are invasive. Here, we developed real-time noninvasive fluorescence imaging of CSTK using NanoLuc (Nluc) and a Z-Leu-Arg-QTZ probe. We found that our two enzyme system preferentially targets osteoclast activity. In vitro studies showed a linear relationship between CSTK probe concentration and intensity, decreased luminescence in the CSTKi probe system, and no luminescence in the D, L probe. In vivo studies evinced greater luminescence in murine tibial bone than in mammary fat pad, indicating the probe's bone niche specificity. Thus, our findings show that CSTK is an effective tool to track pathological osteoclast activity and investigate new treatments.

Assessing Vitamin C Deficiency in Pediatric Cancer Patients

Marissa Giangiorgi | Mentor: Nadia Agha

Background: 70% of cancer patients are vitamin C deficient vs 7.1% of the general population. Deficiency correlates to lower quality of life and faster cancer progression. Current research is limited to adults. Vitamin C deficiency could have more consequences in children due to developmental needs. We aim to determine the prevalence of vitamin C deficiency in pediatric cancer populations and determine associated risk factors. Methods: Cross-sectional study with cancer

patients 6-39 years old at MD Anderson/Texas Children's Hospital. Data included demographic, clinical and physical activity data. Vitamin C blood serum drawn quarterly for 2 years. Dietary intake estimated using food diary. Results: 108 participants, mean age 17.74 (±6.157), 40.7% female, 52.7% non-Hispanic White, 73.1% alive. 45.9% of participants were deficient. Analysis of additional risk factors in progress. Conclusion: It was common for patients to be vitamin C deficient. Older age, male sex, no cancer surgery, and more hospitalizations raised the risk of vitamin C deficiency. Further research is necessary to determine guidelines for the evaluation and management of vitamin C deficiency in this population.

Impacts of tRNA Methyltransferase 1-*like* on tRNA Structure and Function

Cindy Han | Mentor: Catherine Denicourt

Recent discoveries highlight modification of noncoding RNA as a key layer of gene expression regulation. Transfer RNA (tRNA) are the most modified RNAs. Modifications affect tRNA structure and thus function in translating mRNA during protein synthesis. This control at the translational level of gene expression influences adaptation to stimuli. Here, I focus on the understudied tRNA methyltransferase 1-*like* (TRMT1L). Lab CLIP-seq data revealed TRMT1L interacts with tRNA-tyrosine and tRNA-cysteine. While Nanopore sequencing data indicated TRMT1L catalyzes a N2,N2-dimethylguanosine (m2,2G) modification on unprocessed tRNA-tyrosine, mass spectrometry suggests it mediates modifications installed by other enzymes on tRNA-cysteine. To determine if TRMT1L is sufficient to methylate *in vitro* transcribed tRNA-tyrosine and to confirm if tRNA-cysteine is indeed not an enzymatic substrate, I will conduct an *in vitro* methylation assay. This work will clarify a mechanistic model of TRMT1L function drawn mainly from reverse genetics approaches. Future work includes defining required elements of TRMT1L substrates and testing if tRNA-derived fragments are among those substrates.

Development of an *Ex Vivo* Assay for STING Agonist-Mediated Dendritic Cell Activation

Arman Hassan | Mentor: Simon Young

Stimulator of interferon gene (STING) agonists, such as cyclic dinucleotides (CDNs), have potential to drive antitumor immunity in several cancers, including head and neck squamous cell carcinoma (HNSCC). We previously established that peptide-based hydrogel delivery systems improve the efficacy of CDN monotherapy in HNSCC preclinical models. However, the immune mechanism leading to this improved survival is not entirely known. We hypothesize that CDN-mediated dendritic cell (DC) activation may lead to tumor regression in our HNSCC preclinical models. To test our hypothesis, we will develop an *ex vivo* assay to investigate DC activation by CDN treatments. Successful development of an *ex*

vivo dendritic cell culture protocol is critical for our project. Currently, we are optimizing conditions to derive dendritic cells from murine bone marrow. Future studies will include flow cytometric analyses to confirm DC activation. Collectively, these studies will provide tools to better understand the STING agonist CDN-mediated DC activation process and how this plays a role in tumor regression in preclinical HNSCC models of oral cancer (Supported by NIH R01 DE030140 to Simon Young).

Drug-Antigen Combinations to Induce Tumor-Specific Immune Activation in a Local Cancer Vaccine Delivery Platform

Nikitha Kota | Mentor: Corrine Chua

Cancer vaccines aim to mount an anti-tumor response through prolonged immunomodulation. However, effective cancer vaccine delivery to generate a potent anti-tumor response is challenging. To overcome this obstacle, we developed the NanoLymph, a vaccine platform that triggers immune activation through continuous delivery of immune adjuvants and cancer antigens to locally recruit and modulate dendritic cells, thus alleviating the toxicities associated with systemic drug delivery. To establish a clinical relevance for this device, we applied a mixed lymphocyte approach to establish that melanoma associated AH-1 antigen could promote T-cell responses. We co-cultured T-cells with antigen-activated dendritic cells and then subsequently assessed T-cell activation through flow cytometric quantification of surface marker expression. Next, the potency of CCL21 as the strongest dendritic cell chemoattractant was confirmed through a cell migration assay. These results will guide the selection of drug and antigen combinations to apply in the NanoLymph, with the goal of promoting a clinically relevant immune response towards certain solid-state tumors.

Exploration of Peptide Homology Signal Transmission in Dendritic Cells

Arnav Murthy | Mentor: Sharon Amanya

T helper type 1 (TH1) responses are critical for anti-cancer immunity. Previous work suggests that TH1 immunity is elicited by detection of homology between bound antigenic peptides on dendritic cell (DC) MHC class I & II. Sensing is mediated by the multi-aminoacyl-tRNA synthetase complex (mARS) which in turn transmits homology signals through the mammalian target of rapamycin complex 1 (mTORC1). How this signal is transmitted from mARS to mTORC1 is yet to be understood - a gap we aim to fill. My project studies Rags, small G proteins heterodimers known to transmit amino acid sensing signals through mTORC1. CoIP showed direct interaction of RagA with mARS, which diminished following homologous antigenic loading. Western blotting for total RagA was similar across all experimental conditions suggesting that homologous loading specifically inhibits RagA binding to mARS. I plan to explore the effect of homologous loading

on Rag GTP/GDP state through coIP of GTP. Findings from this study will further elucidate mechanisms by which amino acid homology is transmitted from mARS through mTOR to regulate TH1 polarization which may be harnessed to enhance cancer immunotherapy outcomes.

Mutation at Rad21 Cleavage Site Potentially Inhibits Apoptosis

Mary Perez | Mentor: Debananda Pati

Apoptosis is an essential pathway used for programmed cell death when cells deviate from the normal profile. When this pathway is inhibited, it can lead to tumorigenesis and treatment-resistant disease. We suspect we have found a mutation at position 279 on the Rad21 protein that inhibits this apoptotic pathway and leads to chemotherapy resistance. Rad21, a vital structural component in the cohesin complex, is involved in a multitude of crucial functions within the cell. The protein not only contributes to sister chromatid cohesion, but has also been shown to play a role in initiating the apoptotic pathway. The D279V mutation on the Rad21 protein inhibits this initiation of apoptosis by affecting the proteolytic cleavage of Rad21. To illustrate the effects of this mutation, a Western blot analysis was performed and stained with the hRad21 pAb and myc pAb. A cell viability assay with CellTiter-Blue was completed to analyze the apoptosis levels. When cells with this mutation are exposed to apoptosis stimuli, they do not go through programmed cell death as intended. This leads to the possibility of cancer immortality and resistance to chemotherapy.

Nadk Knockout in KC Mouse Model Slows Pancreatic Ductal Adenocarcinoma (PDAC) Progression

Nishita Prasad | Mentor: Sarah Elsea

Pancreatic ductal adenocarcinoma (PDAC) is an aggressive cancer with many hurdles to diagnosis. It is increasingly important to develop effective treatments against PDAC. The progression of PDAC is due to oncogenic drivers - one of which is a gain-of-function NAD kinase variant (NADK), involved in regulating cellular redox levels and NADP/NADPH homeostasis. This variant was only found in one PDAC case during initial study, but even without this variant, wild-type NADK is overexpressed in PDAC cases. This project aims to understand how wild-type Nadk is involved in PDAC tumor development in the KC mouse model. By knocking out Nadk specifically in mouse pancreas cells, we confirmed that the rate of PDAC growth is slowed. Using immunohistochemistry and in vivo/in vitro imaging systems, we also found the number of tumor lesions and percentage of tissue fibrosis were halved in KC-Nadk-/- mice. RNA-seq also indicated lower expression of glutaredoxin and glutathione reductase, genes related to oxidative stress, in some of the knockout mice. Ultimately, these results indicate that developing a

therapeutic targeting NADK may be effective in decreasing the rate of pancreatic tumor growth.

Mathematically Modeling Progression of Low-Grade Gliomas

Devika Shankar | Mentor: David Hormuth

Gliomas are the most common primary brain tumors. Low-grade gliomas (LGGs) typically are slow-growing; however, patient prognoses vary greatly and some LGGs have more aggressive characteristics similar to high-grade gliomas. Mathematical modeling provides insights into the dynamics of aggressive LGGs, facilitating improved therapeutic outcomes. A model representing growth kinetics and simulating tumor progression over time under various conditions has been developed to identify key factors impacting growth rate. To validate the model's accuracy, patient-specific clinical data is used. LGGs are contoured from post-gadolinium T1-weighted and T2 FLAIR MRI sequences taken at different time points. Values for gross and clinical target volume as well as total tumor cellularity are extracted and used to estimate mathematical model parameters to predict progression. This quantitative imaging and mathematical modeling approach may allow for optimizing treatment strategies for aggressive LGGs. By integrating patient data and exploring therapeutic scenarios, the model provides valuable insights into LGG progression dynamics, enabling improved clinical decision-making and patient outcomes.

Barriers and Facilitators to Technology-based Health Interventions Among Rural Adults and Rural Cancer Survivors

Jenna Shi | Mentor: Scherezade Mama

Rural adults and rural cancer survivors in the United States experience disparities in health care access compared to their urban counterparts, which contribute to health behaviors like physical inactivity and obesity. Amidst the COVID-19 pandemic, online health interventions gained popularity, but there is limited knowledge about the experiences of rural adults and rural cancer survivors engaging with these interventions compared to in-person interventions. This qualitative study aimed to explore the barriers and facilitators to participating in technology-based health interventions among rural adults and rural cancer survivors. Participants (N=20) from Northeast Texas participated in a 1:1 interview via Zoom and completed a demographic questionnaire. Interviews were transcribed and coded using a thematic analysis approach, and important quotes were identified and organized into themes. Emergent themes included: 1) Positive aspects of intervention delivery; 2) Negative aspects of intervention delivery and 3) Future steps for delivery improvement. These results depict the multifaceted online health intervention experience of rural adults and rural cancer survivors.

