2025 NORTH CAROLINA POSTDOC RESEARCH SYMPOSIUM

JUNE 20, 2025

NORTH CAROLINA BIOTECHNOLOGY CENTER

ABSTRACT BOOK

AGENDA

Start	End	Session
9:00	9:30	Registration & Poster Setup
9:30	9:45	Welcome/Opening & Sponsor Remarks
9:45	11:00	Postdoctoral Scholar Flash Presentations
11:00	11:15	Break / Networking
11:15	12:00	Poster Session A
12:00	1:00	Lunch & Networking
1:00	2:00	Concurrent Industry / Academia Career Panels
2:00	2:45	Poster Session B
2:45	3:00	Break / Networking & Poster Takedown
3:00	3:45	Keynote Address w/ La Tondra Murray
3:45	4:00	Final Remarks and Prize Winners
4:00	4:30	Additional Networking

SPONSORS

NC STATE UNIVERSITY
RISEUPP AN NSF INCLUDES ALLIANCE
UNC CHARLOTTE
BURROUGHS WELLCOME FUND
UNC RESEARCH Office of Postdoctoral Affairs
North Carolina Biotechnology Center
THE UNC SYSTEM
NORTH CAROLINA AGRICULTURAL AND TECHNICAL STATE UNIVERSITY
ECU
WILMINGTON UNIVERSITY

PANELS

Industry Pathways: Navigating Careers Outside Academia

This panel brings together four accomplished scientists who successfully transitioned from academic research to impactful careers in industry and related sectors. With experience across biotech startups, clinical research organizations, regulatory science, and agricultural innovation, these PhD-trained professionals offer diverse perspectives on what it takes to thrive beyond academia.

Panelists will share their personal journeys, the decisions that shaped their careers, and the skills that helped them succeed outside the university setting. Attendees will hear practical advice on exploring the job market, identifying transferable skills, and understanding workplace expectations in industry. Whether you are early in your exploration or preparing for a career move, the discussion will provide perspective, guidance, and useful takeaways for considering careers beyond academia.

MODERATOR:
Patrick Brandt, PhD
Senior Director of Career Development and Science Outreach, School of Medicine, UNC-Chapel Hill

Dr. Patrick Brandt is Senior Director of Career Development and Science Outreach at UNC-Chapel Hill and Director of the TIBBS Program (Training Initiatives in Biomedical and Biological Sciences). He leads efforts to support graduate students and postdocs as they prepare for diverse scientific careers, with a strong focus on transitions beyond academia. Patrick directs the ImPACT internship program and the Certificate Program in Translational Medicine, both of which provide hands-on experience and professional development opportunities. He is passionate about helping trainees identify career goals and gain the skills and confidence to pursue them. Patrick earned his PhD in Biochemistry from the University of Rochester and completed postdoctoral training at the National Institute of Environmental Health Sciences.
https://www.linkedin.com/in/patrickdbrandt/

PANELISTS:
Bailey Zwarycz, PhD
Business Development Director, Alimentiv

Bailey Zwarycz, PhD is Business Development Director at Alimentiv, a global contract research organization specializing in gastrointestinal diseases. In this role, she leads strategic partnerships and drives growth initiatives by connecting clinical trial sponsors with specialized CRO services. Prior to joining Alimentiv, she held multiple leadership roles at Altis Biosystems, a biotech startup developing in vitro models of the human gut, where she contributed to commercial strategy, scientific sales, and project management. Bailey transitioned into industry after several years as a scientist, gaining deep experience in preclinical research, client relations, and product development. She earned her PhD in Cell Biology and Physiology from the University of North Carolina at Chapel Hill, where she also completed a brief postdoctoral fellowship focused on intestinal stem cell biology.
https://www.linkedin.com/in/baileyzwarycz/

Kimberly Koehn, PhD
Regulatory Scientist II, Rho

Kimberly Koehn is a Regulatory Scientist II at Rho, where she leads and supports cross-functional teams to develop regulatory strategies, coordinate clinical and preclinical submissions, and author key regulatory documents for FDA and international agencies. Kimberly's scientific journey began in natural product total synthesis, followed by postdoctoral work in medicinal chemistry at UNC's Eshelman School of Pharmacy. There, she helped design novel analgesic drug candidates and served as a project manager during the COVID-19 pandemic. Her passion for regulatory science grew out of these collaborative experiences, and she now specializes in product development strategy across therapeutic areas. Kimberly is also committed to professional development and previously co-chaired UNC's Medical and Regulatory Affairs Training initiative to support aspiring scientists in the field.
https://www.linkedin.com/in/kimberlyklaskoehn/

Martin Buchkovich, PhD
Associate Director, Bioinformatics, IQVIA Laboratories

Martin Buchkovich is Associate Director of Bioinformatics at IQVIA Laboratories, where he has worked since 2015 in progressively advanced roles. His work supports the application of bioinformatics in clinical and research settings, with a focus on genomic data analysis. Martin earned his PhD in Bioinformatics and Computational Biology from UNC-Chapel Hill, where his research investigated genetic variants linked to cardiometabolic traits. He also holds a bachelor's degree in bioinformatics from Brigham Young University and has prior experience supporting experimental geneticists in both academic and industry settings.
https://www.linkedin.com/in/martinbuchkovich/

Dale Karlson, PhD
Principal Scientist, Trait Sciences Lead, Terrana Biosciences

Dale Karlson is a plant molecular biologist with over two decades of experience spanning academia and industry. He currently serves as Principal Scientist and Trait Sciences Lead at Terrana Biosciences, driving innovation in trait development for crops. After earning his PhD, Dale completed postdoctoral research in Japan focused on the molecular biology of plant responses to low temperature stress. He later led an NSF-funded academic lab before transitioning to biotech, where he held leadership roles at Monsanto, Pairwise, and GreenLight Biosciences. His work has centered on high-throughput screening technologies, trait discovery, and gene expression strategies across a range of crops. Dale also serves as an Adjunct Professor at NC State, maintaining strong ties to academic research and training.
https://www.linkedin.com/in/dale-karlson-1061b735/

Emir Islamovic. PhD
Scientist, Molecular Biologist at BASF

Dr. Emir Islamovic is a Molecular Biologist at BASF, where he contributes to regulatory science by leading and supporting molecular, biochemical, and bioinformatics projects with a strong focus on good laboratory practices (GLP). He brings over 16 years of research experience across academia, government, and industry, with expertise in DNA and protein characterization and a proven record of managing complex, multi-stakeholder projects. Prior to joining BASF in 2014, Dr. Islamovic held research roles at UC Berkeley and served as a postdoctoral associate with both the USDA Agricultural Research Service and the University of Georgia. He earned his PhD in Molecular Biology from Loyola University Chicago.
https://www.linkedin.com/in/emir-islamovic-951a343/

Academic Pathways: Careers Beyond the Tenure Track

This panel will showcase diverse career opportunities beyond the traditional tenure-track path. It will highlight roles in teaching-focused institutions, research support, non-faculty research positions, and academic administration. The panelists will share their extensive experience in academia and beyond, demonstrating how postdoctoral training can open doors to careers in research administration, program leadership, digital learning innovation, and interdisciplinary research. Attendees will gain insight into a range of fulfilling career paths that contribute to the academic community in impactful ways.

MODERATOR:
Mary Farwell, PhD
Assistant Vice Chancellor at East Carolina University

Dr. Mary Farwell is the Assistant Vice Chancellor for Research Development at East Carolina University, overseeing research development, centers and institutes, postdoctoral affairs, and undergraduate research. She is also a Professor of Biology in the Harriot College of Arts and Sciences. With over 30 years at ECU, Dr. Farwell has extensive experience in biochemistry, biotechnology, and cell biology, and has led programs supporting faculty-mentored undergraduate research and initiatives for first-generation biology students. She earned her PhD in Biochemistry from UC Berkeley.
https://www.linkedin.com/in/mary-farwell-phd-0399aa9/

PANELISTS:
Grace Byfield, PhD
Research Associate, School of Medicine, UNC Chapel Hill

Dr. Grace Byfield is a Research Associate in the UNC School of Medicine, where she contributes to multi-disciplinary research programs. Her career spans academia, biomedical research, and public health outreach. Prior to her current role, she served as Program Manager at the Center for Outreach in Alzheimer's, Aging and Community Health at North Carolina A&T State University and held faculty positions at both North Carolina A&T and Saint Augustine's University. Earlier in her career, she worked as a Research Microbiologist at RTI International, a leading nonprofit research institute, and as a Research Associate at Duke University Medical Center. Dr. Byfield completed her postdoctoral training at UNC-Chapel Hill and earned her PhD in Microbiology from North Carolina State University.
https://www.linkedin.com/in/grace-byfield-20398261/

Wanda White-Walker, Ed.D.
Director of Teaching and Learning- Center for Innovative and Transformative Instruction

Dr. Wanda White-Walker is Director of Teaching and Learning at Winston-Salem State University, where she leads faculty development, digital learning, and instructional innovation through the Center for Innovative and Transformative Instruction. With over 25 years of experience in higher education, corporate training, and instructional design, she has held leadership roles including Interim Dean and Associate Professor, and has trained faculty in pedagogy, curriculum design, and inclusive teaching. She is also CEO and Founder of White Professional Communications, a consulting firm specializing in workplace learning and communications strategy. Dr. White-Walker holds an Ed.D. in Educational Leadership and an M.A. in English from UNC Charlotte, and a B.A. in English and History from Winston-Salem State University.
https://www.linkedin.com/in/drwandawhite/

Trino Ascencio-Ibáñez, PhD
Teaching Professor - Director of Undergraduate Programs at North Carolina State University

Dr. Trino Ascencio-Ibáñez is a Professor and Director of Undergraduate Programs at North Carolina State University, where he has served in various teaching faculty roles for over 16 years. His research expertise includes plant-virus interactions, early virus detection, and multi-omics analysis, which he integrates with a strong commitment to undergraduate education and program leadership. Prior to his faculty career in the U.S., Dr. Ascencio-Ibáñez conducted plant virology research at CINVESTAV in Mexico for over a decade, focusing on transgenic crops and virus characterization. He earned his PhD in Biochemistry from North Carolina State University.
www.linkedin.com/in/trino-ascencio-ibáñez-6733574

Dr. Andrea Walens, PhD
Senior Director of Research Administration, College of Arts & Sciences, UNC-Chapel Hill

Dr. Andrea Walens is the Senior Director of Research Administration in the College of Arts & Sciences at UNC-Chapel Hill, where she leads a team supporting grant awards and administration across the College. Prior to this, she served as Assistant Director of Collaborative Science at UNC Lineberger Comprehensive Cancer Center and was a postdoctoral fellow studying the tumor immune microenvironment and breast cancer mortality disparities. She earned her PhD in Cancer Biology from Duke University and brings extensive experience in research development, grants administration, and fostering transdisciplinary collaborations.
https://www.linkedin.com/in/andreawalens/

Meghan Kraft
Director of Research Core Facilities at UNC-CH

Meghan Kraft is Director of Research Core Facilities at the University of North Carolina at Chapel Hill, where she oversees strategy and operations for 15 research units. With over 10 years of experience in organizational leadership, she specializes in streamlining processes, improving financial performance, and aligning operations with institutional goals. She previously served as Interim Director of Core Strategy and Assistant Director of Research Operations at UNC, and as Director of Operations at Eva Garland Consulting. She holds an MBA from Meredith College and an Associate of Science in Human Resources Management from Wake Technical Community College.
https://www.linkedin.com/in/meghankraft/

KEYNOTE

The Sweet Spot: Mapping Your Unique Career Advantage

In today's challenging job market, candidates need more than just expertise—they need clarity about what makes them uniquely valuable. "The Sweet Spot: Mapping Your Unique Career Advantage" introduces a powerful framework for identifying your professional "unfair advantage" through the intersection of your skills (what you know), experiences (what you've lived), and talents (what you do best). In lieu of dramatic career pivots that implore you to make wild shifts, this approach emphasizes the exploration of adjacencies that build on your existing strengths while revealing new pathways forward. You'll see real-world examples and engage in interactive exercises to map your own sweet spot, recognize options you're already positioned for, and make strategic career moves that honor your investments while expanding your possibilities. This session offers a realistic yet empowering roadmap for navigating uncertainty with confidence, helping you recognize your next opportunity in a competitive landscape.