The Effect of DHPS Gene in Breast Cancer Progression

Jessica Suh | Mentor: Ming Zhu

Breast cancer is the most common cancer that women are diagnosed with, with over 2.3 million cases worldwide in 2020. Although there have been many advancements in the monitoring and treatment of breast cancer, triple negative breast cancer (TNBC) is an aggressive form of breast cancer that lacks positive markers, which means that it is difficult to find proper chemicals and drugs to treat TNBC. This project looks specifically at deoxyhypusine synthase (DHPS) as a potential therapeutic target in TNBC treatment. DHPS is an enzyme involved in hypusination, which is a post-translational modification that converts lysine to hypusine. DHPS is shown to be involved in regulating protein translation and cell proliferation, and past studies have indicated the potential role of DHPS in TNBC. The goal of this project is to better understand how DHPS affects TNBC tumor progression and metastasis. This will be accomplished by knocking out the gene to study its effect on cell proliferation, as well as overexpressing mutations to analyze the effect on the phenotype of the breast cancer cell line, using MDA-MB-231 cells.

A role for the interaction between DNA-dependent protein kinase (DNA-PK) and TAZ in inducing glioma stem-like cell (GSC) radio-resistance

Tiffany Tang | Mentor: Krishna Bhat

TAZ is a transcriptional cofactor highly expressed in 70% of glioblastomas (GBMs), a virtually incurable brain tumor. Glioma stem-like cells (GSCs), a particularly resistant subpopulation of GBM, overexpressing TAZ undergo a proneural to mesenchymal subtype transition, which is accompanied by aggressive phenotypes like increased treatment resistance. However, the molecular mechanisms of TAZ-mediated cell fate transition and GBM treatment resistance remain elusive. We previously identified a novel interaction between DNA-dependent protein kinase (DNA-PK) and TAZ in response to ionizing radiation (IR) treatment in GSCs. Here, we extend our previous findings to contextualize the significance of this novel interaction in altering sensitivity to IR. We demonstrate that prolonged culture of GSCs treated with etoposide increases TAZ expression. Furthermore, siRNA knockdown of TAZ increases the number of γH2AX foci post-IR. A combination of IR and DNA-PK inhibitor treatment in GSCs reduces the half-life of TAZ compared to GSCs treated with IR, implicating the role of the recruitment of TAZ to DNA damage breaks and its resulting interactions with DNA-PK to induce radio-resistance.

Investigating the Role of Antigen Density on CAR Immunological Synapse Avidity

George Tataris and Anvita Wadhwa | Mentor: Sybrina Kerr

CAR T cells are prime immunological tools in combating relapsed or refractory cancers. CAR T cells show remarkable efficiency against leukemia and lymphoma, but not against solid tumors. Our project endeavors to elucidate the intricacies of the interface between a CAR T cell and its target tumor cell and how this influences cytotoxicity. We hypothesize that the diminished efficacy of CAR T cells against solid tumors may be attributed to sub-optimal antigen-dependent activation at the CAR immunological synapse (CARIS). To investigate this hypothesis, we genetically engineered a glioblastoma cell line, LN229, to generate tumor cells expressing a gradient of HER2 antigen densities. This was achieved by subjecting the tumor cells to varying numbers of transduction cycles with HER2-encoding gamma retroviruses. Our findings demonstrate the feasibility of creating a gradient of HER2 antigen density on LN229 cells. In subsequent research, we aim to evaluate CAR T cell cytotoxicity, phenotype, and immune synapse avidity using these engineered tumor cells. Our long term objective is to enhance HER2-specific CAR T cell efficacy against solid tumors by optimizing the CARIS.

The Effects of Light-activated Molecular Jackhammers for Cancer Treatment

Zicheng Wang | Mentor: Ciceron Orozco

Different molecular machines are discovered and utilized to mechanically destroy biological structures. A light-activated MNM with a unidirectional Feringa-type rotating motor was first confirmed to open pores in the cell membrane causing rapid necrotic cell death. Those motors, however, require fluxes of photons with shallow penetration for activation. Further research has revealed that mechanical cell damage can also be accomplished by using modified cyanine dyes. Compared with the Feringa-type motors, the cyanine molecules with cancer-targeted ability can be activated by near-infrared (NIR) light with higher optical penetration in vivo. Those molecules rely on the molecular plasmon for driving a super-fast concerted-whole-molecule vibration in the THz range to first bind and mechanically disassemble the membrane of the cancer cells. These vibrational oscillations at ~40 THz are 7 orders of magnitude faster than the rotation of the fastest Feringa-type motor (3 MHz). The coupling of electronic mode and vibrational modes mentioned is named as vibronic-driven action (VDA). These VDA-capable cyanine molecules are also named Molecular Jackhammers (MJHs) for their vibration pattern.

Quantitative assessment of HSP90-stress-induced genome instability

Zoe Wang | Mentor: Tin Pham

SESSION 3

Human Development, Health, Performance and Disease

A High-Throughput Screen Uncovers Key Regulators of the Mitochondrial Surveillance Pathway

Yvette Acevedo and Alicia Chan | Mentor: Natasha Kirienko

Mitochondrial dysfunction is at the core of a series of metabolic, neurodegenerative, cardiovascular diseases, cancer, and aging. To maintain mitochondrial homeostasis, multicellular organisms have developed multiple surveillance mechanisms. Previous research in *Caenorhabditis elegans* has shown that a key component of mitochondrial surveillance, the evolutionarily-conserved Ethanol and Stress Response Element (ESRE) pathway, is activated in response to reactive oxygen species, liquid-based infection with *Pseudomonas aeruginosa*, and mitochondrial damage. The ESRE pathway acts through a DNA element, which consists of a conserved 11-nucleotide motif found in the promoter region of effector genes. However its regulation remains largely uncharacterized. We set out to find key regulators involved in ESRE pathway activation by conducting a screen on a library of transcription factors and kinases using a transgenic worm line expressing GFP under control of ESRE element, which gives a convenient readout on ESRE activation. This work aims to identify a regulatory cascade for ESRE in order to better understand mitochondrial surveillance and prevent or treat mitochondrial dysfunction.

Assessing Meal Planning and Food Preparation Practices among Houston Food Pantry Users

Catherine Cook | Mentor: Dave Jayna

Objectives:
Food pantries play a crucial role in fulfilling the needs of low-income individuals. Meal planning and food preparation practices are essential for food pantry users to maximize resources and ensure nutritional adequacy and optimal health. This presentation aims to explore the meal planning and food preparation practices among food pantry users.

Methods:
Data was collected from 59 participants from 2 food pantries located in the Houston metro area, Texas. Data was collected using surveys including demographics, meal planning (6 items) and food preparation practices (21 items).

Results:
Majority of the participants were female (90%), Hispanic (70%), >41 years old (56%), married (51%), and with a household income of <$21,000 (46%). Food pantry clients showed low scores of 7.69±4.26 for menu planning and 13.88±7.18 for food preparation skills.

Conclusions:
The data suggests that there is room for improvement in these areas. With the majority of participants demonstrating limited menu planning and food preparation skills, interventions aimed at enhancing these abilities are crucial to promoting better nutritional outcomes and overall health among food pantry users.

Huntingtin-HAP40 Core Complex regulates Cellular Homeostasis through Endolysosomal Trafficking in Huntington's Disease

Daniela Covarrubias | Mentor: Sheng Zhang

Aging-related neurodegenerative diseases (NDs), including Huntington's disease (HD), continue to present a significant societal threat as there remain no treatments or cures. HD is a fatal disease caused by hereditary CAG amplifications in the Huntingtin (HTT) gene. Growing evidence connects NDs to disruptions in endolysosomal trafficking, a major cellular homeostasis process. HTT has already been suggested to function in this cellular protective mechanism, yet the specifics remain unclear. HTT is conserved in Drosophila allowing probing of evolutionarily conserved functions across species. We found evidence that HTT controls the size, acidity, and potentially the fusion of endolysosomes, and that HTT binds to endolysosomes potentially through a structural mechanism. Lastly, validation in neurons showed that HTT depletion leads to increased complexity of dendritic arborization neurons, a phenotype associated with alterations in endolysosomal processes. Future work will address how HTT controls cargo trafficking, the exact steps, if polyQ expansion alters those normal functions, and whether modulating this process is a viable therapeutic approach for HD.

Selective Serotonin Reuptake Inhibitors (SSRIs) as Mitophagy-Dependent Treatments for Neurodegenerative Diseases (NDDs)

Mariam Elsharkawy | Mentor: Natasha Kirienko

Neurodegenerative diseases (NDDs) pose a global health challenge, necessitating therapeutics targeting distinct characteristics of NDDs, such as protein aggregation. Mitochondrial autophagy, a selective process for removing damaged mitochondria, has emerged as a potential therapeutic target due to its role in reducing protein aggregation and neuronal loss associated with NDDs, with PTEN-

induced kinase 1 (PINK1) protein activating mitophagy. Leveraging *Caenorhabditis elegans (C. elegans)* models, we investigated the potential of selective serotonin reuptake inhibitors (SSRIs) to activate mitophagy and mitigate NDD symptoms. Our study identifies sertraline and paroxetine as mitigators of paralysis in a model of Alzheimer's disease characterized by β-amyloid protein accumulation. Additionally, fluorescence imaging assays using the P*pink-1*::PINK-1::GFP reporter in a separate *C. elegans* model suggest a mitophagy-dependent pathway as the mechanism of action for paroxetine and sertraline, highlighting the complexity of SSRIs' therapeutic effects. These findings underscore the potential of repurposing SSRIs for NDDs by targeting mitochondrial health and protein aggregation.

A split and inducible adenine base editor for precise in vivo base editing

Peretz Gilberd | Mentor: Zane Zeng

DNA base editors use deaminases fused to a programmable DNA-binding protein for targeted nucleotide conversion. However, the most widely used TadA deaminases lack post-translational control in living cells. Here, we present a split adenine base editor (sABE) that utilizes chemically induced dimerization (CID) to control the catalytic activity of the deoxyadenosine deaminase TadA-8e. sABE shows high on-target editing activity comparable to the original ABE with TadA-8e (ABE8e) upon rapamycin induction while maintaining low background activity without induction. Importantly, sABE exhibits a narrower activity window and higher precision than ABE8e, with an improved single-to-double ratio of adenine editing and reduced genomic and transcriptomic off-target effects. Furthermore, when delivered via dual adeno-associated virus vectors, sABE can efficiently convert a single A•T base pair to a G•C base pair on the PCSK9 gene in mouse liver, demonstrating in vivo CID-controlled DNA base editing. Thus, sABE enables precise control of base editing, which will have broad implications for basic research and in vivo therapeutic applications.

Fibrosis of Ganglionic Intestine May Contribute to Bowel Dysfunction in Human Hirschsprung Disease

Britney Hsu | Mentor: Cheng Lily

Hirschsprung disease (HSCR) is characterized by a deficit of enteric neurons in the distal bowel. Although the proximal ganglionic bowel is considered normal, many patients continue to have persistent bowel dysfunction post-surgery. Our previous study in mice revealed abnormal collagen levels and ECM-related gene expression in ganglionic proximal HSCR colon. In this study, we aimed to characterize differences in collagen content in human proximal ganglionic intestine of HSCR patients (n=6) compared to age-matched controls (n=3), who underwent stoma closure after trauma. Collagen content in submucosa and muscularis propria was

quantified via trichrome staining. Results indicate significantly higher collagen content in HSCR proximal intestine compared to controls. To determine the effects of distension alone, proximal and distal intestine segments from atresia patients (n=3) were compared. Collagen levels were similar between proximal and distal segments, suggesting the elevated collagen content in HSCR is specific to the condition rather than distension. Increased collagen content in the proximal HSCR intestine may contribute to the abnormal function of ganglionic intestine.

Oral microbiome assessment in Alzheimer's disease patients by 16S sequencing

Connie Huang | Mentor: Gena Tribble

Alzheimer's disease (AD) has been linked to dysbiosis of the oral microbiome. At least one pathway through the toxic proteases of oral microbe Porphyromonas gingivalis has been elucidated. The aim of this study was to identify bio markers of AD progression through 16S rRNA gene sequencing of oral swab samples from patients from four groups: healthy control, mild cognitive impairment (MCI), mild dementia due to AD, and moderate/severe dementia to AD. Using Atima software, significant changes in bacterial communities was assessed by disease state, and other demographic variables. Gender did not impact alpha diversity measures (observed species, Shannon index, Simpson index, and Chao1 index). Comparing each progressive AD stage revealed a decrease in both number of bacterial species and diversity in favor of select dominant bacteria, particularly from the Rothia genus. Notably, Shannon index rose between MCI to mild dementia, but decreased more so while going to the moderate/severe AD stage for both hard and soft tissue swab samples. These data suggest a dynamic and changing oral microbiome in correlation to AD progression so that we may further illuminate the causes of Alzheimer's.

Analysis of Cellular Markers in Differentiated Macrophages

Sarah Johnson | Mentor: Holt Christopher

Food allergy is a condition that affects nearly 10% of the United States population. Biomarkers in the food-allergy response include genes such as galectin-3 and TGFβ-1. Research into these molecules has indicated expression in conjunction with esophageal eosinophilia, a physical symptom of the food-allergic response. This work used the human monocytic cell line THP-1 to analyze changes in cellular expression between monocytes and macrophages, immune cells that can initiate food allergic responses. The degree of THP-1 differentiation was tested using phorbol 12-myristate 13-acetate (PMA) in three concentrations, with the morphology being documented after 72 hours of stimulation. Following this, the monocytes and macrophages were analyzed using a flow cytometry panel to

confirm differentiation by analyzing cell-specific markers. The two cell types were then stimulated using lipopolysaccharide (LPS) and raw shrimp extract. Expression of galectin-3 and TGFβ-1 post-stimulation was quantified with qPCR. By analyzing the changes in cellular expression, we hope to gain insight into the role of galectin-3 and TGFβ-1 in the THP-1 post-stimulatory response in food allergy.

Elucidating the Role of Peroxisomal E3 Ligases in Pexophagy

Sydney Lagard | Mentor: Sydney Lagard

Peroxisomes are metabolic organelles essential to eukaryotic life. In plants, such as Arabidopsis thaliana, peroxisomes are involved in stress response, fatty acid β-oxidation, ROS/RNS detoxification, etc. Peroxisomal quality control is maintained via pexophagy and ubiquitination. Pexophagy facilitates peroxisomal degradation via phagophore formation and nutrient recycling. Ubiquitination is a post-translational modification that attaches ubiquitin to a target protein to facilitate degradation. Little is known about the relationship between pexophagy and ubiquitination. Stub1, a mammalian E3 ligase, plays a role in pexophagy. MIEL1, an Arabidopsis E3 ligase, localizes to peroxisomes and disrupts peroxisomal morphology when mutated. By comparing AtCHIP (a homolog of Stub1 found in Arabidopsis) to other E3 ligases, such as MIEL1, ubiquitin-dependent pexophagy and overall peroxisomal dynamics will be better understood. My research could potentially answer outstanding questions about peroxisomal disorders in humans, which range from minor implications to lethality.

The effects of Transforming Growth Factor Beta (TGF-β) receptor inhibition in an aged mouse model of chronic cerebral hypoperfusion

Karen Marquez | Mentor: Michael Maniskas

Transforming Growth Factor-Beta (TGF-β) proteins are necessary for recovery following cerebral damage due to their pro-inflammatory response. However, in older adults TGF-β may become elevated, potentially exacerbating white matter injury and astrogliosis, which are implicated as primary drivers of vascular cognitive impairment. We investigated the pathological effects of TGF-β inhibition in a longitudinal sex-difference study of chronic cerebral hypoperfusion, induced by Bilateral Carotid Artery Stenosis (BCAS) surgery. We hypothesize that TGF-β inhibition will result in decreased astrogliosis and decreased white matter injury compared to control (drug and surgical) mice. TGF-β concentrations in brain homogenate were assessed through TGF-β ELISA. Female mice in the BCAS vehicle group had significantly higher concentrations of TGF-β than females in the sham drug group. Additionally we stained for Glial Fibrillary Acidic Protein (GFAP) to assess astrogliotic differences across groups in this study. White matter injury in the striatum, corpus callosum, and hippocampus is currently being analyzed to

assess whether the TGF-β antagonist resulted in observable differences in pathology.

Enzymatic Methylation Sequencing of Mouse Embryos Deficient in Folic Acid Metabolism Protein MTHFD1L

Pratyush Mohapatra | Mentor: John Steele

Folic acid (FA), also known as vitamin B9, is a vitamin that helps form the neural tube of a developing fetus. It plays an integral role in preventing neural tube defects (NTDs) such as spina bifida, anencephaly, and other congenital malformations. Once ingested in the form of a multivitamin, folic acid must be reduced to tetrahydrofolate (THF), a derivative of folic acid, in order to participate in mitochondrial and cytosolic one-carbon metabolism. During the former process, MTHFD1L is an enzyme that catalyzes the last step in the pathway, creating formate from 10-formyl-tetrahydrofolate. Variants of MTHFD1L can interfere with the ability of folic acid to prevent NTDs, and give rise to FA-resistant NTDs. A common MTHFD1L variant (rs3832406) has been associated with NTDs due to altered splicing efficiency of the mRNA transcripts of *Mthfd1L*. The one-carbon metabolism pathway also results in the synthesis of methionine, which can serve as a methyl donor during DNA methylation. Thus, this project centered around enzymatic methyl sequencing of the genome of *Mthfd1L*-deficient mice to investigate potential epigenetic mechanisms that could induce NTDs.

Analysis of Novel Children's Diabetes Prevention Education Program

Dillan Patel, Mia Baumann, Ashley Zhang, Cecile Nguyen and Aditi Velgekar | Mentor: Cassandra Diep

This study investigated the effectiveness of a diabetes prevention curriculum created and delivered by Kid Power: Building Healthier Communities from The Ground Up, health education initiative led by Rice University undergraduates, in Summer 2021. Underprivileged students in a community center participated in an educational program about diabetes prevention education, which was created by the study team of Kid Power. Students were surveyed three times to gauge changes in understanding and lifestyle: once prior to the program and twice following its completion. Overall, there was a demonstrated increase in understanding of diabetes for students participating in the program. There was also an increase in self-reported vegetable consumption and physical activity. Limitations, such as attrition and self-reporting bias, must be noted. However, the results support the curriculum's positive impact for underprivileged students.

Development of High Throughput Phenotypic Assays for Uncharacterized Bacteria

Kathryn Rhatigan | Mentor: Yousif Shamoo

Early response to the spread of disease-causing pathogens can mitigate harm. Wastewater surveillance has proved a useful tool for tracking the spread of known pathogens and can be expanded to search for potential emerging pathogens. Phenotypic assays that can be scaled to screen hundreds of samples are necessary to identify pathogenic traits in unidentified bacteria in wastewater. In this project, two high-throughput phenotypic assays for traits associated with pathogenic behavior were developed. Many human pathogens can lyse red blood cells, so an assay was developed to screen for hemolysis. Hemolysis showed a distinct color change in a narrow range around each colony. Furthermore, the ability to degrade the extracellular matrix is a common aspect of pathogenesis. Gelatinase activity was seen in gelatin agar that was clear around bacterial colonies. Both of these assays were developed to be fast and high-throughput. In the future, these two assays will be used to screen wastewater isolates for hemolysis and gelatinase activity and further assays will be developed to analyze for additional pathogenic traits.

AstroCapsules: a Novel Tool to Detect and Modulate the Neurotrauma Microenvironment

Kat Rosner | Mentor: Samira Aghlara-Fotovat

While neuroinflammation plays a critical role in the host response to injury, it can shift temporally from a reparative to harmful state by inducing fibrosis and scarring, and can lead to severe cognitive and motor impairments when it persists. Building upon previous evidence implicating interleukin-1 receptor antagonist (IL1Ra) as a potential mitigator of inflammation, we transduced human pluripotent stem cell-derived astrocytes to constitutively produce transgenic IL1Ra. Subsequently, we utilized alginate encapsulation technology to form “AstroCapsules”, which were conceived to test the effect upon indirect cocultures in vitro and to protect transplanted cells in the CNS in vivo without need for immunosuppression. We first determined that exposing inflammatory neural organoids to IL1Ra AstroCapsules resulted in a significantly reduced production of inflammatory biomarkers (i.e., CXCL8 and CCL2) compared to control groups. Additionally, we successfully transplanted AstroCapsules into mouse pup brains and found detectable amounts of IL1Ra in the homogenized tissue. Overall, our findings highlight the feasibility of transplanting IL1Ra AstroCapsules to alleviate neuroinflammation.

Exploring Caregivers‘ Perspectives on Technology To Support Caregiving and Aging in Place for Homebound Older Adults

Esha Shenoy | Mentor: Carina Katigbak

Homebound older adults (≥ 60 years) and their informal family caregivers face multiple challenges to meeting their instrumental, emotional, and informational needs which results in lower functional status, multiple comorbidities and poorer mental health. Caregivers are tasked with providing uncompensated care for medically complex older adults often without formal healthcare training. These high levels of burden and greater vulnerability to social isolation and loneliness may precipitate chronic stress which in turn can compromise caregiver health. In recent years, numerous health-focused technologies assisting with health promoting behaviors such as physical activity, stress management, and nutritional tracking have emerged. However, little is known about the acceptability of these tools for homebound older adults and their caregivers. The purpose of this qualitative study is to explore how caregivers of home bound older adults perceive technology in the context of supporting caregiving and aging in place using focus group and one on one interviews.

Loss of the E2 SUMO-conjugating, *Ube2i*, in embryonic oocytes causes impaired ovarian development in mice

Tegan Tien | Mentor: Stephanie Pangas

Errors in meiosis cause infertility and faulty ovarian reserve establishment. SUMOylation, a post-translational modification using the essential enzyme UBE2I, has been implicated in meiosis in the formation of the synaptonemal complex (SC) during Prophase I in yeast cells, but remains unexplored in mammalian models. A novel mouse line was generated by mating female mice with a floxed *Ube2i* allele *(Ube2iloxP/loxP)* with male mice expressing a pre-meiotic germ cell-specific cre recombinase *(Stra8P2Acre)* to investigate the effects of a pre-meiotic loss of *Ube2i*. Preliminary data showed that compared to control littermates, *Ube2i* cKO mice were sterile, producing no pups per litter. Ovaries of 4-week-old control and *Ube2i* cKO females display morphological differences. Histologic analysis of ovaries from of postnatal day 4-week-old control and *Ube2i* cKO females showed a significant decrease in follicle number in the conditional knockout. *Ube2i* cKO females displayed errors in the molecular pathways involved in folliculogenesis which led to impaired oocyte quality, suggesting that UBE2i SUMOylation is required for mammalian oocyte development.

Investigating the impact of ALCAM gene knockout on Lupus Nephritis symptoms in mouse models through systematic testing.