Biography

La Tondra Murray is a strengths-based leadership coach and educator with a background in information technology, business, and academia. As the founder of ONA Partners, LLC she helps emerging leaders and lean teams use evidence-based, data-driven techniques to create epic results through the delivery of customized workshops and coaching services. La Tondra has coached 1000+ individuals in the areas of talent assessment, work-life integration, productivity, and emerging leadership. She is a Certified Personal and Executive Coach (CPEC) as earned through the Coaching and Positive Psychology (CaPP) Institute. She is also a Certified Gallup Strengths Coach with over a decade of experience with the Clifton Strengths® assessment.

La Tondra has 25+ years of leadership experience in corporate, research, and higher education technology-based environments. She holds a Ph.D. in Industrial Engineering from North Carolina State University as well as undergraduate degrees in Electrical Engineering and Computer Science from Georgia Tech and Spelman College, respectively. In addition to running her own coaching practice, La Tondra serves as an Executive-in-Residence and Adjunct Professor with a focus on Leadership and Management at Duke University's Pratt School of Engineering.

FLASH TALKS

1. **Mpox Isn't Over: A Call for Urgency and Preparedness | *Tom Carpino***

This flash talk will offer a concise update on the global mpox landscape—formerly known as monkeypox—and outline why it remains a pressing public health concern. I'll also highlight steps we can take to reduce harm and better support affected communities.

As we gather during Pride Month—a time of celebration, reflection, and connection—it's crucial to consider how emerging infections intersect with stigma, equity, and community health. Mpox has disproportionately affected gay, bisexual, and other men who have sex with men and in the summer of 2022, it drew worldwide attention as outbreaks spread to over 110 countries and affected more than 100,000 people.

Yet today, public concern has largely faded. Mpox continues to spread, with multiple strains in circulation, no approved treatment regimen, and limited vaccine access in many endemic countries. Despite early efforts, vaccination and education campaigns have stalled amid waning political will and defunded research.

Mpox isn't just a past or niche issue. It's a wake-up call to reimagine how we respond to emerging infections—with urgency, compassion, and inclusion. Without sustained investment, public awareness, and global collaboration, we risk allowing mpox to become a neglected disease once again—one that resurfaces with greater force and deepens existing health inequities.

https://www.linkedin.com/in/tomcarpino

2. **Electronic Cigarettes: A Pregnancy Risk? | *Samuel Cripps***

The past decade has seen an epidemic of electronic (e) cigarette use, popularly referred to as 'vaping'. When an e-cigarette user puffs on the mouthpiece, the battery-powered device heats and aerosolizes a viscous liquid for inhalation. Typically, this contains nicotine and a diversity of artificial flavoring chemicals. Concerningly, the health effects of e-cigarette flavorings independent of nicotine are largely unknown. Vaping is most popular among individuals of reproductive age. As a result, an estimated 8-10% of women in the US vape during pregnancy, reinforced by the notion that vaping is safe compared to smoking. However, e-cigarettes are associated with pregnancy complications including fetal growth restriction, characterized by an abnormally small fetus. A causal relationship remains unknown. Thus, we hypothesize that flavored e-cigarettes can compromise maternal and fetal health by interfering with early pregnancy processes. These include timing of embryo implantation into the uterus and establishment of the placenta, a transient organ that facilitates oxygen and nutrient delivery to the fetus.

To investigate the impacts of vaping on early pregnancy outcomes, we treated human placental cells with e-cigarette components and exposed pregnant mice to e-cigarette vapors to accurately model human vaping. Pregnant mice exposed to flavored nicotine e-cigarettes exhibited abnormal timing of embryo implantation and reduced fetal to placental

weights. Moreover, nicotine e-cigarette vapor modulated the function of cultured human placental cells, and some flavors exhibited greater harm than others. Interestingly, flavored e-cigarette vapor without nicotine induced the greatest genetic changes in the mouse placenta and human placental cells, further highlighting toxic effects specific to flavorings. Overall, these results indicate that e-cigarettes disrupt early pregnancy processes which can lead to fetal growth restriction. Given the unprecedented levels of vaping during pregnancy, it is critical to caution against this practice.
www.linkedin.com/in/samuel-cripps-0498922b7

3. **Investigating the implications of nanostructure surfaces on the bacterial adhesion, growth and biofilm formation | *Parth Desai***

Understanding bacterial interactions with nanostructured surfaces is crucial for advancing biomaterial applications. In this study, we fabricated titanium dioxide (TiO_2) nanostructures and systematically compared them with planar TiO_2 surfaces to assess bacterial attachment, growth dynamics, and metabolic activity. Using a combination of water contact angle measurements, crystal violet (CV) staining, tetrazolium chloride (TTC) assays, confocal laser scanning microscopy (CLSM), and scanning electron microscopy (SEM), we evaluated surface characteristics, bacterial adhesion, and viability.
Our findings reveal that TiO_2 nanostructured surfaces significantly influence bacterial growth and attachment compared to non-structured TiO_2 surfaces. Notably, bacterial viability and metabolic activity were distinctly modulated by nanoscale surface architecture, independent of the titanium dioxide material composition. These results provide the first evidence that bacterial response is primarily driven by nanoscale surface topography rather than chemical composition alone. Such insights pave the way for optimizing biomaterial design in antimicrobial and bioengineering applications especially in the bio implants.
https://www.linkedin.com/in/drphdesai90369/

4. **Rhythm and Blues: Brain Waves Behind the Craving Cues | *Joaquin Douton***

People recovering from cocaine addiction often experience intense negative emotions during withdrawal, including stress, anxiety, or dysphoria. Importantly, these emotional states are a major reason why many people relapse. To prevent relapse, we need a better understanding of what happens in the brain as these negative feelings emerge and how to intervene. In our research, we use a rat model in which a sweet taste (like saccharin) becomes unpleasant after repeated pairings with cocaine, mimicking how drug use can alter emotional responses. When rats show aversive responses to the sweet, it reflects a shift toward a negative emotional state that is linked to greater drug-seeking behavior. We also developed a rat model of noninvasive brain stimulation called transcranial alternating current stimulation (tACS), that can help restore healthy brain activity. Our goal was to characterize the effects of cocaine on the coordinated activity of the “control center” and the “emotion center” of the brain in response to the sweet taste and assess if tACS could reverse these effects. To do so, as a measure of brain activity, we recorded brain waves

using local field potentials (LFP) in the prelimbic cortex and the nucleus accumbens core, regions of these centers involved in relapse, during the intraoral infusions of a grape-flavored saccharin solution before and after 7 pairings with cocaine injections. We found that cocaine altered synchronized activity between these regions, leading to stronger negative reactions to the sweet taste. However, after 5 days of 20 Hz tACS stimulation, both the negative reactions and the brain wave disruption were reduced. Collectively, our data reveal important changes in brain wave synchronization associated with cocaine-related negative emotional states. Most importantly, we show that tACS stimulation may offer potential noninvasive treatment to reduce these negative emotional states, restore healthy brain function and potentially prevent relapse.
www.linkedin.com/in/joaquin-douton-5627ab71

5. **Targeting Lipid-Microbiome Interactions to Improve Treatments for C. difficile Infection | *Abigail Gancz***

Poop. Everybody does it. But for patients with *Clostridioides difficile* infection (CDI), a life-threatening gut disease, something as ordinary as digestion can turn deadly, causing over half a million infections and 30,000 deaths in the U.S. each year. CDI doesn't just disrupt lives; it also adds over $5 billion in hospital costs annually. Fecal microbiota transplants (FMTs)- yes, transferring healthy poop into sick patients- have been a breakthrough and life-saving treatment, often succeeding where antibiotics fail. But because FMTs involve transferring live microbes from donors, they carry risks like introducing unexpected infections, and we urgently need safer, more precisely targeted therapies. My research dives into how FMTs actually heal the gut by reshaping the lipidome- the collection of fats and fat-like molecules that regulate inflammation, maintain the gut barrier, and interact closely with our microbiome. Using cutting-edge technology capable of detecting over a thousand types of lipids, we found that FMTs dramatically rewire the gut's chemical environment, shifting it toward a healthier state and promoting conditions that suppress the growth of dangerous bacteria like *C. difficile*. In particular, we discovered specific lipid changes tied to bacteria that promote recurring CDI, offering key clues into why some patients relapse. These findings open new doors for developing next-generation treatments that mimic the benefits of FMTs without the risks. By better understanding how poop, fats, and microbes team up to keep us healthy or make us sick, we are helping to transform the way we fight one of today's most serious and costly infectious diseases.
https://www.linkedin.com/in/abbygancz/

6. **What Does an Embryonic Heart Feel? | *Kirsten Giesbrecht***

Even if you don't consider yourself a multitasker, your heart was before you were born. First your heart must pump blood through the developing embryo and is our first organ to begin functioning during our development. The heart starts pumping blood before it has developed any of its four chambers. But the embryonic heart is also tasked with growing and developing itself, all the while constantly pumping blood. The embryonic heart does this in part, by relying on physical forces, including friction, generated from the blood it is pumping against

its inner walls, as cues for how to develop. You might imagine, then, if we changed those forces, then the heart itself will change how it develops. And in fact, congenital heart defects are the most common birth defect worldwide and only about a third of them can be traced to known genetic causes, meaning that many congenital heart defects might arise from altered blood flow. Unfortunately, it's difficult to study regular blood flow, let alone abnormal blood flow in developing human hearts. Instead, I study blood flow in developing chick hearts, because surprisingly they have a very similar size and order of development to human hearts, and they are much easier to access. I increase the thickness of their blood during heart development to understand how the heart reroutes its development in response to the change in blood flow. Using a combination of highly detailed imaging techniques and computational modeling, I can both quantify the structural changes that occur in the heart and simulate the rerouted blood flow through these hearts. This work can lead to identifying unhealthy changes in blood flow before a congenital heart defect emerges during pregnancy and possibly contribute to therapies to interrupt unhealthy heart development.
https://www.linkedin.com/in/kirsten-giesbrecht

7. **Mapping the Infant Brain: A New Frontier in Early Childhood Health | *Khoi Huynh***

The first five years of life are a whirlwind of brain development, shaping how we think, learn, and relate to the world. Yet, many of the tools scientists use to understand the brain were designed for adults, leaving a critical gap in how we study early childhood. Our work tackles this challenge by developing the first brain mapping tools specifically built for infants and toddlers. Why does this matter? Because many lifelong conditions—like autism, ADHD, or learning disabilities—trace their roots to early brain development. By the time symptoms appear, the brain's foundational architecture is already in place. What if we could see the signs earlier? What if we could chart the brain's growth like we do height and weight, and spot when something starts to go off course? Our project delivers just that: a new framework to map the brain's wiring in its earliest stages. Using advanced MRI techniques, we track how white matter pathways—highways for brain signals—grow, branch, and connect across infancy and early childhood. We are building the first age-specific atlases and "growth charts" of these pathways, offering a powerful new lens into how the brain develops. This research isn't just academic—it lays the groundwork for earlier, more accurate diagnosis of neurodevelopmental disorders. It gives doctors and scientists new tools to understand how each child's brain develops, and where interventions might help most. Ultimately, this work empowers families, clinicians, and researchers with knowledge that could change the trajectory of a child's life. In a world where mental health and developmental challenges are on the rise, understanding the infant brain has never been more important. Our mission is to make the invisible visible—so we can act sooner, care better, and give every child the best start possible.
https://www.linkedin.com/in/khoi-minh-huynh/

8. **Smart Bandage: Water-Powered, Electronics-Free Dressings for Rapid Wound Healing | *Rajaram Kaveti***

Chronic wounds, such as diabetic foot ulcers, affect millions globally and represent a growing public health crisis—leading to amputations, reduced quality of life, and over $28 billion in annual treatment costs in the U.S. alone. While electrotherapy is a promising solution known to accelerate healing by promoting cell migration and blood flow, its clinical adoption has been limited by high costs, bulky equipment, and restricted patient mobility. I have developed a novel, water-powered, electronics-free dressing (WPED) that delivers therapeutic electric stimulation to wounds—without the need for wires, batteries, or external power, and remain effective in extreme temperatures, humidity, and pressure. These soft, flexible dressings activate instantly with a drop of water, producing a localized electric field aligned with natural healing processes. With a manufacturing cost of just ~$1, WPEDs provide an affordable, point-of-care treatment option suitable for low-resource settings, remote communities, and disaster zones. In diabetic mouse models, WPEDs accelerated wound closure significantly (~30%) compared to conventional and FDA-approved treatments. Histological analysis confirmed enhanced epidermal regeneration, increased blood vessel formation, and reduced inflammation—hallmarks of accelerated, high-quality healing. Importantly, the device operates reliably under extreme environmental conditions and does not impair mobility, making it ideal for real-world use. By combining materials science, biomedical engineering, and translational research, this work introduces a disruptive solution to an urgent medical need. WPEDs pave the way for accessible, scalable wound care technology that could dramatically reduce healthcare burdens and improve outcomes for underserved patients worldwide.
https://www.linkedin.com/in/rajaram-kaveti/

9. **Can gut bacteria influence the way we walk? Exploring the role of the gut microbiota in ALS progression | *Maria Emilia Panzetta***

Amyotrophic lateral sclerosis (ALS) is a multifactorial and devastating disease that gradually paralyzes people by attacking the neurons that control movement. However, not everyone with ALS experiences the disease in the same way. Some decline rapidly, while others live for years with a slower progression. We still don't fully understand why. One surprising clue may lie in the gut. Our gut is home to trillions of bacteria that help digest food, regulate our immune system, and even communicate with the brain. Recently, it has been discovered that these bacteria, the gut microbiota, can influence how diseases develop, including those that affect the brain. In our study, we asked: Could gut bacteria play a role in how fast ALS progresses? To find out, we collected stool, saliva, and blood samples from people with ALS who had either fast or slow disease progression. We also transferred their gut bacteria into mice that develop ALS. We found that mice that received gut bacteria from fast-progressing patients got sicker more quickly than those that received bacteria from slow progressors. We also identified specific changes in the gut and blood chemistry of these mice. This suggests that gut bacteria may actively influence how the disease progresses. Furthermore, we isolated a specific bacterial strain from slow-progressing patients, and it was sufficient to slow down the disease in mice acting as a probiotic. We aim to develop

new probiotic therapies and/or generating biomarkers that help predict how the disease will progress, bringing us closer to more personalized treatment options for ALS. This research highlights how something as simple as gut bacteria might help change the future of a complex and devastating neurological disease.

10. A Spatial Agent-Based Model to Evaluate Ecosystem-Based Adaptation Through Mangrove Restoration | *Fatemeh Rezaei*

Rising sea levels and intensified flooding events pose growing threats to coastal and estuarine communities and ecosystems, and infrastructure. Ecosystem-based Adaptation (EbA), such as mangrove restoration, leverages biodiversity and ecosystem services to enhance climate resilience, offering both cost-effective and environmentally sustainable solutions. Effective adaptation relies not only on ecological restoration but also on understanding the complex decision-making processes that guide stakeholder actions. This study applies a spatial agent-based modeling (ABM) approach to simulate the decision-making processes of multiple stakeholders including local communities, NGOs, and policy-makers in the context of mangrove restoration for EbA. Our approach is based on Ostrom's social-ecological systems model which helps structure the interactions between stakeholders and ecosystems under uncertainty. By capturing the interactions between the stakeholders and their environment, the model compute how variations in social, financial, and technical capacities among communities and NGOs influence the effectiveness of restoration strategies. Our model also examines how the scale of restoration efforts and the severity of cyclone-related damage affect long-term community resilience and coastal protection. Our findings from the ABM that models feedback in social-ecological systems aims to (i) identify feedbacks in EbA systems; (ii) support policy-makers in designing effective coastal protection policies and (iii) provide recommendations for communities in vulnerable coastal regions toward resilient and adaptive planning.

11. The future of climate adaptation is Indigenous | *Savannah Swinea*

Environmental challenges such as biodiversity loss, pollution, and climate change are symptoms of a deeper issue: the legacy of centralized, command-and-control approaches to managing nature. These approaches often rely on scientific models to simplify complex ecosystems and optimize resource use, yet have frequently failed to ensure resilience or sustainability. One way to combat these historical pitfalls is to use a novel approach called co-producing knowledge, in which we consider the knowledge of local people in tandem with technical expertise. Those who interact closely with nature develop place-based knowledge situated within their environment, which can be essential in contexts where scientific data are limited or uncertainty is high. Our project exemplifies this knowledge co-production approach through research with the Eastern Band of Cherokee Indians (EBCI), a federally recognized Tribe in North Carolina whose cultural, ecological, and economic well-being is deeply tied to place. EBCI's lands lie within a region experiencing increased climate impacts including storms, flooding, and increasing temperature, which threaten access to species, habitats, and landscapes that are crucial for maintaining ancestral ties. In partnership with EBCI, NC State University, and the US Geological Survey, we are co-developing a participatory study focused on characterizing Tribal habitat priorities and

threats under climate change. The results will inform a Tribally-led climate adaptation plan and support cross-boundary coordination to ensure continued access to important land, air, and water. Tribes like EBCI are uniquely positioned to contribute environmental expertise developed through legacies of stewardship. Climate change is a wickedly complex problem that threatens both nature and culture, so leveraging Indigenous knowledge is not only a matter of equity, but must be viewed as vital for designing meaningful conservation strategies. Failing to engage the full spectrum of knowledge systems constrains our ability to respond to environmental change and manage natural resources effectively. As climate impacts accelerate and conventional approaches fall short, supporting locally informed solutions will be critical to sustaining both ecosystems and the communities that depend on them.
https://www.linkedin.com/in/savannahswinea/

12. **Tiny Organs, Big Answers: Uncovering Why Some Cells Respond to Messages and Others Don't | *Pelin Yasar***

Breast cancer is one of the most common cancers in the world, and nearly 70% of cases depend on a hormone called estrogen to grow. These cancers are usually treated by blocking estrogen's messages to cells. But the challenge is, not all cancer cells respond the same way, some continue growing despite treatment. Understanding why is a major question in breast cancer research. Interestingly, this kind of unpredictable response isn't limited to cancer. Even in healthy breast tissue, similar types of cells can behave very differently when exposed to hormones. To explore what drives this variability, we built 3D mini-organs called "organoids" from mouse breast cells. These lab-grown structures act like real breast tissue, they can produce milk proteins and form layered architectures and allow us to track how individual cells respond to hormones like estrogen and progesterone. We found that some organoids continue responding to hormones for months, while others lose their responsiveness. These differences appear to depend on the type of cell the organoid originally came from. We also discovered that the levels of hormone-responsive genes change throughout the cell division process, and because the cells in each organoid tend to divide in sync, we gain a unique opportunity to study how hormone messages affect gene activity throughout the cell. By using advanced imaging techniques that let us visualize single RNA molecules, we can see exactly when and how estrogen-responsive genes turn on in single cells. Our work offers a powerful window into how hormone messaging breaks down in cancer, like a group chat where most people reply, but a few ignore the message entirely. Figuring out why some cells stop listening could lead to better diagnostics and more targeted treatments for patients with hormone-driven cancers.

POSTER PRESENTATIONS

1. **Estrogen-Dependent Exacerbation of Ethanol-Induced Cardiac Dysfunction: Role of Circadian Clock Protein Period 2 Suppression and Ferroptosis Augmentation | *Syed Anees Ahmed***

Background: Alcohol exacerbates cardiovascular dysfunction in females in an estrogen (E2)-dependent manner. While E2 confers cardioprotection in premenopausal women and experimental menopause models, its interaction with circadian clock proteins and ferroptosis in the female heart under ethanol (EtOH) exposure is still unexplored.
Aim: We tested the hypothesis that suppression of the cardioprotective circadian protein Period 2 (Per2) contributes to E2-mediated exacerbation of EtOH-induced cardiac oxidative stress and dysfunction.
Methods: Female Sprague-Dawley rats (n = 6–8) underwent bilateral ovariectomy (OVX) and received either EtOH (5% liquid diet) or a control diet, with or without E2 supplementation, for 8 weeks. Cardiovascular function was assessed using radiotelemetry and echocardiography, while the biochemical and molecular analyses evaluated underlying mechanisms.
Result: Treatment with E2 reduced the body weight and fat mass in OVX as well as in OVX+EtOH+E2 rats. Echocardiography showed improved cardiac function in OVX treated with E2 alone vs. exacerbated cardiac dysfunction when EtOH was added to E2. Molecular analyses revealed higher Per2 expression, redox enzyme activity, GPX4, and cardioprotective microRNAs (1, 133a, 208a, 499) levels in OVX+E2, while suppressed Per2, glutathione depletion, GPX4 degradation, reduced cardioprotective microRNAs, and ferroptosis markers were increased in OVX+EtOH+E2.
Conclusion: E2 preserves cardiac function under physiological conditions but exacerbates EtOH-induced dysfunction via Per2 suppression, oxidative stress, and ferroptosis. The loss of E2-mediated Per2 upregulation plays a critical role in ethanol-induced myocardial ferroptosis in E2-replete rats. These findings highlight a potential cardiovascular risk for menopausal women consuming ethanol while on E2 replacement therapy.
https://www.linkedin.com/in/syed-anees-ahmed-m-pharm-phd-098455135/

3. **Mapping out the active site Schiff base nucleophile in the dRP lyase activity of mitochondrial DNA Polymerase Gamma (Pol Î³) | *Chioma Aloh***

DNA polymerase γ (Pol γ) is the only replicative polymerase in the mitochondria and has been implicated in the repair of DNA damages encountered during mitochondrial DNA replication. Failure to correct these lesions leads to point mutations, deletions and depletion of the mitochondria DNA which is observed in patients with mitochondrial disorders. In single-nucleotide base excision repair (SN-BER), the dRP lyase activity of Pol γ catalyzes the release of the terminal 5' 2-deoxyribose 5-phosphate (dRP group) of the DNA to produce a substrate for DNA ligase which seals the nick. This finding suggests that the excision of the dRP group would proceed via a Schiff base intermediate as evidenced by the trapping of the Pol γ amino-substrate by reduction with sodium borohydride ($NaBH_4$). Mapping of Pol γ by $NABH_4$ cross-linking, limited proteolysis and mass spectrometry revealed that the Schiff base nucleophile is Lys^{512}. Alanine and methionine variants of Lys^{512} were expressed to investigate the mechanism of the dRP lyase activity of Pol γ. Results from DNA binding studies of WT Pol γ and the variants with dsDNA show comparable binding affinities, but differing affinities for ssDNA substrates. DNA polymerase assay of WT Pol γ, K512A Pol γ and K512M Pol γ gave burst amplitudes of 80 nM, 18 nM and 16 nM and k_{cat} values of 0.07 s^{-1}, 0.35 s^{-1} and 0.33 s^{-1} respectively. Crosslinking of WT Pol γ and the variants by reduction with $NABH_4$ revealed a trapped product which suggests that though the active site Lys^{512} may have been mutated, another lysine is substituting for its activity. Future studies will investigate the dRP

lyase activity of WT Pol γ and the variants and neighboring active site lysine residues which may be acting as substitutes for Lys^{512} will be analyzed.