Julie Trinh | Mentor: Chandra Mohan

Lupus nephritis (LN), a common complication of systemic lupus erythematosus (SLE), is primarily caused by T cells. CD6 and its ligand – activated leukocyte cell adhesion molecule (ALCAM) – play roles in T cell activation and trafficking. Recent studies have found that ALCAM was expressed by renal structural cells, whereas CD6 expression was limited to T cells, with a higher number of CD6+ and ALCAM+ cells in LN. Thus, proving that CD6/ALCAM pathway plays a role in LN and SLE and its use as a disease biomarker. This study aims to confirm the contribution of this pathway using n=50 ALCAM KO mouse models. CD6 and ALCAM expression was assessed in LN kidney and spleen cells where we saw a significant difference in CBC analysis in mutant versus wild-type (WT) mice. ALCAM KO mouse models seems to ameliorate anemia and thrombocytopenia in SLE males, while also helping inflammation recovery in anti-GBM LN. Interestingly, there was no statistical significance in BUN, Proteinuria, and GFR analyzed between the mutant and WT mice, as well as, male mice survival rate fell short of expectation for this experiment. These results indicate a need for further testing in 7-8 month old ALCAM KO mice.

Characterizing Growth and Interactions of Three Potentially Beneficial Nasal Bacteria: *Dolosigranulum pigrum*, *Corynebacterium accolens*, *Corynebacterium pseudodiphtheriticum*.

Christina Walker | Mentor: Christina Walker

The bacterial composition of the nasal microbiota has a close association with the severity of respiratory infections. Specifically, infection severity lessens when colonized with commensal bacterium *Dolosigranulum pigrum*. Some microbes that colonize the nasal passages, like *D. pigrum* and *Corynebacterium spp.,* may have inhibitory effects on harmful pathogens like *Staphylococcus aureus* and *Streptococcus pneumoniae*. Studying how these nasal bacterial species interact with each other, genotypically and phenotypically, could help us understand how these bacteria interact in the nasal microbiota. To test this, I cocultured the bacteria and harvested them to determine colony forming unit (CFU) numbers. My poster will discuss how growing *D. pigrum, C. accolens,* and *C. pseudodiphtheriticum* together altered the CFU count versus when grown separately. I will also discuss my process in extracting RNA from the bacterial pellets for sequencing. In the future, I will analyze what genes are differentially expressed as a result of growing these bacteria together. Understanding all components of how these nasal bacteria interact will lend knowledge to the future development of novel therapeutics.

Effect of Metformin Treatment on KSR2 Mutation Induced Oxidative Stress

Jade Xu | Mentor: Stephanie Sisley

Kinase suppressor of ras 2 (KSR2) is an intracellular scaffolding protein modulating AMPK signaling. KSR2 mutations are associated with early onset obesity and insulin resistance in humans. These mutations decrease AMPK activation and binding affinity, which affects cellular metabolism rate and impairs fatty acid oxidation. Previously, metformin was found to activate AMPK and restore fatty acid oxidation rate in variants with KSR2 mutations. In addition, these variants may lead to decreased antioxidant activity, however the effect of metformin has not been studied. Thus, this study explores how metformin treatment on KSR2 mutations affects antioxidant activity. We used HEK293 cells to transfect KSR2 constructs containing mutations. Next, we treated cells with metformin to measure gene expression of the antioxidant enzyme, Glutathione Peroxidase (GPX), in our variants. After metformin treatment, we performed RNA extraction and RT-qPCR to detect GPX expression. Preliminary results showed that metformin increased GPX expression in KSR2 Wild Type transfected cells and partially restored GPX expression in KSR2 variants. We will continue to investigate the role of KSR2 in this pathway.

Aberrant Inactivation of FOXO1 in SCA1

Leo Zhang | Mentor: James Orengo

Spinocerebellar ataxia type 1 (SCA1) is a neurodegenerative disorder caused by a CAG repeat expansion mutation in the ATXN1 gene. Although the primary driver of many clinical features appears to be the loss of cerebellar Purkinje cells, recent studies have implicated a neuromuscular component that causes late-stage atrophy of breathing muscles, ultimately resulting in premature death. Additionally, preliminary studies by the Orengo Lab suggest increased activity of the JNK signaling cascade in motor neurons of a well-characterized SCA1 mouse model. In other neuromuscular disorders, aberrant JNK activation appears to inhibit the activation of FOXO1, a transcription factor involved in pathways that regulate cell death. This study establishes a potential linkage between our JNK findings and motor neuron death by analyzing phosphorylation of FOXO1 at Ser249, which induces nuclear translocation. The results of Western blot and immunofluorescence experiments show decreased Ser249 phosphorylation in SCA1 brainstem and spinal cord samples. Combined with prior experiments studying phosphorylation of FOXO1 at Ser256, these findings show promise for uncovering a novel role of FOXO1 in SCA1.

Elucidating the Role of Candidate Disease Gene *Ccdc136* in the Retina

Karen Zheng | Mentor: Jiaxiong Lu

The Effect of Carboplatin on the Brain

Shungu Zimbwa | Mentor: Anand Singh

More than 75% of cancer patients who receive high-level chemotherapy treatment experience chemotherapy-related cognitive impairment (CRCI) known as chemobrain. Currently, no treatment to cure or prevent these long-term, debilitating effects exists, and the mechanism is poorly understood. To gain a better understanding of the mechanism underlying CRCI, we have created a preclinical mice model using the chemotherapy agent carboplatin to study long-term neurological deficits and performed single nuclear RNA sequencing (snRNAseq) of the hippocampus. Our preliminary data demonstrated dose-dependent deficits in executive and sensorimotor function 7-9 weeks after carboplatin administration in the mice of both sexes. snRNAseq of the hippocampus showed changes in the glial cell number as well as genes associated with oxidative phosphorylation and neurodegeneration at early and late time points. This study established a preclinical model that can be leveraged to mechanistically understand the long-term neurocognitive side effects of chemotherapy. Future studies will aim to identify potential targets to prevent and/or treat the neurotoxic effects of cancer treatment in pediatric patients.

The Earth: Geology, Ecology and Environment

Impact of freshwater inputs on oxygen levels in Bahia Almirante

Liana Awe | Mentor: Mark Torres

Both climate and land cover change are altering the ecological landscape of the tropics. As an example, Panama's extensive coral reefs have been at the forefront of recent discussions involving the impacts of climate change on bodies of water, particularly in relation to oxygen levels. Low dissolved oxygen levels were first documented in Bahia Almirante, Bocas Del Toro in 2010 and cycles of such have persisted ever since. Using a suite of water quality analysis tools, we measured solute concentrations in water samples from the Changuinola, Nigua, Osete, and Pastores rivers, which all flow into Bahia Almirante, to help determine what role, if any, freshwater inputs play in driving oxygen depletion in the bay. Our data may help to paint a clearer picture of how both natural and anthropogenic processes affect oxygen levels in Bocas de Toro, as well as improve the overall paucity of data from tropical regions.

The Effect of a Single Controlled Burn on Soil Nutrient Concentration, pH, and Bacterial Diversity Six-Months and One Year Post Controlled Burn

Amélie Baca, Maia Figueroa, Faustina Ironkwe, Makenna Mack and Emily Rainbolt | Mentor: Caroline McNeil

Controlled burning has many impacts on soil properties. Previous studies have shed light on changes in soil biodiversity, pH levels, and nutrient composition following repeated burns. However, it remains unclear how these properties change over time as soil recovers from a single controlled burn. This project aims to investigate the impact of controlled burning on soil properties over one year. We show the effect of prescribed burning on soil pH levels, diversity and quantity of bacterial communities, and nutrient concentrations, such as nitrogen, phosphorus, and potassium. Soil samples were collected from burned and unburned plots of soil in the Prairie Plots and surrounding areas at Rice University. Samples were plated to analyze bacterial presence and diluted to measure pH levels and determine nutrient concentrations. Preliminary results suggest the biodiversity of bacteria recovers as time elapses from the initial controlled burn.

How do microbes influence aggressive behavior in *Drosophila melanogaster*?

Raleigh Bellard | Mentor: Marina Hutchins

Microbial communities play a vital role in the development and health of their host; in turn the host is physiologically and behaviorally influenced by their presence. Often, how microbial communities influence social behavior is studied in isolated, pairwise interactions. However, this approach ignores how microbes can influence dyadic interactions within larger social groups. Aggression is an important social behavior which influences social structures. I conducted an experiment with *D. melanogaster* to investigate the differences in aggressive behavior in social groups of axenic flies, who have their entire microbial communities removed (n= 22 groups), and flies with an intact microbiome (n = 13 groups). *D.melanogaster* is amenable to this study, as they have a well characterized set of aggressive behaviors. Studying the influence of microbes on aggressive behavior contributes to our understanding of their impact on social behavior in group settings.

Analyzing the Bacterial and Chemical Compositions of Soil Samples at Rice University

Rachel Huber, Jihra Hill, Joy Kim, Megan Phung and Rocky Ren | Mentor: Carrie McNeil

Microbial diversity and chemical contents of soil are essential for ecosystems to thrive. This study evaluates the bacterial and fungal abundance and chemical composition of undisturbed, prescribed-burn, and construction soil samples across Rice University's campus. It is expected that disrupted soil samples will have fewer

microbes, a pH < 6.2 or > 6.8, and lower concentrations of nitrogen, potassium, and phosphorus than soil that was unaltered. UV-vis was used to assess N, P, and K contents of the soil. pH was measured via pH probes. Omega Biotek extraction kits were used to remove and amplify eDNA from the samples. Preliminary results show a sharp decrease of DNA in soil samples from the campus' construction site, and the soil samples from the prescribed burn site show an increase in DNA concentration and diversity. Microbes were quantified by streaking on R2 agar and counted using ImageJ software. The results show the burned soil to have the most microbes, the undisturbed soil to have fewer microbes, and the construction soil to have the fewest. This research directly applies to the ecosystem on Rice's campus and may have implications for the broader ecosystem of Houston.

Geologic Implications of Seismicity Associated with the 2018 Kilauea Eruption

Adam Leff | Mentor: Juli Morgan

In May 2018, the Kilauea volcano on the big island of Hawaii began to erupt along the East Rift Zone. This volcanic activity abruptly ended in mid-August. The initial eruption was accompanied by several large earthquakes and a period of intense seismic activity. While the eruption ended in mid-August, the associated seismic activity continued through September to varying degrees. The seismic activity has been documented in papers others; however, the exact locations of the earthquakes have not yet been determined. Therefore, we do not understand their implications for the volcano's subsurface structures, particularly with regards to the offshore portion. By plotting the earthquakes with depth, magnitude, and time we have been able to identify several interesting features along the onshore and offshore portions of Kilauea volcano. By comparing data from several sources and relocating the earthquakes, we intend to analyze the geological and topographic implications of these interesting events and gain a more complete understanding of the active offshore structures of the Kilauea volcano.

Microbial Growth and Diversity in Water Dispensers from Popular Rice University Locations

Matthew Ochoa and Sophiya Sami | Mentor: Carrie McNeil

Despite filtration and chlorination in public water dispensers, post-filtration analyses of drinking water still reveal bacterial growth. Due to their widespread use in educational institutions, including Rice University, water dispensers pose health concerns due to the risk of microbial pathogen proliferation. In this analysis, we compare the bacteria count and microbial diversity of water dispensers of popular locations on Rice's campus. Water samples were collected from the Recreation Center, Rice Coffeehouse, Audrey's Cafe, Brochstein, and Fondren and then plated on Reasoner's 2A agar plates. The resulting colonies were counted and screened on MacConkey agar for gram-negative bacteria. Our data revealed that Brochstein's

water had the most microbial growth and diversity. This water contained gram-negative bacteria, which has the potential to be more resistant to antibiotics and disinfectants. Our analysis emphasizes the importance of water dispenser maintenance to enhance public safety and minimize the risk of harboring opportunistic pathogens. Further research may elucidate our understanding of the causes of microbial growth in public dispensers.