4. **Oral Stem Cell Behavior in Alcohol Exposure | *Amber Altrieth***

The oral mucosa are critical to overall human health, playing a role in essential tasks like chewing and digesting food and maintaining a first line of defense against pathogens and chemicals. The oral mucosa are exposed to many stressors and need to be replenished frequently. They comprise stratified epithelia containing a proliferative basal layer and differentiated suprabasal layers, which provide barrier function. Basal cells balance proliferation and differentiation through oriented cell division and delamination. Dysregulation of these processes can lead to an alteration in oral mucosa architecture and/or function ultimately impacting overall health. According to the NIAAA 62.5% of Americans 12 years and over have consumed alcohol in the past year, contributing to 4.1 million alcohol-related emergency room visits. Alcohol use disorder is also one of the strongest comorbidities with oral cancer. Alcohol consumption has systemic effects due in part to its metabolites, which can cause inflammation, oxidative stress, and cell death. While it is well known that alcohol impairs neural stem cell proliferation, survival, and cell fate, little is known about its local effects on oral mucosa. In collaboration with the McElligott and Hodge labs, mice were administered alcohol via either two-bottle choice intermittent access (IA) or chronic intermittent ethanol (CIE) using vapor and palate and tongue were harvested. Palatal and tongue epithelium were stained to identify changes in stem cell behaviors, including proliferation, cell death, DNA damage, and differentiation. Male IA tongues and female CIE palates both had increased suprabasal thickness, suggesting an increase in differentiation following alcohol exposure. Next steps include identifying the potential mechanism of increased differentiation, which could be due to alterations in oriented cell divisions or increased delamination. Dysregulation of oral stratified epithelium can have negative implications for human health, which would likely impair wound healing and in severe cases could lead to cancer.
www.linkedin.com/in/amber-altrieth

5. **Diagnostic Point-of-Care Biosensor for Differentiating Allergic and Non-Allergic Asthma | *Ayemeh Bagheri Hashkavayi***

Asthma presents as a multifaceted respiratory disorder involving ongoing inflammation and narrowing of the airways. Proper management of asthma depends on correctly identifying whether the condition is allergic or non-allergic, as each subtype can respond differently to treatment strategies. In 2019, asthma impacted 262 million individuals globally and contributed to nearly 455,000 fatalities [1]. The impact is especially severe in resource-limited regions, where gaps in diagnosis and treatment are more common. Standard diagnostic procedures such as spirometry, skin tests, and IgE-based assays are often resource dependent and qualitative, making them less suitable for decentralized assessment [2]. Consequently, they are unable to provide the prompt and accurate quantitative differentiation necessary for efficient point-of-care diagnosis. We introduce a portable biosensor developed to measure asthma biomarkers and distinguish between allergic and non-allergic forms [3]. The device integrates lateral flow assay (LFA) technology with electrochemical signal readout to enhance sensitivity and enable real-time detection. Numerous bioprobe pairs were screened using ELISA and LFA to identify the most sensitive and specific antibodies for incorporation. Electrochemical detection allows precise quantification of selected biomarkers from minimal sample volumes, overcoming the limitations of conventional colorimetric LFAs, which typically produce binary or semi-quantitative outcomes. When paired with a portable potentiostat, the biosensor becomes a compact, user-friendly diagnostic tool, capable of delivering rapid results with minimal user input, ideal for both clinical and decentralized environments. By streamlining the diagnostic process, this system accelerates clinical decisions, reduces reliance on centralized labs, and improves accuracy. Next steps include assay refinement, multiplex integration, and broad validation for clinical use and regulatory approval.

6. **Exploring Experts' Uncertainties about Gene Drive Technology for Agricultural Pest Control in the U.S.: A Qualitative Study to Inform Policy Development | *Nourou Barry***

As experts consider what it might look like for gene drives to manage agricultural pests, there remain several uncertainties across a broad range of issues, including technical, ecological, regulatory, and social implications.

Drawing on 25 expert interviews, we parse out these uncertainties and the potential for Adaptive Management to help guide development, deployment, and governance of gene drives for invasive agricultural pest management. Adaptive Management emerged specifically to attend to uncertainties in complex social-ecological systems, prescribing collective learning and responsiveness to stakeholder feedback to effectively reach management goals. Thus, Adaptive Management provides clear direction on how to account for and make decisions in the face of considerable uncertainties surrounding these gene drive tools. We also give some attention to the ways in which the uncertainties that are specific to agricultural applications are somewhat distinct from or consistent with global discourse around gene drive development across sectors.

8. **Quantum Federated Learning for Healthcare: a new paradigm for collaborative learning | *Amandeep Singh Bhatia***

The healthcare sector deals with highly sensitive patient data, bound by stringent privacy regulations that limit direct data sharing between institutions. Federated Learning (FL) offers a promising paradigm for collaborative model training without centralizing data, preserving privacy and meeting compliance requirements. In this work, we present a novel Quantum Federated Learning (QFL) framework that integrates quantum-inspired optimization techniques to enhance convergence efficiency, reduce communication overhead, and significantly reduce model size. Our proposed QFL framework achieves up to 2–39% reduction in communication rounds, and improves model convergence by 5–60% through quantum-aware optimization methods. Furthermore, by leveraging quantum-inspired model architectures, we achieve a 99% reduction in parameter count compared to conventional deep learning models, significantly lowering the memory and communication cost for edge devices. We evaluate our framework on diverse medical imaging modalities, including chest radiographs, CT scans, ultrasound images, and dermatoscopic skin lesion data, demonstrating its strong adaptability across data types. Despite highly non-IID client data distributions, our QFL models consistently outperform locally trained models and classical federated baselines in both performance and robustness. These results highlight the potential of quantum techniques to enable scalable, privacy-preserving, and resource-efficient federated learning in healthcare and other sensitive domains.
https://www.linkedin.com/in/amandeep-singh-bhatia-ph-d-07b83822/

9. **Targeting the CXCR3 axis in HER2+ breast cancer with self-replicating RNA Lipid Nanoparticles to enhance anti-tumor immunity | *Anchit Bhagat***

Breast cancer (BC) is the most frequently diagnosed cancer in women worldwide with more than 2 million new cases in 2020. The efficacy of immune checkpoint blockade (ICB) for BC is limited, with response rates of <10% for anti-PD-1/PDL1 monotherapy in subtypes that express human epidermal growth factor receptor 2 (HER2+) and/or hormone receptors. Hence, there is an urgent need to improve immune based strategies for BC. One possible approach to enhance response is the application of intra-tumoral (IT) immunotherapy. We have previously reported the efficacy of intratumorally injected plasmid IL-12 (pIL-12-EP) followed by electroporation in a TNBC mouse model. Following pIL-12-EP there was a striking enrichment of the CXCL9/10/11/CXCR3 family in tumor infiltrating immune cells. This led us to hypothesize that this axis may be the critical component downstream of pIL-12-EP treatment that is responsible for anti-tumor responses. In this work, we have gone on to validate the expression of CXCR3 and its ligands by tumor infiltrating lymphocytes (TILs) in biopsies of human HER2+ BC using single cell resolution spatial transcriptomics. We used an IT adenoviral injection to treat an implantable HER2+ mouse model and observed tumor growth inhibition in our Ad-IL12 treated group as compared to the control group with higher CD8 T cell, higher effector memory CD8 T cells, CD8 PD1 cells and higher expression of PD-L1 on myeloid cells along with lower infiltration of neutrophils. Ad-CXCL9 alone was not sufficient to inhibit tumor growth or alter immune cell infiltration. Ongoing efforts to develop a more efficient way of delivering our targeted therapy are focused on lipid nanoparticles (LNPs) containing self-replicating RNA as they possess a number of advantages. We conclude that CXCL9 monotherapy has not been effective and propose that a combination or sequential therapy of CXCL9 with IL12 or another immunostimulatory agent may be required.
https://www.linkedin.com/in/anchit-bhagat-phd-msc-858ab063/

10. **Cloneable nanoparticles: enhancing molecular contrast in biological imaging| *Kanda Borgognoni***

The pathogenesis of many diseases can be difficult to identify because the native mechanisms of many biological pathways are poorly understood. Ribosome biogenesis is an extraordinarily complicated pathway involving hundreds of proteins for pre-ribosome assembly. Structural defects in mature ribosomes are known to cause ribosomopathies and can be oncogenic. Ribosome assembly has been traditionally studied by characterizing isolated intermediates. However, the absence of crucial transient interaction partners as well as extraction from the tissue can paint an incomplete picture of ribosome formation. I hypothesized that by developing methods to noninvasively investigate ribosome biogenesis, I would discover unique assembly steps not apparent in traditional studies. Bioimaging methods, like an MRI, create real-time feedback of cellular processes. Molecular bioimaging, specifically electron cryotomography (cryoET), can provide real-time feedback at atomic-level detail that breaks down the biochemical mechanisms of native pathways as well as how bioprocesses become pathogenic. cryoET produces image information in the form of contrast from every atom in the cell. This volume of information makes it challenging to study specific proteins since images are grayscale mosaics of all cellular proteins which produce similar image contrast. Thus localizing specific proteins *in situ* requires genetically labeling them with a high contrast cryoET tag, similar to how GFP can genetically label proteins for fluorescence microscopy. As no analogous label for cryoET existed, I developed and optimized a novel cloneable Selenium nanoparticle (cSeNP) tag, which is an enzyme that produces a high contrast inorganic SeNP. I am endogenously labeling ribosomes with cSeNP to create molecular beacons that allow us to image ribosomes and their intermediate structures within their native environment, revealing new insight into the intricacies of this complex assembly pathway. This approach has broad appeal as cSeNPs can be genetically incorporated onto other proteins and facilitate the investigation of many native biochemical pathways.

11. **An In Vitro Microscopy Screen Identifies Novel Regulators of *Cryptococcus neoformans* Morphology. | *Eduardo Caro***

Cryptococcus neoformans, a basidiomycete fungus, is a significant opportunistic pathogen responsible for meningoencephalitis, especially in immunocompromised individuals. Understanding its cellular biology and virulence mechanisms is crucial for developing targeted therapeutic and preventive strategies. In this study, we systematically investigated how host-like conditions influence cryptococcal cell wall composition, a critical factor in pathogenicity. Specifically, we examined the effects of RPMI medium, elevated CO_2 levels, and 37°C incubation on cell wall morphology. Using an automated high-throughput 96-well plate imager (ImageXpress Pico), we screened a large-scale mutant library annotated for gene function. By comparing cell morphology under host-relevant conditions with standard laboratory conditions, we identified genes crucial for maintaining cryptococcal morphology during infection. An initial selection strategy focusing on pronounced phenotypes (e.g., impaired budding separation) enabled rapid identification of relevant candidates, followed by functional analyses related to cell wall synthesis. Our approach facilitated the efficient screening of extensive mutant libraries, demonstrating that even subtle morphological changes can be detected using brightfield imaging metrics. This study offers valuable insights into the biology of *C. neoformans*, highlighting the interplay between environmental conditions, cellular architecture, and gene function. Future research will assess selected mutant strains as potential vaccine candidates, aiding in the development of innovative antifungal interventions.

12. **Numeric analysis of the bioenergy production potential of agricultural wastes using a microbial fuel cell coupled with anaerobic digestion | *Sourabh Chakraborty***

Anaerobic digestion (AD) and microbial fuel cells (MFC) have been studied to convert organic wastes such as animal manure and crop residues into energy products. A MFC coupled with AD can convert the wastes into electricity and biogas. This study was to develop a mathematical model to predict and optimize the bioenergy production potential of agricultural wastes using a MFC coupled with AD. Corn stover (CS), cattle manure (CM) and its mixture at various fractions are used as representative agricultural wastes. Aspen plus is used to develop the process models of MFC and AD. RYield reactor was used for simulating hydrolysis reactions of AD, while two separate RCSTR reactors were

utilized for modelling acid generation (Acidogenesis and Acetogenesis) reactions and methanogenesis. Additionally, RCSTR reactor was utilized for modelling MFC (based on digestate obtained from AD). The model is validated by comparing the predicted yields of biogas and electricity with the data reported in literature. The simulation revealed that the biogas quantity formed was highest for CS and lowest for CM. However, lowest amount of biogas from CM corresponded to highest methane content in it. When AD was performed on the binary mixture (1:1 wt/wt CS: CM; with C:N ratio = 24.3), significant quantity of biogas and methane content in it was obtained within the range of that obtained from AD for individual CM and CS. From this, it was realized that co-digestion of CS and CM is helpful in getting considerable quantity of biogas with significant methane content.

13. **Evaluation of neutrophil antiviral responses to HIV-1 | *Haleigh Conley***

Background: Neutrophils, the most abundant leukocyte in the blood, perform robust antimicrobial effector functions to destroy pathogens. These functions include phagocytosis, reactive oxygen species (ROS) production, and cytotoxic granule release. Neutrophil effector functions are triggered by pathogens or through the binding of antibody-antigen immune complex (IC) to cell-surface Fc receptors. Despite their important role in combatting infection, neutrophil responses to HIV-1 and HIV-antibody ICs (HIV-1-ICs) are not well studied. We hypothesized that neutrophil antiviral responses are enhanced in the presence of HIV-1-ICs and the ability of these responses to eliminate infectious virus is influenced by antibody specificity and subclass.

Methods: HIV-1-antibody immune complexes were generated by incubating human monoclonal antibodies (mAbs) with green fluorescent protein (GFP)-expressing HIV-1 virions. These immune complexes were incubated with peripheral blood neutrophils. Phagocytosis was determined by detection of internalized GFP virions using flow cytometry and confirmed using immunofluorescence microscopy. To determine if virus was inactivated following phagocytosis, immune complex-loaded phagocytes were co-cultured with permissive cells containing an HIV-driven luciferase reporter gene. ROS production was measured using luminescence. Levels of cytotoxic granules in the supernatant were measured to evaluate degranulation.

Results: HIV-1-ICs generated with IgG3 mAbs induce at least 2x more binding and phagocytosis of GFP-HIV than IgG1 mAbs, and 30-fold more than uncomplexed HIV. Neutrophils that bind HIV-1-ICs transfer infectious virus to permissible cells. However, transfer is prevented by trypsin washing, suggesting that only extracellular HIV-1-ICs remain infectious. Neutrophils do not induce robust ROS responses or significant cytotoxic granule release in response to HIV-1-ICs.

Conclusions: HIV-1-ICs generated with IgG3 mAbs elicit greater neutrophil phagocytic responses than IgG1 mAbs. Neutrophils bind to and transfer HIV-1 to permissible cells, but neutrophils that phagocytose HIV-1 do not transfer HIV-1 to permissible cells. Neutrophils do not release cytotoxic ROS or MMP-9 granules in response to HIV or HIV-1-IC.

www.linkedin.com/in/haleigh-conley

14. **Generating Panoramas from Ultrasound Videos for Field-Based Longitudinal Injury Surveillance** | ***Matthew Daunis***

Longitudinal injury surveillance systematically monitors injury patterns over time to better understand risk factors and interventions that optimize population outcomes. Current research that employs diagnostic ultrasound to study dose-response relationships causal to tissue adaptation and maladaptation is limited by resources and environments accessible in clinical and laboratory settings. The purpose of this project was to extend longitudinal injury surveillance to field settings by developing a novel approach for generating panoramas from ultrasound videos obtained using a portable, cost-effective ultrasound device. Ultrasound sessions were conducted with 10 men's and 13 women's collegiate soccer student-athletes at the mid-point of their competitive seasons. Ultrasound videos of six lower body muscles and tendons were collected. Panoramas of the tissues were generated using key features within the frames of each video to determine which frames should be included in the panorama and how those frames should align with each other. Four variables within the process (i.e. dimensional-, confidence-, and threshold-based variables impacting feature quantity and alignment criteria) were manipulated, producing 300 panorama variations, for each video to evaluate how changes within the process affect the resulting panoramas. Ten frames from each panorama were compared to their corresponding region within their respective panorama using eight metrics associated with pixel-,

structure-, and distribution-based differences between images. Preliminary results of a 4-way GLMM ANOVA showed all panorama variables had significant main and interaction effects on pixel- and structure-based metrics ($p<0.05$), while three panorama variables had significant main and interaction effects on distribution-based metrics ($p<0.05$). The panorama variables' effects on the evaluation metrics support further evaluation and development of the panorama generating process, including the integration of a machine learning strategy for converging on an optimal configuration for an ultrasound video.

15. **Automated Data Curation for AI Drug Repurposing| *Marcello DeLuca***

Drug repurposing represents a vital approach to medicine, especially for rare diseases where de novo development is prohibitively expensive. Here we introduce the Medicines, Diseases, and Indications (MeDI) resource, designed to accelerate AI-guided drug repurposing by addressing critical data limitations. MeDI consists of three components: a comprehensive list of over 4,300 legally repurposable drugs with 14 filtering options, sourced directly from regulatory authorities; a rationally separated list of distinctly treatable diseases, ontologically harmonized for computational use; and an authoritative collection of drug-disease relationships extracted from approval documents.

A distinguishing feature of MeDI is its enumeration of combination therapies, which constitute nearly 25% of approved medications but are underrepresented in existing resources.

Another distinguishing feature of MeDI is the quantity of training data it makes available. We implemented a novel approach using hierarchical disease ontologies to infer treatment relationships, allowing drugs indicated for parent disease classes to be connected to relevant disease descendants. This methodology expanded our dataset to over 340,000 drug-disease connections—an order of magnitude increase compared to existing knowledge sources. To validate MeDI's impact, we integrated it with state-of-the-art AI models for drug repurposing, documenting significant improvements in prediction performance.

All components of MeDI are machine-readable, ontologically harmonized, and designed for seamless integration into biomedical knowledge graphs. The resource provides provenance links to original approval documents, enabling straightforward verification of each drug-disease relationship.

MeDI addresses a fundamental limitation in the field—insufficient high-quality training data for AI-guided drug repurposing. By establishing clear boundaries for repurposable drugs and treatable diseases while substantially expanding available training connections, this work enables researchers to focus on prioritizing nomination efforts based on current medical needs. MeDI represents a significant advancement in computational medicine resources that may accelerate drug repurposing, target nomination, and AI-driven precision medicine efforts.

https://www.linkedin.com/in/marcello-deluca/

16. **Investigating the implications of nano-structure surfaces on the bacterial adhesion, growth and biofilm formation | *Parth Desai***

Understanding bacterial interactions with nanostructured surfaces is crucial for advancing biomaterial applications. In this study, we fabricated titanium dioxide (TiO_2) nanostructures and systematically compared them with planar TiO_2 surfaces to assess bacterial attachment, growth dynamics, and metabolic activity. Using a combination of water contact angle measurements, Fluorescence microscopy, Atomic Force microscopy (AFM), Scanning Electron Microscopy (SEM), we evaluated surface characteristics, bacterial adhesion, and viability. Our findings reveal that TiO_2 nanostructured surfaces significantly influence bacterial growth and attachment compared to non-structured TiO_2 surfaces. Notably, bacterial viability and metabolic activity were distinctly modulated by nanoscale surface architecture, independent of the titanium dioxide material composition. These results provide the first evidence that bacterial response is primarily driven by nanoscale surface topography rather than chemical composition alone. Such insights pave the way for optimizing biomaterial design in antimicrobial and bioengineering applications especially in the bio implants.

https://www.linkedin.com/in/drphdesai90369/

19. **Structure-guided discovery and small molecule targeting of a regulatory pseudoknot in ABL1 mRNA | *Simon Felder***

RNA structures within coding sequences are increasingly recognized as regulators of translation, yet structurally and functionally validated examples in human mRNAs remain limited. Here, we combined in-cell chemical probing with 3D modeling to uncover a novel pseudoknot within the coding region of human *ABL1* mRNA. Modeling predictions guided in vitro validation by chemical probing and cryo-electron microscopy, confirming the existence of a stable, compact loop–loop pseudoknot. Synonymous mutations that disrupted the pseudoknot led to increased *ABL1* protein levels, establishing its role as a translational repressor. Additionally, we identified a small-molecule fragment that binds the pseudoknot with moderate micromolar affinity in vitro. Ongoing experiments are investigating how these mutations and the ligand influence *ABL1* expression and oncogenicity.