Investigating Anthropogenic and Environmental Influences on Mammal Food Web Structure in African Ecosystems

Mallory Tucker | Mentor: Annie Finneran

Understanding the structure of food webs offers insight into the stability of ecosystems. However, the primary variables which drive food web structure have yet to be determined. In this study, we investigated whether anthropogenic disturbances or population structure are the main drivers of different metrics of food web structure (connectance, linkage density, and mean food chain length). We assembled community and environmental data for African mammal populations at 170 sites representing tropical, desert, and savannah ecosystems and created food webs documenting interactions at these sites. We created linear models to determine whether anthropogenic disturbances (proportion of endangered species, habitat fragmentation, climate warming, and hunting by humans) or population structure (phylogenetic and functional diversity) were better predictors of food web structure. Preliminary results indicate that climate change reduces primary productivity in African ecosystems, thereby influencing basal consumers in food webs, demonstrating the importance of identifying the influence of anthropogenic impacts on overall food web structure in order to guide conservation efforts.

Materials from the Fundamental to the Complex

Novel Biological Applications of Light-Activated Molecular Motors: Modulating Cell Signaling and Dark Toxicity Studies

Gautam Chaudhry | Mentor: James Tour

Light-activated molecular nanomachines have emerged as promising tools for various applications, including the control of biological processes. Feringa-type molecular motors, which exhibit unidirectional rotation in response to light, have been shown to stimulate muscle contraction through intracellular calcium signaling. However, the limited penetration of visible light hinders their potential for in vivo applications. To address this limitation, we investigated a new class of molecules, aminocyanines, which can be activated using infrared (IR) light and have been shown to kill cancer cells. In this study, we assessed the capacity of

aminocyanines to elicit Ca2+ release and evaluate their toxicity in the absence of light on HEK293 cells. Our results showed that aminocyanines induced strong Ca2+ release when stimulated with IR light, reaching levels of 4 times stronger than baseline values. Toxicity studies revealed EC50 values of 1.23 μM for Cy7.5 amine and 0.92 μM for BL-273 after 24-hour incubation. These findings suggest that aminocyanines present an option for future applications, combining the light-activated control of biological processes with enhanced tissue penetration.

Antibacterial Material for Future Space Travel

Kara Fan | Mentor: Albert Yee

A big challenge of long term space travel is bacteria proliferation in the spacecraft. Bacteria form threatening biofilms, jeopardizing equipment and the health of astronauts. In this study, nanomaterials that can inhibit bacterial growth without cleaning chemicals were created. The antibacterial mechanisms of the nanomaterials were analyzed by comparing how polymer polarity affects bacterial growth. The hypothesis is that polar nanopillar polymers can prevent bacteria growth, which may help explain the mechanisms of bacteria death. Nanopillars were fabricated on polar polymers, polymethyl methacrylate and polycarbonate , and nonpolar polymers, cyclic olefin copolymer and high-density polyethylene via nanoimprint lithography. Pseudomonas (PAO1) were incubated on each surface and biofilm growth was visualized with scanning electron microscopy. The PAO1 colony forming units were measured. Polar nanopillar polymers significantly prevented bacteria growth compared to the control while nonpolar polymers did not prevent bacteria growth. The results suggest that electrostatic interactions between polar nanopillar surfaces and bacterial membrane proteins yield high antibacterial effects.

Elucidating the Mechanism of Secondary Light-switching Response of Rhenium(I) Dipyridophenazine Complex

Cole Holladay | Mentor: Angel Martí

Amyloid-β (Aβ) peptide aggregation has been linked to the development of Alzheimer's disease. Earlier efforts from the Martí group proposed the use d6 metal complexes to probe and modify Aβ aggregates. The photoluminescence emission of the rhenium(II) dipyridophenazine complex ([Re(CO)3(dppz)(Py)]+) increased in the presence of Aβ fibrils. Remarkably, another emission enhancement of the mixture of [Re(CO)3(dppz)(Py)]+ and Aβ fibrils was observed when irradiated with UV light. Previous studies showed that [Re(CO)3(dppz)(Py)]+ oxidized methionine 35 of Aβ fibrils upon UV irradiation. However, the mechanism of this secondary response has not been established. To determine this, dimethyl sulfide (DMS) and the [Re(CO)3(dppz)(Py)]+ complex are used to mimic the microenvironment of the

rhenium complex bound to Aβ. This solution is irradiated with UV light (365 nm) to cause the emission enhancement. Following High Performance Liquid Chromatography (HPLC), mass spectroscopy and NMR data provide information that elucidates the structures of two important interactions between Aβ and [Re(CO)3(dppz)(Py)]+, from which the mechanism in question can be deduced.

Studies Towards the Preparation of Highly Strained Substituted Bicyclic Carbocycles through Ring-Contractive Methods

Pierre Loch-Temzelides | Mentor: Laszlo Kurti

The use of strained carbocycles as bioisosteres for substituted aromatic rings has garnered significant attention in the development of novel active pharmaceutical ingredients (APIs). Structures such as substituted cubane derivatives, bicyclo[2.2.2]octane derivatives (BCOs), bicyclo[2.1.1]hexane derivatives (BCHs), and bicyclo[1.1.1]pentane derivatives (BCPs) have proven viable linkers to preserve spatial orientation of substituents of aromatic rings while avoiding electronic "cross-talking" effects. BCPs and BCHs have attracted particular interest, with incorporation into several novel and existing APIs, but widespread adoption of these motifs has been hindered by difficulties in their preparation.

Herein, studies have been undertaken to access these strained carbocycles through ring-contractive methods utilizing conventional reactivity (Favorskii, Quasi-Favorskii, and Wolff rearrangements). This novel approach would allow the preparation of BCHs and BCPs from corresponding BCOs through double and triple ring contractions respectively, and would simultaneously allow for increased substitution on the bridge methylenes, regions currently difficult to functionalize otherwise.

Exploring *SpySwitch*-Mediated Antibody Fragment Binding to Gas Vesicles: A Step Towards Enhanced GV Cell Purification

Rishab Mandyam | Mentor: Eugene Chung

Gas vesicles (GV) are gas-filled nanostructures made of proteins used for buoyancy in certain prokaryotic organisms. The inside of the protein shell is extremely hydrophobic while the outer membrane is hydrophilic, creating a nanobubble. A particular protein in GVs, called GvpC, wraps around a GV and is used for stability and structure. The ease of binding by GvpC makes it a suitable candidate to synthetically bind a protein of interest to. Recently, there's been growing interest in SpySwitch, a SpyCatcher variant that can create switchable bonds with SpyTag based on pH and temperature, and Lu Lab believes that this may be a suitable connecting protein to bind GvpC to. With previous success in binding GvpC to SpyTag, it is thought that making a temperature/pH dependent binding system

that is reversible may be very beneficial in purifying target cells. The end goal is to be able to bind a gas vesicle to a nanobody through the SpySystem which can then bind to a targeted protein/cell that will ultimately be purified through buoyancy. SpySwitch can enable us to purify proteins even more efficiently by allowing the detachment of gas vesicles after initial purification.

Fabrication of Negatively Charged Crosslinked Microparticles for Inflammation Modulation

Prerna Mohan | Mentor: Ghanashyam Acharya

Both acute and chronic inflammation are associated with several disease pathologies, with 3 out of every 5 people, worldwide, dying due to a chronic inflammatory disease including heart disease, stroke, autoimmune and neurodegenerative diseases.1 During infection or injury, an immune response is initiated, triggering monocyte differentiation into inflammatory macrophages, which secrete proinflammatory cytokines, leading to tissue damage and scar formation.2 Currently, the only available therapeutics targeting inflammation are broad-acting steroids and non-steroid anti-inflammatory drugs (NSAIDs). As a result, there is a need for a therapeutic approach that can target the underlying causes of inflammation to reduce the local inflammation in the target tissue. Previous studies have demonstrated the importance of a negative surface charge of microparticles in inflammatory monocyte sequestration and the capturing of positively charged, proinflammatory cytokines.3,4 Herein, we report several microparticle fabrication methods to produce negatively charged, cross-linked microparticles for applications in reducing local inflammation via a non-pharmacological approach.

Adaptive Microscopy for Phenotype-Activated Single-Cell Screening

Nathan Nguyen | Mentor: James Lee

Microscopy is a backbone in neuroscience research to understand neuronal activities and develop protein tools to visualize cellular and molecular dynamics. Current microscopy relies heavily on preprogrammed imaging protocols that generate data for post-hoc analysis. This manual process limits the complexity and scale of the experiments and lengthens the troubleshooting of protocol design. Here we report SPOTlight, a high-throughput adaptive technique to isolate cells with unique spatiotemporal profiles from heterogeneous populations. The SPOTlight technique involves imaging cells via microscopy, real-time analysis, quantification, visualization, and archiving of multiple visual phenotypes, optical tagging of target cells, and retrieval of tagged cells via fluorescence-activated cell sorting. We demonstrate that smart microscopy can save time and reduce data variation by developing mGold2, a protein for extended imaging experiments with the most photostable yellow fluorescent protein reported to date. Ultimately, we

envision SPOTlight and closed-loop microscopy technologies will accelerate research by discovering tools and methods for recording and understanding neuroscience.

Nanofibrous Peptide Hydrogels Leveraging Histidine to Modulate pH-Responsive Supramolecular Assembly and Antibody Release

Gabriel Saenz | Mentor: Jeffrey Hartgerink

Developing a Sex-Sorter to Control Neural Circuits

Anuska Santra | Mentor: Herman Dierick

Separating males from females for experiments with Drosophila melanogaster is normally done by sorting them under a microscope with a paintbrush based on their morphological differences. The aim of my research is to simplify this sex-sorting strategy by placing drug resistance and drug sensitivity markers directly on the Y-chromosome. This strategy can then be used to specifically select for males or counter select against males depending on the drug that is fed to the population. To make these transgenic constructs, I am using Goldenbraid 2.0 to combine the selection and counterselection marker with a physical marker (green or red fluorescence in the eyes) into a cassette situated between two attPCC sites. I am using Crispr/Cas9 genome editing to introduce the markers in different regions of the Y-chromosome. In the future, I will switch the cassette out with different combinations of selection and counterselection factors using the attPCC system to conduct robust drug testing and determine the efficacy of the sex sorter. Here I present the result of my ongoing selection and counter selection Y chromosome transgenesis.

Synthesis of Glycosylated Peptides and Lipids for Biomedical Applications

Adam Thomas | Mentor: Jeffrey Hartgerink

Glycosylated biomaterials have attracted interest for the treatment of cancer and other complex diseases. As scaffolds for the proliferation of cells and vehicles for the controlled release and targeted delivery of small molecule drugs, glycosylated hydrogels and liposomes demonstrate promise as tunable materials for biomedical applications. Recent work in the Hartgerink lab has shown that loading cargo-containing liposomes into our nanofibrous MultiDomain Peptide hydrogels slows the release of this cargo. This creates a biomaterial combination that enables controlled, localized release of a desired small-molecule payload. Inspired by these findings and the interesting properties of glycosylated biomaterials, this work presents the synthesis of a glycosylated lipid and series of glycosylated Multidomain Peptides. An acetylated carbohydrate is first conjugated to a serine

linker. This can then be used as a versatile synthetic intermediate, able to be amidated to a lipid or used in solid-phase peptide synthesis. These syntheses represent foundational work that will ultimately enable the development of new glycomaterials for applications in drug delivery and regenerative medicine.