These findings reveal a structured regulatory element within an oncogene and underscore the potential of coding-region mRNA structures as novel targets for small-molecule therapeutics.

www.linkedin.com/in/simon-felder

21. **Comprehensive Probing of RNA Structure in Human Pre-mRNAs | *Claire Fleurisson***

While over 90% of the human genome is transcribed into RNA, more than 95% of therapeutic drugs still target proteins. RNA-targeting drugs remain scarce, with Risdiplam, approved in 2020, being the first and only small molecule to modulate an RNA–protein complex. Developing small molecules that act on RNA remains challenging due to two major obstacles. First, RNA is highly dynamic and negatively charged, making selective and high-affinity binding difficult. Past efforts have improved affinity using polyamines and achieved structural specificity with complex scaffolds such as spirocycles and paracyclophanes. Second, although RNA can fold into 3D structures with druggable pockets, similar to proteins, identifying these structural motifs remains difficult, especially in pre-mRNAs with short half-lives. This project addresses both challenges by expanding the chemical space of spirocyclic synthetic RNA-binding molecules and by developing strategies to identify and study structured motifs in pre-mRNA especially in splicing sites. Together, these advances aim to pave the way for novel RNA-targeted therapeutics.

https://www.linkedin.com/in/clairefleurisson/

22. **Impact of satellite imagery spatial scale on small water body methane emission estimates | *Mollie Gaines***

A critical gap in understanding the global methane (CH^4) budget is quantifying emissions from small artificial waterbodies. CH^4 is a potent greenhouse gas with a global warming potential 28 times higher than carbon dioxide over a 100-year period. One mechanism that may be driving increased CH^4 emissions is an increase in natural emissions from inland aquatic ecosystems, such as small waterbodies (<0.1 km^2). The number, location, and seasonal changes in small waterbodies—particularly artificial (or man-made) waterbodies (i.e., irrigation or stormwater management ponds)—are still relatively unknown, despite their critical importance in CH^4 emissions. Data from satellite imagery is a promising way to map the presence and area of small water bodies, as they acquire data systematically over space and time. However, most prior research has used medium-resolution satellite imagery (30 m), which has been shown to underestimate the area of small waterbodies. In this study, we used machine learning (random forest) and deep learning (U-Net) to classify small water bodies from higher resolution imagery (10 m and 3 m). We found that each resolution could detect seasonal changes in surface water area; however, the higher resolution imagery detects larger area for the same water bodies. We also found that the higher resolution imagery detected more small water bodies than the moderate resolution imagery. Finally, we found that the higher resolution surface water areas had a stronger correlation with CH^4 concentrations (R^2 0.68) than the lower resolution imagery (R^2 0.16). We conclude that higher resolution imagery can 1) identify more small waterbodies than moderate resolution imagery; and 2) produce more accurate estimations of methane concentrations. High resolution imagery can be used to provide a more accurate estimation of local, regional and global methane emissions. Such estimates can help countries better plan to meet their Global Methane Pledge.

https://www.linkedin.com/in/mollie-gaines/

24. **Wood smoke exposure-mediated modulation of sputum proteome depends on airway inflammation and GSTM1 genotype -a pilot study | *Arunava Ghosh***

Background: Increased incidence of wildfire events is a major concern in the US and globally. Previously we reported that the percentage of polymorphonuclear neutrophils (%PMN) in sputum (Non-responders vs Responders) and *GSTM1* genotype (sufficient vs null) play an important role in determining wood smoke exposure-derived pulmonary effects (Inhal Toxicol. 2022). However, detailed examination of sputum proteome following exposure and comparison between known susceptible phenotypes is understudied. Our current study addresses this aspect by examining modulation of protein levels in sputum samples, post controlled exposure.
Methods: The current study cohort included 21 healthy volunteers without any lung diseases. Sputum samples collected from the participants were analyzed by LC-MS. Normalization was done by a factor calculated from the total sum intensity and the median intensity. T-test was used to compare between the groups, and a p-value <0.05 with abs. $\log_2$ Fold Change >0.5 was considered significant.
Results: An overall decrease in protein levels in sputum was noted in 24 hour post exposure samples. When participants were categorized based on sputum %PMN, non-responders demonstrated more changes, predominantly downregulation of protein levels compared to the responders. Changes in the non-responders were mostly associated with protein structure and polymerization processes. When *GSTM1* genotype of the participants were considered, more proteins were significantly altered (mostly downregulated) in SUFF genotype than NULL group.
Conclusion: Overall, sputum proteome of participants from non-responders and *GSTM1* SUFF genotype groups showed intensified response and more downregulated proteins in the post wood smoke particle exposure timepoint. The study observations imply a role of individual characteristics in the determination of susceptibility or vulnerability towards wildfire smoke inhalation-mediated pulmonary effects.
https://www.linkedin.com/in/arunavagin/

25. **GRIP: a one-pot in vitro library display platform for massively parallel evolution of proteins | *Victoria Goldenshtein***

Library display technologies have enabled the discovery of proteins with specific affinity for target substrates, accelerating progress across immunology, oncology, infectious disease research, and drug discovery. These platforms rely on physically linking a protein (phenotype) to its encoding nucleic acid (genotype), enabling selection from vast variant libraries. Traditional in vivo methods like Phage Display offer high genotype-phenotype linkage stability but are limited to ~10^9 variants due to bacterial transformation constraints. In contrast, in vitro approaches can support much larger libraries (~10^{12} variants), but suffer from other limitations. For example, Ribosome Display, which relies on the ribosome to link protein and mRNA, is hindered by linkage instability. mRNA Display covalently links mRNA to its protein but is technically challenging and suffers from low efficiency, reducing effective library size.
Here, we present a novel *in vitro* protein display technology called **GRIP Display** (Gluing RNA to Its Protein) that permits generation and simultaneous screening of vast libraries (>10^{12} variants) against a target of interest. The binding pocket optimization of a protein had proven to be a difficult task for the existing technologies previously. Here, we demonstrate **1**) GRIP Display's utility in optimization of a large binding tunnel of HaloTag protein (HTP) to enhance the covalent capture of its chemical ligand (HTL); **2**) the development of high affinity orthogonal HTP/HTL pairs with minimal cross-reactivity.
GRIP Display retains at least 10,000-fold more genetic material than Ribosome Display, with minimal genetic cross-talk and significant selection enrichment, without imposing any additional experimental steps. GRIP Display represents an unrivaled alternative to the existing technologies by eliminating the trade-off between library size, linkage stability, and ease of use.
https://www.linkedin.com/in/victoria-goldenshtein

26. Non-fibrillar collagens IV and VI have opposing impacts on macrophage migration and pro-regenerative marker expression: implications for the tumor microenvironment | *Jennifer Hammel*

Within the tumor microenvironment (TME), the extracellular matrix is remodeled to suppress anti-tumor immunity and promote tumor progression. We have previously demonstrated that collagen VI, an immunosuppressive non-fibrillar protein, alters T cell behavior in prostate cancer and sarcoma (1,2). Another key immune element of the TME is tumor-associated macrophages (TAMs) that exhibit a pro-regenerative phenotype, supporting tumor progression. Thus, we sought to understand how collagen VI could alter macrophage behavior in the TME to promote tumor survival and immunosuppression. To do so, we isolated monocytes from umbilical cord blood, differentiated them into macrophages, and polarized them toward pro-inflammatory and pro-regenerative phenotypes. Then, we cultured them on uncoated, collagen I (as a fibrillar collagen control), collagen IV (as a non-fibrillar collagen control), or collagen VI coated plates and performed live imaging and flow cytometry for polarization markers and antigen presentation. We found that collagens I and IV, but not collagen VI, promoted the migration of unpolarized macrophages compared to the uncoated control. Interestingly, in pro-inflammatory and pro-regenerative macrophages, only collagen IV promoted migration, demonstrating key differences between all collagen types. This pairs with our findings that only collagen VI promoted the expression of CD206, a pro-regenerative marker, in unpolarized and pro-inflammatory macrophages. Overall, we have demonstrated that collagen VI is able to alter macrophage behavior in 2D. Our results suggest that collagen VI reduces the migratory capacity of macrophages while polarizing them toward a TAM phenotype. We will next study macrophage behavior in 3D using a collagen I+IV and collagen I+VI hydrogel system that we have established and characterized with controlled stiffness and fiber density. We will further increase complexity by including vasculature and tumor cells to better model the TME.

https://www.linkedin.com/in/jh-hammel/

27. Developing Isoquinolinone Carboxamides as Orexin Receptor Antagonists | *Rhashanda Haywood*

G protein-coupled receptors, orexin type 1 and orexin type 2 (OX_1R and OX_2R) have become molecular targets of interest for the development of novel treatments for disorders of the central nervous system (CNS). Neuropeptides orexin-A and orexin-B are endogenous ligands for the OX_1R and OX_2R receptors found throughout the CNS. Upon binding to OXRs, they are responsible for physiological functions such as reward seeking, stress, food intake and the sleep–wake cycle. Disruption of normal orexin receptor action can lead to neurological disorders, obesity and inflammation. Studies have shown that loss of orexin neurons leads to the onset of narcolepsy type I. Isoquinolines are a privileged structural motif found in bioactive molecules and have demonstrated potential as therapeutics to treat numerous human diseases. A class of isoquinolines are currently marketed as dual orexin receptor antagonists (DORAs) and selective OXR antagonists (SORAs) as chemical probes to study orexin signaling, thus showing the utility of structurally similar molecules to study biological pathways. We have investigated octahydroisoquinolin-1-one-8-carboxamides for novel biological activity via high-throughput screening (HTS) through the NIH Molecular Libraries Program. Several analogs were identified as potent, G protein-biased kappa opioid receptor agonists. Other analogs and additional screening led to the discovery of exemplars that were inhibitors of the OX_1R with moderate activity and promising selectivity. In this study, we will further optimize the potency and physical properties of this series to develop complementary chemical tools for studying orexin signaling.
https://www.linkedin.com/in/rhashanda-haywood-phd-4b75b166/

29. Scalable Personalization of Robotic Prostheses: A Reinforcement Learning Approach for Real-World Mobility| *Woolim Hong*

Lower-limb amputation presents a significant physical and psychological impact, increasing the risk of falls, injuries, and secondary impairments while limiting individuals in daily activities and community participation. In the U.S., over 2 million people are living with limb loss, and this number is projected to increase by 145% by 2060 due to the rising

prevalence of vascular diseases and diabetes. Many individuals with lower-limb amputations struggle to perform daily tasks such as walking on slopes or climbing stairs, largely due to the lack of active control and net power generation in conventional prostheses. Robotic prostheses have emerged as a promising solution, enabling more natural and adaptive gait across diverse locomotion tasks. However, these devices often lack personalized control, failing to account for individual user needs. This lack of personalization can result in suboptimal performance and increase the risk of secondary complications. Although clinicians and prosthetists attempt to optimize prosthetic parameters manually, this process is time-consuming and becomes increasingly complex in environments involving varied terrain. To address these challenges, this study introduces a reinforcement learning (RL)-based automatic tuning framework to deliver personalized control of a robotic knee prosthesis and enhance gait performance. The underlying control strategy is impedance control, designed to emulate human joint behavior. We propose a two-stage tuning mechanism designed to ensure both efficiency and safety during user interaction. In the first stage, the RL agent learns an optimal policy through a data-driven offline process that incorporates human knee trajectory resemblance, phase alignment, and penalization of safety-critical conditions. In the second stage, the offline-trained agent is deployed in a human-in-the-loop setting to fine-tune the knee stiffness parameters in real time as the user walks with the prosthesis. This method enables adaptive, user-specific control without manual parameter tuning, offering a scalable and intelligent approach to next-generation lower-limb assistive technologies.
https://www.linkedin.com/in/woolim-hong/

31. **Pigment-Dependent Mitochondrial difference in Retinal Pigment Epithelium: Implications for AMD Susceptibility in Albino Mice | *Md Jahirul Islam***

Albinism, a genetic condition marked by melanin deficiency, is associated with significant ocular abnormalities, including reduced visual acuity, foveal hypoplasia, and nystagmus [1–3]. The absence of melanin in albino mice (Balb/c strain) renders their RPE particularly vulnerable to oxidative stress and light-induced damage, suggesting a potential mechanistic link to age-related macular degeneration (AMD) [4, 5].

To investigate this susceptibility, we cultured and characterized RPE cells ex vivo from pigmented (C57BL/6J), depigmented (passaged C57BL/6J RPE), and albino (Balb/c) mice. Using immunocytochemistry, we confirmed RPE identity via RPE65 and tight junction integrity via ZO-1 expression. Scanning electron microscopy revealed a higher number of mitochondria with reduced size in de-pigmented and albino RPE compared to pigmented RPE. Quantification of mitochondrial DNA (mtDNA) corroborated this increase in mitochondrial count.

We further assessed the expression of key mitochondrial dynamics proteins. Mitochondrial fusion proteins—Mitofusin 1 (Mfn1), Mitofusin 2 (Mfn2), and Optic atrophy 1 (OPA1)—were significantly downregulated in depigmented and albino RPE, while the fission protein Dynamin-related protein 1 (Drp1) was upregulated, indicating a shift towards mitochondrial biogenesis.

Using the Seahorse XF Analyzer, we measured mitochondrial function. Albino and de-pigmented RPE exhibited reduced basal respiration and spare respiratory capacity. Intriguingly, in vitro re-pigmentation of albino RPE using melanin extracted from B6-derived RPE restored mitochondrial function to levels observed in pigmented RPE. This was further validated by the Seahorse ATP Rate Assay, which showed diminished ATP production in de-pigmented and albino RPE, with restoration upon re-pigmentation.

These findings suggest that pigment (melanin) may regulate mitochondrial dynamics and energy metabolism in RPE cells. Given the central role of mitochondrial dysfunction in the pathogenesis of AMD [6], our data provides a potential mechanistic basis for the increased susceptibility of albino eyes to degenerative retinal diseases. Ongoing studies aim to elucidate how light exposure, particularly blue and white light, influences mitochondrial biogenesis and bioenergetics in pigmented versus non-pigmented RPE cells, with the goal of uncovering mechanisms underlying AMD susceptibility and identifying potential therapeutic targets for intervention in both pigmented and albino models.

33. **Electrochemical Assay for Real-Time Monitoring of Gas-Reducing Enzymes: A Case Study on Laccase and Formate Dehydrogenase | Nisha Jangir**

Electrochemical assays have emerged as an efficient and cost-effective approach to measure the real-time activity of redox enzymes. Traditionally, gas-reducing enzyme activity has been assessed with spectrophotometric method using secondary substrates. The electrochemical assay, however, can detect enzyme activity using gas as a substrate, highlighting the need to develop an electrochemical assay method specifically tailored for gas-reducing enzymes. In the current study, we developed an electrochemical assay designed to measure the activity of laccase and formate dehydrogenase (FDH), two key enzymes involved in biocatalysis, bioenergy production, and environmental applications. Laccase catalyzes the reduction of oxygen to water, while FDH plays a role in converting carbon dioxide into formate and vice versa. The current method utilizes mediators to facilitate electron transfer between the enzyme's active site and the electrode surface, enabling the real-time detection of enzymatic reactions. This includes monitoring the reduction of oxygen by laccase and carbon dioxide by FDH through electrochemical signals. Key factors such as enzyme loading, mediator concentrations, and substrate/gas concentration were investigated to optimize the assay's sensitivity and stability. The developed electrochemical assay demonstrated reproducibility for enzyme activity which makes it a promising alternative to traditional methods and offering a robust and scalable approach for studying and utilizing gas-reducing enzymes in diverse fields, including environmental monitoring and industrial biocatalysis.

https://www.linkedin.com/in/nishajangir

34. **Ultrasound Parameter Optimization for Effective Drug Delivery to MRSA Diabetic Wound Biofilms in Mice with Passive Cavitation Detection | *Jyoti Jethe***

Background: Chronic wounds are often colonized by bacterial biofilms, that impede drug penetration facilitating drug tolerance, prolonging healing process in wounds and increasing risk of relapse. Persister cells, a subpopulation that survive high doses of antibiotics, are a key reason for relapses. Our previous studies showed that using ultrasound, nanodroplets, and an anti-persister drug significantly improved the effectiveness of gentamicin in treating methicillin-resistant Staphylococcus aureus MRSA-infected diabetic wounds in mice. This study introduces real-time feedback mechanisms utilizing passive cavitation detection to refine ultrasound parameters for the intervention of preclinical wound infections.

Methods: In a MRSA wound model using SKH-1 hairless mice (n=40), wounds were treated twice daily with gentamicin and palmitoleic acid from days 2 to 4 post-infection. One treatment each day was followed by nanodroplet administration and ultrasound (800 kPa or 2 MPa) using a 1.1 MHz focused transducer (9.09% duty cycle) equipped with a central element for passive cavitation detection. Ultrasound was applied for 5 minutes with nanodroplet replenishment every minute and recording signals every 15 seconds to quantify stable and inertial cavitation. On day 5, wounds were harvested and plated to assess the bacterial burden.

Results: Ultrasound and nanodroplets potentiated the antibiotic effect of gentamicin. Passive cavitation was successfully implemented, and cavitation signal was quantified and compared for 800 kPa and 2 MPa. This data was compared to bacterial burden reductions and wound size changes. The regression analysis revealed a negative correlation between cavitation and bacterial burden, indicating that greater cavitation may enhance bactericidal efficacy.

Conclusion: Passive cavitation detection effectively quantifies stable and inertial cavitation across ultrasound pressures and offers a real-time feedback tool to optimize ultrasound parameters for enhanced antibiotic efficacy. Future work will explore improved probes for better wound coverage, refine acoustic settings, and develop more effective nanodroplets for targeted delivery and enhanced cavitation advancing clinical translation for treating resistant biofilm infections.

www.linkedin.com/in/dr-jyoti-jethe-755602185

35. **Functional Characterization of Long Noncoding RNA KCNQ1OT1 in Rhabdomyosarcoma | *Ara Jo***

Rhabdomyosarcoma (RMS) is the most common soft tissue sarcoma in children and adolescents, with survival for high-risk cases stagnant at less than 30%. Contemporary molecular classification of RMS is into fusion-positive (FP)

and fusion-negative (FN) groups, based on expression of fusion oncogenes. Although the majority of FN-RMS tumors exhibit mutations in protein coding genes, especially in the RAS pathway, about 25% instead show only copy number alterations and LOH at chromosome 11p15.5, which harbors tumor suppressor genes (TSGs) *CDKN1C*, *PHLDA2*, and *SLC22A18*. The 90kb long noncoding RNA KCNQ1OT1 (OT1) is a known *cis* silencer of this locus. We hypothesize that OT1 is upregulated in RMS, contributes to RMS tumorigenesis by repressing critical TSGs, and that targeting OT1 could provide a novel therapeutic approach. Using qPCR and epigenomic interrogation of available RMS tissue, we find OT1 highly expressed in FN-RMS cell lines and banked tumor samples. Complementary genomic methylome data of RMS tumors shows silencing and activation of the *CDKN1C* and *OT1* promoters, respectively. Suppression of *OT1* using shRNA against various sites along the transcript, or a dual excision CRISPR knockout (DECKO) of the promoter, inhibits RMS cell proliferation, induces apoptosis, and recovers TSG expression. In a candidate approach, using both gain and loss of function approaches, the Hippo pathway YAP1 transcriptional co-activator was found to modulate OT1 expression. Unbiased genomic screens are planned. Finally, using *in silico* binding prediction models, we designed OT1-directed anti-sense oligonucleotides (ASOs), demonstrating they can be delivered to RMS cell lines. These ASOs, designed to degrade or inhibit OT1 function, will be tested in RMS cell-based and xenograft models to determine their efficacy and specificity. To generate additional information about regions of OT1 that might be therapeutically tractable, antisense DNA capture probes will be applied to OT1 in RMS cells to generate higher nucleotide resolution maps of OT1 structure and protein binding. This study not only deepens our understanding of OT1's role in RMS but also advances the development of innovative RNA-based treatments, addressing a critical need for effective therapies in this aggressive childhood cancer.
www.linkedin.com/in/ara-j-0bb723117

36. **The Development of a Low-Cost Liquid Crystal Module for Cancer Cell Imaging Using White-Light Microscopy | *Udayakumar Karuppanan***

Background: Quantitative phase microscopy (QPM) is evolving in the field of microscopy, capturing the interest of cell biologists and microbiologists. Quantifying the phase in cellular imaging means estimating the total shift of interference light. Due to cell thickness, the refractive index varies, creating an optical path length difference (OPD) between the sample path (cell) and the reference path (fixed mirror), which creates interference light. By shifting this interference light temporally, the total phase shit is achieved. Several phase-shifting methods exist; however, they are sensitive to environmental disturbance and need multiple phase-shifted images for phase extraction, which requires a longer exposure time of light on the bio sample, which creates phototoxicity.
Objectives: To develop a low coherence white-light QPM incorporating a compatible liquid crystal (LC) module to get a cellular phase map.
Methods: A common-path interferometry was adopted to create interference between the sample and reference, and a liquid crystal (LC) based optics for phase-shifting. Interferometry and azobenzene-based LC modules are aligned to make the setup simple, compact, and straightforward. This LC module generates optical phase delays of both single and total cells (dry mass) without any moving parts of the LC, compensating for temporal movement on conventional phase shifting. A polarization camera captures a single frame of four-quadrant, high-contrast phase-shifted images (generated by LC), enabling easy real-time and post-lateral phase retrieval of cells.
Results: A phase map of the cancer cells was retrieved from a single-shot phase-shifted image, and its thickness was estimated.
Conclusions: A low-cost white light QPM integrating LC module is configured, which is compact enough to image cancer cells. We aim to refine it further to integrate it into conventional microscopes. QPM, a label-free imaging, meaning no dying of the bio-sample, upon integrating our LC module, may offer affordable and biologically safe QPM systems, enhancing phase imaging.

37. **The effect of optical flow perturbations on walking foot placement control in people with multiple sclerosis | *Kavya Katugam-Dechene***

Lateral foot placement is adjusted step by step to maintain balance while walking. Impaired control of this process may underlie increased fall risk observed in people with multiple sclerosis (PwMS), even before the onset of significant physical disability. Prior studies, including our own, have shown that PwMS are especially vulnerable to balance

perturbations, but traditional metrics like step width variability offer limited insight into how foot placement is regulated over time. In this study, we applied detrended fluctuation analysis (DFA) to assess the temporal persistence of step width (SW) and step length (SL) during treadmill walking with and without optical flow perturbations. DFA α exponents >0.5 indicate persistent (same-direction) step-to-step changes, <0.5 indicate anti-persistent (opposite-direction) changes, and =0.5 indicate uncorrelated changes. Fifteen adults with relapsing-remitting MS and fifteen matched controls walked on a treadmill while viewing a virtual hallway with either unperturbed, AP-perturbed, or ML-perturbed optical flow. Mixed-factorial ANOVAs showed a significant main effect of condition on αSW and a group×condition interaction for αSL. Across both groups, αSW was lower during ML perturbations compared to AP or unperturbed conditions, indicating less persistent SW regulation. For PwMS only, αSL was significantly lower during AP perturbations compared to unperturbed walking, suggesting less persistent SL regulation. These findings suggest that ML perturbations impair SW regulation in all participants, while AP perturbations specifically disrupt SL regulation in PwMS. By applying DFA, we captured a more nuanced picture of control than traditional variability measures allow. PwMS demonstrate less consistent step-to-step adjustments under visual perturbations, suggesting impaired regulation of foot placement that may contribute to fall risk.

38. **Trends in dental care use among adolescents and young adults (1994-2018): Impact of school-based dental care education and neighborhood context. | *Amandeep Kaur***

Purpose: Dental visits declined over time, yet prior research overlooks preventive education and structural barriers. This study assessed dental care use (DCU) trends, its association with school-based dental care education (SDCE), and neighborhood conditions.

Methods: We used data from the National Longitudinal Study of Adolescent Health (Add Health), including 6,504 valid cases at wave 1. Dental exams (past 12 months) and school-based dental education were binary variables. Neighborhood conditions were re-coded as well-kept vs poor. Covariates include race, language, grade, land use, and insurance. We accounted for complex survey design, using "Proc Surveyfreq" and assessed associations using "Proc Surveylogistic", reporting weighted percentages and odds ratios.