Patterns and Origins in Nature

Applying Neural Networks to Regress Scattering Variables at a Novel Muon-Ion Collider

Arturo Amarilla | Mentor: Darin Acosta

This research project explores the application of neural networks to reconstruct the physics variables of Deep Inelastic Scattering in the context of collisions at a novel Muon-Ion Collider. The approach of the MuIC is to substitute the electron beam in the electron-ion collider (EIC) that is in development with a high-energy, high-intensity muon beam as an upgrade. This design allows the generation of muon-proton and muon-nucleus collisions at an unprecedented center-of-mass energy of approximately 1 TeV. These muon-ion collisions will give us important insights into how matter behaves. Thus, by harnessing the collective strengths of different methods, the research seeks to achieve optimum precision in measuring key parameters associated with deep inelastic collisions.

Characterization of the Extracellular Matrix of Migratory Neural Crest Cells in Enteric Nervous System Development of Zebrafish

Jorge Arnez Gonzales | Mentor: Hannah Johnson

The extracellular matrix (ECM) has been identified as a key structural component involved in the migration of neural crest cells (NCCs). NCCs give rise to the enteric nervous system (ENS), a network of neurons that dictate digestive tract functions, such as nutrient absorption and hormone regulation. Danio reiro, the zebrafish, shares 70% of human genes and makes an ideal organism to study ENS development. However, the characterization of ENS ECM throughout development is limited. A bioinformatics approach using zebrafish gene datasets to identify ECM genes of interest related to ENS formation and NCC migration led us to identify syndecan-4 (sdc4) and tenascin-Cb (tncb) as genes of interest due to them being enriched in biological processes related to cell migration. In vivo mRNA labeling in a transgenic zebrafish line with sox10 reporter expression at various time points in ENS development suggests colocalization of tncb and sox10 along important NCC domains in zebrafish, suggesting that NCCs express ECM genes during development. Such colocalization could suggest further ECM gene expression along other developmental stages and thus rationale for further ENS ECM characterization.

Generating and Isolating an Apo Conformation of Stearoyl-Coenzyme A Desaturase 1

Disha Bhattacharya | Mentor: Zhou Ming

Overproduction of SCD1, a fatty acid desaturase, contributes to obesity and cancer progression. Designing SCD1 inhibitors requires a detailed understanding of the enzyme's catalytic mechanism and various conformations. Although the structures of substrate- and product-bound SCD1 imply the existence of a fatty acid-free apo state, this apo state has yet to be isolated. Therefore, we will electrochemically reduce SCD1 in a substrate-free environment, potentially forcing the release of fatty acid products to yield the apoprotein. Product retention will be measured by reverse-phase chromatography, and these data will demonstrate whether fatty acid release by SCD1 is motivated by redox interactions or by substrate intake. Furthermore, the resulting apoprotein may be used for structure determination in future studies. Such a structure could help identify lipid desaturase inhibitors to reverse excessive fat accumulation and slow tumor growth.

Circadian Rhythm Regulators Modulate Neurodegeneration in a *Drosophila* Model of Spinocerebellar Ataxia Type 1

Rhea Cho | Mentor: Ismael Al-Ramahi

Expressing and Pulling Single Molecules of a Novel Pentameric Viral Fiber

Cynthia Deem | Mentor: Yizhi Tao

A newly discovered virus called the Orsay Virus (OV) is currently the only known viral pathogen to naturally infect C. elegans, though its mechanism of cell infection remains largely unknown. The Tao lab has previously shown that OV expresses a fibrous δ protein that functions in both entry and egress stage of the virus life cycle. The OV δ fiber is primarily made of a novel b-bracelet motif. In this project we will use single molecule force spectroscopy via AFM to study the protein domain unfolding and ligand binding potentials of this novel viral fiber. To facilitate AFM analysis, we have made a δ protein construct with three tandem titin Ig-like (I27) domains fused to both N- and C-termini of the δ polypeptide to allow us to observe the pulling of single fiber molecules with AFM. We are currently expressing and purifying this protein before moving on with AFM. We expect to use titin I27 unfolding force peaks as standard to calibrate the virus fiber unfolding and unbinding signals. Determining binding potential of the protein will lead to increased knowledge about the mechanisms of cell entry and may also have interesting biomaterial applications due to its unusual stability.

Understanding the role of pyocins in intraspecific competition in *Pseudomonas aeruginosa* clinical isolates

Yanhan Deng | Mentor: Natasha Kirienko

Pseudomonas aeruginosa is a common nosocomial pathogen that has developed multi-drug resistance to many frontline antibiotics. In addition to its numerous virulence factors that promote bacterial colonization and pathogenesis, scientists also found that some *P. aeruginosa* strains can inhibit the growth of other strains. In our previous research, we found that certain multi-locus sequence types (MLST) such as ST111 are predominant in microbial infections of clinical settings, which seems to be related to their production of R pyocins, a group of bactericidal factors. In this study, we use isolates from pediatric cystic fibrosis patients and 20 isolates from leukemia patients to study the ability of their suppressed culture to restrain the growth of our model strain naturally sensitive to R pyocins.Isolates that inhibit sensor strain are likely of higher risk in hospital settings, dominating other types of *P. aeruginosa*. Characterizing these isolates will help us to understand the role of pyocins in intraspecific competition and characterize the relationship between the pyocin productions and the prevalence of certain *P. aeruginosa* sequence types.

Skin Color Development and CRISPR Genome Editing in the Brown Anole Lizard *Anolis sagrei*

Zoe Griffin | Mentor: Richard Behringer

Visual communication key in many vertebrates. *Scarb1* is a receptor associated with yellow pigment development in birds and fish, and reverse cholesterol transport in mammals. Although *scarb1*'s role is well-studied in many vertebrates, its function in reptiles remain unexplored. In anole lizards, which rely on visual communication cues, *scarb1* expression is correlated with yellow coloration in the dewlap, a flap of neck skin anoles use to communicate. Here, we investigate the role of scarb1 in skin color development of the brown anole, *Anolis sagrei*. We find that this gene is well conserved in *Anolis* and across vertebrates and successfully target *scarb1* with guide RNAs. The goal of this project is to utilize these CRISPR gRNAs to create mutants to study the functional role of *scarb1* in color development in reptiles. We hypothesize *scarb1* mutants will lack yellow pigment in the skin. These data will further our understanding of whether color patterning genes play a conserved role in development across tetrapod species, strengthening our understanding of color-based signaling and the development of these signals in an understudied phylum.

Promotion of Collagen Fibrils Through Phosphoserine and Lysine Pairwise Interactions

Megan Hoang | Mentor: Jeffrey Hartgerink

Characterizing the Role of Peroxins in Pexophagy

Priscilla Ibrahim | Mentor: Makaela Jackson

Peroxisomes have many important roles in the metabolic and biochemical processes within Eukaryotic cell organelles. Peroxisomal structures and functions have been studied in mammals, yeast, and plants to gain better understanding of their role within cellular activities such as pexophagy. Here we take advantage of the ease of working with Arabidopsis to analyze the role of PEX proteins in pexophagy. We isolated A. thaliana plants containing different PEX mutations and performed microscopy and biomolecular assays on transformed plants to monitor fluorescent-reporter cleavages and determine if there are any measurable differences in pexophagy induction or observable physiological differences between wildtype lines and pex mutant lines. These findings can impact the way researchers study and manipulate autophagy in organelles, and even cells in future efforts in this subject.

Agroforestry Impacts on Rodent Populations and Communities Relative to Intact Forests and Intensive Farmland

Maddie Jeffery | Mentor: Amy Dunham

In cultivating daily commodities like coffee, cacao, and vanilla, agroforestry aims to maximize production and habitat conservation. However, its impacts on fauna compared to other habitat types, especially for generalist species like rodents, remain unclear. Most habitats are assumed equally suitable for this flexible order, but diversity in functional traits may yield unknown disparate effects with conservation implications. To address this knowledge gap, I conducted a meta-analysis - screening sources for data on rodent population diversity, abundance, and community composition in response to agroforestry. A preliminary vote-count revealed the relative suitability of agroforests for variably sized rodents, while study sites were assessed for geographic bias. Consistent with studies on other fauna, I anticipate that agroforests support rodents less than intact forests but more than intensive farming systems, though data is likely biased towards the Americas. While future data of broader geographic scope will refine regional trends, this study exposes the need for tailored conservation systems that recognize rodent heterogeneity and fortify knowledge of agroforestry impacts.

Single Cell Sequencing Identifies a Novel Regulator of the Intestinal Stem Cell Lineage

Christina Ko | Mentor: Tyler Jackson

Understanding how intestinal stem cells (ISCs) become dysregulated is significant because this can lead to the development of cancer or gut degeneration. However, much remains to be known about the molecular mechanisms that contribute to such dysfunction. I employ the Drosophila melanogaster midgut as a model for studying how ISCs can become impaired. This is a crucial system as Drosophila stem cells share high orthology with human genes and stem cells. The ISC lineage is as follows: ISCs, enteroblasts (EBs), pre-enteroendocrine cells, enterocytes (ECs), and enteroendocrine cells (EEs). With single-cell sequencing and differential gene expression analysis, I found several uncharacterized genes that may influence ISC function. One of these candidates was Cph (Chronophage), an ortholog of human BCL11A/B transcription factor. Upon knockdown of Cph, there was a significant decrease in the number of EBs, EEs, and ECs suggesting an inability for ISCs to differentiate properly. In addition, there were defects in ISC proliferation. The converging evidence of the above defects demonstrates the power of Drosophila and single-cell sequencing to discover novel stem cell regulators.

Utilizing PARP1 to Improve Large Insertions and Deletions in *Danio rerio*

Katherine Lachman | Mentor: Daniel Wagner

CRISPR-Cas9 technology in zebrafish *Danio rerio* presents exciting opportunities to further understand the human genome and human diseases. Creation of indels is efficient, but creation of larger deletions and homologous recombination remains challenging. We hypothesize that introducing specific chromatin modifications at cleavage sites can modify repair mechanisms in ways that will be useful to engineer the zebrafish genome.

Modification of chromatin by the addition of poly ADP ribose (PAR) can recruit DNA repair machinery to the site of DNA damage. We have fused Poly [ADP-ribose] polymerase 1 (PARP1), to Cas9 to promote the production of PAR at the sites of Cas9 mediated cleavage. We are targeting the *golden* gene which is required for pigment formation as an easily observable output of Cas9 mediated mutagenesis. In our preliminary experiments, we hypothesize that Cas9-PARP will promote larger deletions between Cas9 target sites rather than local indels. In future experiments we will test the efficiency of homologous recombination using Cas9-PARP.

Well-Defined Sodium Complexes for the Hydrogen-Isotope Exchange of Arenes

Ian Lin | Mentor: Samantha Yruegas

Deuteration enables the isotopic labeling of compounds, which has applications in medicinal studies, imaging techniques, and analytical chemistry. Hydrogen isotope exchange (HIE) leads as the most developed method for deuteration, mainly through transition metal mediated C-H activation pathways. However, precious metals of the d-block are rare, expensive, and potentially toxic, which brings up the question of whether using s-block metals could be used as a more abundant, affordable, and biologically compatible alternative. Compared to the environmentally exhausted lithium amides, sodium amides are more reactive than lithium, providing a promising alternative as a sustainable metal catalyst. Currently, sodium amide complexes bearing stabilizing bidentate ligand scaffolds are the only well-defined complexes of this type that have been isolated. Considerable focus has been put to further explore the coordination of these complexes and their activation mechanism in HIE processes. This study demonstrates the feasibility of synthesizing well-defined sodium amide complexes formed from anionic tridentate ligand systems and explores their reactivity for the HIE of organic molecules.

Quantum Corrections to Electronic Transport in Carbon Nanotube Bundles with Ultrahigh Conductivity

Zhengyi Lu | Mentor: Douglas Natelson

Previous studies have revealed the weak localization quantum correction to conduction in solution-spun aligned CNT fibers at low temperatures. However, these studies lack a deterministic explanation to the microscopic electronic transport process in these CNT fibers, especially to the transport dimensionality. Here we present the results of low-temperature magnetic field dependent conductivity measurements conducted on aligned CNT bundles. Using scotch-tape exfoliation and electron-beam lithography, we prepared electrically interfaced bundles. Numerical analysis of the weak localization magnetoresistance provided further insight of the dimensionality of the quantum-coherent transport in aligned cylindrical CNT structures. Moreover, we observed and investigated magnetic field dependent universal conductance fluctuations (UCFs) in conductivity in CNT bundles, which functioned as an additional quantum correction to the electronic transport in CNT bundles. By analyzing the electron phase coherence lengths in these CNT bundles indicated by both quantum correction theories, we discovered a mismatch in scales between different approaches of estimating coherence lengths in CNT bundles.

Determining the enzyme kinetics and structure of Tulane virus protease

Jalen Nguyen | Mentor: Son Pham

Tulane virus is a gastrointestinal virus being used as a research surrogate to human norovirus, a pandemic-causing gastrointestinal virus. Both Tulane viruses and human noroviruses encode for a protease within their genome that cleaves the viral polyprotein into non-structural proteins with different functions, a process necessary for viral replication to proceed. Thus, inhibition of protease activity would effectively hamper viral replication and proliferation, making the viral protease of Tulane viruses invaluable for understanding norovirus protease activity and mechanism. In this study, we expressed the viral protease through recombinant expression in E. coli and purified the protein through immobilized metal affinity chromatography and size exclusion chromatography. For the protease structure, we ran a crystallization screen to screen for protein crystals. We further determined the kinetics of protease cleavage activity using a FRET assay with fluorogenic peptide substrates.

Understanding the Complement of Signaling Genes in Biomphalaria Glabrata

Daniel Peinado | Mentor: Daniel Wagner

Biomphalaria glabrata is a relatively understudied species of freshwater snail that has the ability to become a key model organism due to its adaptability to a lab setting, its well-documented embryonic developmental period, and its reported genome sequence. Many significant genes which exist in key model organisms are also present in B. Glabrata, and understanding the role that these genes play in its development can enhance our current understanding of this species. Through techniques that include PCR, agarose gel electrophoresis, cell transformation, and minipreps, we hope to more clearly understand the role of Wnt genes in B. Glabrata. Future investigation will utilize in. situ hybridization to provide details regarding the expression patterns of these pathways.

Monolithic segmented-blade ion trap system

April Sheffield | Mentor: Guido Pagano

Trapped atomic ions are a promising platform for quantum simulation and computation. Ions are trapped in a radiofrequency electric field generated by a trap with a quadrupole electrode structure to create a psuedopotential well. Their internal (hydrogen-like) electronic levels are addressed by lasers and used as qubit states. Hand-assembled 3D traps offer deep trapping potentials, robustness to stray electric fields, lower surface noise ion heating rates, and a higher degree of optical access, but can also have lower precision in alignment of electrodes and becomes more difficult to build with more complex electrode structures. Microfabricated planar surface traps manufactured from a single substrate avoid

these downfalls and are able to scale more effectively but lack the advantages of 3D geometry. The subject of this poster is a 3D monolithic blade trap system (using 171Yb+ ions) which allows for the advantages of both microfabrication and 3D geometry. This system will be used as a programmable long-chain quantum simulator, allowing the controllable simulation of complex quantum phenomena that are otherwise difficult or impossible to study in laboratories.

Investigating the Role of uif in Mitotic Growth and Wing Development in Drosophila Melanogaster

Sebastian Sy | Mentor: Kathleen Beckingham

The Toxicity of YwqJ in Bacillus subtilis

Christine Wu | Mentor: Marcos de Moraes

We seek to investigate how YwqJ, a bacterial toxin in the LXG family, affects Bacillus subtilis communities. In our approach, we will characterize the toxicity of YwqJ and its toxin domain through toxicity assays. In these experiments, we will culture various B. subtilis strains with YwqJ and observe how the bacterial growth is affected by the toxin. In our results, we found that YwqJ was indeed toxic to B. subtilis, as bacterial growth was greatly limited. Our results also further supported YwqJ's mechanism of toxicity as deaminase activity. Through these experiments, there is a concrete foundation for evidence of YwqJ toxicity, which can be built upon by future research into YwqJ effects and regulation mechanisms on B. subtilis biofilm communities.

An Integrated Machine Learning Approach to De-orphaning G-protein Coupled Receptors

Catherine Zhou | Mentor: Xiang Menglan

G-protein coupled receptors (GPCRs) are key drug targets, but there are many orphan receptors that lack known ligands and functions. We present an integrated machine learning framework that combines ligand-based, structure-based, spatial, and genomic approaches to systematically predict ligands and functions for orphan GPCRs. The model identifies chemical features associated with GPCR binding to different ligand types, screens receptor-ligand interactions using AlphaFold, evaluates binding site interactions, and compares tissue and cell expression across multiple datasets. Using previously de-orphaned GPCRs, these complementary approaches are integrated through transfer learning and ensemble learning, with multi-task architectures leveraging diverse data modalities. Benchmarking on de-orphanized GPCRs showed our integrated framework outperformed traditional and individual machine learning methods, and the model was able to accurately

predict ligands for two orphaned GPCRs that were verified in vivo. This framework provides an effective and efficient computational platform for mapping orphan GPCRs and their ligands, unlocking new therapeutic opportunities for future studies.

Cancer: Biology, Prevention and Therapy

Investigating the Function of Hsp90 in a Hybrid Diploid Yeast Model

Morike Ayodeji | Mentor: Georgios Karras

Hsp90 is a highly conserved protein-folding chaperone that assists in the folding and maturation of proteins. Hsp90 function is closely related to essential processes associated with cancer development. Although there is evidence of Hsp90's involvement in these processes, there is uncertainty surrounding what factors can alter its functioning. The aim of this project is to develop a functional assay of Hsp90 in a hybrid yeast strain. The development of the genome involves the deletion of the ADE2 gene and the incorporation of growth and fluorescence markers. The strains are crossed to obtain heterozygous diploids. Then, growth curves are generated with the hybrid yeast strains in four different conditions: glucose, maltose, and +/- radicicol. The procedure culminates with a glucocorticoid receptor (GR) assay based on the heterologous expression of the GR in yeast. It is expected that the functional assay will reveal a reduction in Hsp90 function in a hybrid yeast model in comparison to its haploid counterpart. The development of this functional assay will provide insight into proteotoxic stress emerging from genomic alteration and the resultant Hsp90 function.

Evaluating the Origin of Intrahepatic Cholangiocarcinoma by Identifying the Mechanisms of Transdifferentiation in Cholangiocytes and Hepatocytes

Priya Bapna | Mentor: Lawrence Kwong

Intrahepatic cholangiocarcinoma (ICC) is a highly lethal cancer of the bile ducts, and understanding its formation mechanism amidst its heterogeneous nature is crucial for developing effective treatments. This investigation aims to induce transdifferentiation of immortalized hepatocytes into cholangiocytes in vitro. The purpose of this is to observe the lineage plasticity of hepatocytes in ICC, identify the origin of ICC, and determine the mechanisms of differentiation, specifically focusing on the role of the Notch pathway and its transcription factors, Hes1, Hey1, Sox4, and Sox9, as well Hnf1b, in the pathogenesis of ICC. The experiment is currently in the process of transfecting the hepatocytes with the cholangiocyte genes and observing changes, both physically and genetically. If successful such that the hepatocytes begin to exhibit biliary lineage morphology and cholangiocyte markers, the study may reveal new insights into the cellular differentiation process

and identify potential therapeutic targets. This could ultimately improve early detection and patient outcomes for cholangiocarcinoma.

Developing Predictive Models for Patients with MEN1-associated Pancreatic Neuroendocrine Tumors

Madeline Belknap | Mentor: Landry Jace

Multiple endocrine neoplasia type 1 (MEN1) is an autosomal dominant hereditary tumor syndrome characterized by mutations in the MEN1 tumor suppressor gene occurring in about 1 in 30,000 people. MEN1 patients have a have a high risk of developing pancreatic neuroendocrine tumors (PNETs) and can develop multiple PNETs within the pancreas. PNETs have been observed in 80-100% of patients in postmortem studies and are the leading cause of death for MEN1 patients. We aim to conduct a retrospective review of patients with MEN1 treated at MD Anderson Cancer Center that have abdominal CT or MRI images available for review to create artificial intelligence (AI) models to predict the development and aggressiveness of PNETs in MEN1 patients. Initial findings will focus on associations between clinical, biological and visual features of PNETs, the surrounding pancreas, soft tissue and adjacent viscera to elucidate predictors of tumor development and prognosis in MEN1 patients, as well as which PNETs are likely to become metastatic without intervention. This research holds promise for early detection and management of PNETs in the context of MEN1, potentially improving patient outcomes.

Optimizing In Vitro Transcription Efficiency using a T7 RNA Polymerase Mutant

James Cheng | Mentor: Francis Tsai

The use of DNA-dependent RNA polymerases (RNAP) is an elegant approach to synthesizing RNA molecules to be used for biochemical and structural studies, gene therapy, and vaccine development. For in vitro transcription, bacteriophage T7 RNAP is widely used because of its high affinity and specificity to its promoter, function without the need for transcription factors, and strong activity. However, T7 RNAP is subject to abortive cycling, wherein unwanted, shorter RNA molecules are generated. A mutation of Proline 266 to Leucine (P266L) in the C-linker region has previously been shown to reduce short abortive transcripts (5-8 nt) compared to wild-type T7 RNAP, thereby ensuring efficient in vitro transcription and sample purity. Here, I show that while the T7 RNAP mutant yields a purer sample of the desired RNA molecule of ~60 nt with less abortive cycling, the catalytic activity of the mutant is lower than T7 RNAP wild-type. I hypothesize that the P266L mutation decreases the transcription rate and propose a change in the experimental procedure to mitigate this tradeoff.

A cytotoxic HLA molecule protects adoptive NK cells from recipient allorejection

Lauren Ginn | Mentor: Robin Parihar

Adoptive natural killer (NK) cell therapy involves infusing genetically engineered NK cells into patients to eliminate tumor. NK cells can be isolated from the patient (autologous) or a matched donor (allogeneic). Despite logistical benefits of allogeneic cells, their long-term persistence post-infusion is limited by elimination by T cells upon recognition of mismatched HLA, a process called allorejection. We hypothesize engineering allogeneic NK cells to express a cytotoxic HLA molecule, termed Chimeric HLA Accessory Receptor (CHAR), will increase NK persistence by preventing NK killing and promoting T cell death. Allogeneic CHAR-NK cells were cultured in a mixed lymphocyte reaction (MLR) assay with alloreactive T cells. While unmodified controls were killed, allogeneic CHAR-NK cells survived and limited T cell proliferation. NK cells co-expressing CHAR and a tumor-directed Chimeric Antigen Receptor (CAR) were cultured with tumor targets and exhibited similar tumor killing to non-CHAR controls. Thus, CHAR expression is protective from allorejection and permissive of continued NK function. Our study supports further clinical development of CHAR into allogeneic NK cell therapies.

Optimization of CEST MRI Clinical Phantoms for Enhanced Instrument Calibration

Leah Gomez | Mentor: Kasey Leigh Yearty

Exploring the Role of the IL-1β Pathway in the Context of Kras Mutant Lung Cancer

Vivian Ha | Mentor: Seyed Moghaddam

Lung cancer continues to be the leading cause of cancer-related deaths worldwide in both men and women. KRAS mutant lung adenocarcinoma (KM-LUAD) is a key hallmark of cancer that promotes tumorigenesis and is mediated by activation of the nuclear factor-κB (NF-κB). Understanding tumor-promoting events as well as targeting inflammation has proven to be important, especially when establishing immunotherapeutic and preventative treatments. IL-1β is a potent activator of the NF-κB pathway and must bind to the IL-1 receptor (IL-1R). We have previously seen a reduction in angiogenesis upon IL-1R blockade. Thus, there is further interest in exploring the effects this receptor has on angiogenesis in tumor development. By extending on these previous findings, we can determine the extent of IL-1β involvement in KM-LUAD tumorigenesis. Additionally, there is significant interaction between the tumor cell/-epithelial IL-1R and IL-1β that elicits a tumor promoting immune microenvironment. Targeting this interaction may contribute

to the development of potential novel therapeutic or preventative modalities for KM-LUAD.

Constructing an AAV Vector for Introducing Esr1 D538G and Pik3ca H1047R Mutations in Rats to Study Their Impact on Breast Tumor Characteristics

Lillian He | Mentor: Yi Li

This research project aimed to create an Adeno-associated virus (AAV) vector for CRISPR-Cas9/Homology-directed repair (HDR) editing in rats to produce breast tumors with Esr1 D538G and Pik3ca H1047R mutations. 70-75% of all breast cancers are estrogen receptor α-positive (ER+) and are usually treated with endocrine therapies. Mutations in the Esr1 gene, specifically D538G, are linked with endocrine therapy resistance and breast cancer metastasis. However, the differences in tumor characteristics caused by the D538G mutation remain largely unknown. A syngeneic rat tumor model carrying the Esr1 D538G mutation is needed since rats readily develop ER+ tumors. Pik3ca H1047R was chosen as the breast cancer-driver mutation as it is one of the most common mutations present in ER+ breast cancers. The AAV vector carrying guide RNAs and HDR donors for Esr1 and Pik3ca (AAV-PE) was constructed using In-Fusion cloning. Following the production of the AAV virus, intraductal injection into rats will be used to confirm genome editing. With this construct, we hope to eventually compare the characteristics of the Pik3ca H1047R/Esr1 D538G tumors with Pik3ca H1047R tumors.

Gene X Modulates Colorectal Cancer Growth Through Interactions with Immune Populations in the Tumor Immune Microenvironment (TIME)

Abhi Jain | Mentor: Lily Cai

Targeting Chronic Lymphocytic Leukemia: The Synergistic, Antiproliferative Effect of B-I09 and ADU-S100

Abigail McKellop | Mentor: Chih-Chi Andrew Hu

B-cell chronic lymphocytic leukemia (CLL) is the most prominent leukemia in adults, creating a demand for treatments. The IRE1/XBP1 pathway is critical for B-cell function and development, and malignant progression of CLL is facilitated by increased expression of XBP1. Another important B-cell pathway involves a critical immune regulator in cancer, STING, of which prolonged agonism causes B-cell apoptosis. Although studies found an interaction between STING and IRE1, a gap remains in understanding the effects of simultaneous pathway modulation. We hypothesized that B-I09, an IRE1 inhibitor, and ADU-S100, a STING agonist, will have a synergistic, antiproliferative effect on human CLL. We investigated the combined

effects of B-I09 and ADU-S100 in human CLL through XTT assays and immunoblotting to understand cellular proliferation and protein expression. Current results produced evidence for an antiproliferative, synergistic effect between B-I09 and ADU-S100. Anticipated results would demonstrate increased expression of apoptotic proteins. This work will develop mechanistic understanding of the synergistic effect, thus contributing to the identification of novel therapeutic targets.

Next Generation Sequencing Analysis of Genomic DNA From A Combinatorial CRISPR-Cas9 Screen To Identify Lethal Interaction in Colorectal Cancer Cell Lines

Bela Nelson | Mentor: Shen John Paul

Genetic interaction refers to the phenomenon that mutations between 2 genes can result in a phenotype that differs from the sum of the mutated genes' individual effects. Understanding genetic interactions are important in cancer biology because it can illuminate the cell signaling pathways that drive tumorigenesis. This is particularly applicable to Colorectal Cancer (CRC) due to its heterogeneous nature. Furthermore, the interactions of CRC genes are not explored and understood. This project uses a CRISPR-Cas9 screen in a CRC-specific cell line. The screen uses a combinatorial RNA library to target all possible genetic interactions between 114 selected CRC genes, totaling 6,441 genetic interactions. Systemically mapping these interactions will provide insight into potential synthetic lethal therapies in which two genes that interact strongly are simultaneously perturbed to cause cell killing.

Reducing varenicline to 1mg QD (daily) for maintaining abstinence from smoking, after 4 weeks of abstinence

Connor Nguyen | Mentor: Connor Nguyen

Cigarette smoking remains a significant cause of premature mortality globally. Despite advancements in nicotine dependence treatments, including Nicotine Replacement Therapy (NRT) and bupropion, varenicline has emerged as a leading pharmacological option. Approved by the FDA in 2006, varenicline's mechanism involves a dual agonist-antagonist action on nicotinic acetylcholine receptors, particularly targeting the α4β2 and α6β2 subunits, making it highly effective for smoking cessation. This study explores the efficacy of reducing varenicline dosage to 1mg daily for maintaining abstinence after an initial 4-week cessation period. With concerns over adverse events and cost implications of varenicline, especially after Pfizer ceased production in 2022, a lower dose could offer a more tolerable and financially accessible option for sustained abstinence. We hypothesize that halving the dose after four weeks of abstinence will not increase cravings or relapse

rates, potentially reducing adverse events. This approach aims to generate data for a broader analysis on dose efficacy, contributing to the optimization of smoking cessation treatments and addressing the financial burden on patients

Generation and characterization of a glioblastoma stem cell model with acquired resistance to LSD1 inhibition

Kareena Patel | Mentor: Joya Chandra

Lysine-specific demethylase 1 (LSD1) is a histone demethylase that is overexpressed in glioblastoma stem cells (GSCs) and functions to promote proliferation. Previous work has investigated LSD1 as a therapeutic target in glioblastoma (GBM) and identified five pro-tumorigenic genes which are HKDC1, RAB3IL1, RAB39B, FTH1, and FAM213A and were associated with LSD1 inhibitor (LSD1i) resistance. In order to determine whether selection pressure from LSD1 inhibitor treatment caused upregulation of these genes, we created a model of acquired resistance in GSC lines in vitro. Resistant lines were generated by treating MDA-GSC17 cells with increasing concentrations of LSD1i, starting at 50 uM. In parallel, MDA-GSC17 controls were exposed to DMSO. The resistant line was created over 4 weeks and monitored by cell number and viability. To assess the change in gene expression, we conducted qPCR for the five genes in the parental and resistant MDA-GSC17 line and saw upregulation in 3 of the 5 genes. Understanding the changes in gene expression as the cells acquire resistance will help us understand the mechanism of resistance to LSD1 inhibitors in GBM and to design new treatment strategies.

CRISPR Inactivation of Mitochondrial Biogenesis Genes in Cancer Cells

Mira Srinivasa | Mentor: Mario Escobar

Mitochondria are the metabolic powerhouses of cancer cell proliferation. When altered, normal processes such as oxidative phosphorylation and glycolysis become harmful due to a variety of factors including the production of mutated enzymes and metabolites, abnormal mitochondrial fission/fusion dynamics, and mitochondrial metabolism of many non-glucose substrates. Subsequently, tumor growth, metastasis, and responsiveness to drug treatment are heavily impacted by the increased abnormal mitochondrial metabolism that is a hallmark of cancer cells. Given its crucial role, inhibiting mitochondrial energy production and mitochondrial biogenesis genes, such as *PPARGC1a*, serves as a potential therapeutic target for cancer. In this study, we use CRISPR inactivation (CRISPRi) technologies to target and repress the mitochondrial biogenesis gene *PPARGC1a*. We then analyze whether treatment of human cancer cell lines with this targeted CRISPRi decreases *PPARGC1a* expression and ultimately decreases cell proliferation. Preliminary results suggest a successful decrease in *PPARGC1a* expression and cell proliferation with the treatment, emphasizing its potential role in cancer therapy.

Diet Composition Influences CD8+ Cytotoxic T Cell Effector Function and Metabolic State in Hepatocellular Carcinoma

Jessica Wen | Mentor: Jessica Wen

Hepatocellular carcinoma (HCC) is the most common form of liver cancer, with over 1 million people diagnosed with this condition each year. While hepatitis virus-associated HCC cases have been declining due to effective treatments and vaccines, the obesity epidemic has contributed to a drastic increase in non-alcoholic/alcoholic steatohepatitis (NASH/ASH) associated HCC cases. Studies have shown that diet and alcohol consumption can induce a shift in the distribution of T cell subpopulations. However, the extent of this effect on the development of HCC has yet to be fully elucidated. This project aims to understand how food composition and alcohol composition impact the function of CD8+ cytotoxic T cells. Mice were placed on diets of varying macronutrient composition with and without alcohol, and disease progression was monitored. Flow cytometry and RT-PCR analyses revealed that long-term dietary intervention altered T-cell metabolism and function, impacting the progression and development of HCC. With a better understanding of the mechanisms underlying cytotoxic T cell dysregulation in steatohepatitis-induced HCC, we can hopefully develop more ways to prevent and treat HCC.

Mucin 5AC inhibition via intratracheal RNAi delivery as an effective alternative strategy for prevention and treatment of Kras mutant lung cancer

Melvin Zarghooni | Mentor: Seyed Moghaddam

Lung cancer, including lung adenocarcinoma (LUAD), is the leading cause of cancer-related deaths in the United States. KRAS mutations are the most prevalent oncogenic driver alteration in human LUAD. We have previously shown that high expression of Mucin 5 AC (MUC5AC), a main airway secretory mucin, is significantly associated with poor prognosis. Mucins are essential for mucociliary clearance and the maintenance of airway homeostasis, however, their overproduction could negatively affect the lung immune microenvironment and has been shown to promote airway diseases such as chronic obstructive pulmonary disease (COPD) and lung cancer. Previously, we have shown that genetic deletion of MUC5AC in a murine model of K-ras mutant lung adenocarcinoma (KM-LUAD) impedes tumor development and reduces pro-tumor inflammatory and immune phenotypes. These findings indicate that MUC5AC is a potential druggable target against KM-LUAD. In this project we looked at MUC5AC RNAi as an effective indirect preventive and therapeutic strategy in highrisk individuals (smokers with COPD) and patients with early stage KM-LUAD, respectively.