Results; Our weighted sample included males (50.8%), non-Hispanic (87.8%), White (74.3%), US-born (92.3%), English-speaking (92.8%), high schooler (65.8%), suburban residents (37.9%), well-kept neighborhoods (86.9%), and private insurance holders (51.5%). About 67.2% received SDCE, which varied by nativity and grade level. Female (χ^2=10.25, p=.007), non-Hispanic (χ^2=91.14, p<.0001), White (χ^2=128.66, p<.0001), English-speaking (χ^2=72.05, p<.0001), privately insured (χ^2=294.35, p<.0001), and those in suburban (χ^2=55.91, p<.0001) or well-kept neighborhoods (χ^2=66.76, p<.0001) were more likely to use dental care; foreign-born adolescents (χ^2=16.01, p=.009) were less likely. DCU declined across waves—67.4%, 69.7%, 56.6%, 55.8%, 62.3% (P<.0001), even among consistently surveyed. The adjusted analysis confirmed this trend (W2: OR=1.16, p=.099; W3: OR=0.60, p<.0001; W4: OR=0.51, p<.0001; W5: OR=0.65, p=.0002). SDCE showed no significant effect (OR_{Adj}=0.93, p=0.514), while poor neighborhoods were linked to reduced DCU (Crude OR=0.58, p<.0001; Time-adjusted OR=0.58, p<.0001; Fully adjusted OR=0.82, p=0.088).

Conclusion: Dental care use declined from 1994 to 2018, with disparities driven more by neighborhood conditions than school-based dental education. Addressing structural barriers may help improve access to care. A non-significant weak relationship between SDCE and DCU draws attention to the need for better-translating knowledge into action.
https://www.linkedin.com/in/amandeep-kaur-ak91a60a150

39. **Optimization of Electrotransformation Protocol for Vaginal Lactobacillus crispatus | *Eun Sol Kim***

The vaginal microbiome plays a crucial role in maintaining women's health, with *Lactobacillus crispatus* being one of the dominant species in health state. This bacterium helps maintain a low vaginal pH and provides protection against infections. Bacterial vaginosis (BV) represents a shift away from a healthy, *Lactobacillus*-dominant state in the vaginal microbiome. Although antibiotics such as metronidazole are commonly used to treat BV, the microbiota does not always return to a stable, *Lactobacillus*-rich state. This underscores the need for strains with improved persistence and colonization potential. Engineered *Lactobacillus* strains offer a promising strategy to restore healthy microbiota and deliver therapeutic functions. While gut- and food-derived *Lactobacillus* species have been widely used in bacterial engineering, vaginal isolates remain underexplored due to their slow growth and low transformation efficiency.

This study aims to establish an optimized electrotransformation protocol for *L. crispatus* isolated from a clinical vaginal swab. To enhance transformation efficiency using plasmid pTRK892, we tested various culture conditions to promote robust bacterial growth and evaluated multiple pretreatment strategies. Optimization of media components and incubation conditions provided insights into cell viability and growth behavior, which informed the setup of transformation experiments for vaginal *Lactobacillus*. Glycine pretreatment enhanced electrocompetence, and the optimized protocol yielded up to ~10^3 transformants per µg of plasmid DNA in one representative strain.
To assess protocol generalizability, we applied the same conditions to twelve additional clinical *L. crispatus* isolates. While transformation efficiency varied across strains, most yielded transformants at levels around ~10^2 per µg DNA, demonstrating the protocol's adaptability across diverse vaginal isolates.
By overcoming key challenges in culturing and transforming vaginal *Lactobacillus*, this study contributes a practical and reproducible method for advancing genetic manipulation of *L. crispatus*. These findings lay the groundwork for future studies in functional genomics and therapeutic probiotic development targeting vaginal health.
www.linkedin.com/in/eunskim43

41. **Impact of Stakeholder Engagement on the Design and Knowledge Transfer of Automated Quality Assurance (QA) Tools in Radiation Oncology Prior to Implementation| *Elizabeth Kwong***

This work aims to examine the impact of stakeholder engagement on the knowledge transfer and pre-implementation outcomes of acceptability, appropriateness, and feasibility when designing an automated quality assurance (QA) tool between two different radiation oncology departments: University of North Carolina (UNC) and University of California San Diego (UCSD).

43. **Novel approach to measuring enzyme activity at sea | *Chad Lloyd***

Heterotrophic microorganisms transform and ultimately respire a substation fraction of the organic matter produced by phytoplankton in the surface ocean. Much of this organic matter is composed of polysaccharides, high-molecular weight (HMW) carbohydrates. To initiate degradation of these polysaccharides, microorganisms must produce the structurally-specific enzymes necessary to hydrolyze these complex substrates. Polysaccharides range substantially in the number of enzymes needed for degradation; the number of enzymes needed to degrade a polysaccharide scales with its complexity (Bligh et al., 2022). By adapting a method using fluorescently-labeled polysaccharides linked to agarose beads (Arnosti, 2003), we investigated degradation of laminarin—a common marine polysaccharide (Becker et al., 2017)—at 11 unique sites in the western North Atlantic Ocean. This novel approach to measuring enzyme activity in the ocean can give us a quicker snapshot of hydrolysis, as we can measure hydrolytic activity over the course of 1-3 days, while normal measurements for polysaccharide hydrolytic activity takes multiple days to collect samples, analyze them, and calculate activity rates. This method can also be applied to measurements of enzyme activity more quickly in the field. We found that laminarin activity was detected at nine stations, and the amount of activity differed from region to region in the ocean.
https://www.linkedin.com/in/cchadlloyd/

44. **Transient Dynamics of Open Quantum Systems using the Multiparticle Holstein Hamiltonian | *Sreeja Loho Choudhury***

Polarons are key quasiparticles that govern the electronic and optical properties of organic semiconducting polymers and molecular aggregates. Understanding the dissipative dynamics of polarons is crucial for elucidating how quantum systems evolve in realistic environments, with applications spanning quantum technologies, condensed matter physics, and chemical/biological systems [1]. In this work, we investigate the dissipative dynamics of polarons in a one-dimensional linear chain coupled to a bath of harmonic oscillators, with a focus on understanding the phenomenon of decoherence [2]. We employ an efficient quantum dynamical approach based on unitary time evolution, where the dynamics is governed by the exponential of Holstein-style vibronic Hamiltonians diagonalized using a multiparticle basis set. We extend this theoretical framework to compute charge carrier mobility from the quantum dynamical results [3]. To explore environment-induced effects, we systematically increase the dimensionality of the bath and observe a

clear trend of coherence and purity decay in the system [4,5]. The subsystem purity is obtained by computing the trace over the bath degrees of freedom of the total time-evolved density matrix [6]. Our model system begins with a dimer, initially excited at one site, coupled to a bath of harmonic oscillators, enabling controlled investigation of system-bath interactions and their impact on quantum coherence and charge carrier mobility.

45. **Exploring the Role of Stress and piRNA Regulation in Germ Cell Immortality | *Lu Lu***

Healthy germ cells maintain themselves in a pristine unstressed state and can be transmitted from generation to generation, indefinitely. Understanding how this germ cell immortality is maintained could provide insights relevant to cell aging and potential rejuvenation of somatic cells. Germ cell immortality is promoted by several pathways, including telomerase and piRNA-mediated genome silencing. piRNAs mediate transcriptional silencing of many loci, such as transposons, and prevent inappropriate silencing of rDNA and histone loci that are important for maintaining the epigenomic integrity of germ cells. The loss of piRNA silencing pathway in *C. elegans* results in a transgenerational sterility phenotype, termed the Mortal Germline phenotype (Mrt). Our previous studies on *prg-1*/Piwi mutants suggest that small RNA imbalance underlying the *prg-1*/Piwi pathway disruption results in the transmission of hereditary stress that builds up across generations, ultimately leading to germ cell atrophy and sterility of late-generation mutants. We are studying the role of a potential stressor that may contribute to the Mrt phenotype in *prg-1*/Piwi mutants and are exploring the regulatory mechanism of this stressor.

46. **A Brain Aging-on-a-Chip Platform Modeling Metabolism-Restricted Neurodegeneration | *Surjendu Maity***

The risk of neurodegenerative diseases rises considerably with aging, yet the cellular mechanisms that contribute to the initial decline of brain function remain inadequately understood because of the constraints of conventional research models. To address this gap, we developed a human-relevant brain aging-on-a-chip platform that integrates 3D neurospheroids and microglia within a microfluidic co-culture system. This innovative approach allows us to simulate key features of aging-related metabolic stress by depleting nicotinamide adenine dinucleotide (NAD^+), a critical metabolic cofactor essential for mitochondrial function and DNA repair. A decrease in NAD^+ levels causes structural changes in neural cells, including axonal fragmentation and synaptic loss, as well as reduced expression of NAD-dependent genes. This results in decreased neuronal activity and impaired synaptic transmission. To further explore the role of immune aging in neural dysfunction, we introduced microglia exhibiting aging-like characteristics into our co-culture system. These microglia showed a reactive phenotype that impaired neuronal firing and reduced synaptic density, even when interacting with healthy neurospheroids. These adverse effects were observed in both direct and indirect co-culture setups, highlighting the role of soluble inflammatory factors. Our model illustrates the relationship between metabolic decline and immune activation that triggers early neurodegenerative changes. This platform allows for the real-time observation of the deterioration of brain cells, supporting studies on mechanisms, and the testing of therapies by providing new opportunities for tackling age-related neurological conditions.

https://www.linkedin.com/in/surjendu-maity-45306259/

47. **Design Principles for Introducing Paramagnetic Spin Centers in Two-Dimensional Polymers | *Mohammed Zahid Malik***

Understanding the design principles underlying the formation of paramagnetic-conjugated structures with high spin density is essential for developing next-generation room-temperature organic ferromagnets (RT-OFMs). However, progress in RT-OFMs development is still limited by key challenges, including radical instability, the lack of spontaneous magnetic moments, and weak magnetic exchange interactions. Motivated by recent experimental observations [1], we theoretically investigate how light-matter interactions impact magnetism and charge transport in 1D and 2D conjugated systems. Understanding these phenomena in doped polymers is particularly challenging: at low doping levels, polarons serve as the primary charge carriers, while at higher doping levels, more complex multipolaron species such as bi-, tri-, and tetra-polarons emerge. Their interactions with counterions and polymer microstructure further complicate our

fundamental understanding of the processes governing magnetism and charge transport. In this study, we employ a modified Hubbard model that incorporates spin-dopant interactions, anion-anion repulsion, and static defects to investigate the formation mechanisms of polarons and bipolarons in 1D and 2D conjugated structures [3]. Our goal is to understand how these factors influence magnetic and charge transport properties and to develop design rules for achieving high spin density in purely organic molecules.

48. **Orchestrated sarcomeric protein regulation in donor-derived skeletal muscle microphysiological system | *Vinicius Mariani***

The development of donor-derived skeletal muscle microphysiological systems (MPS) have become powerful tools to study mechanisms of muscle dysfunction and test potential therapeutic interventions. However, it is unclear whether skeletal muscle produced in these platforms can replicate the orchestrated contractile protein regulation that happens inside the sarcomere of human skeletal muscle fibers during contraction. In this study, we prepared and activated permeabilized single fibers from our muscle MPS developed from primary myoblasts of female (F) and male (M) donors (3-4 fibers per muscle bundle, 4-5 muscle bundles per group). Permeabilized muscle fiber preparations allow for titration of intracellular calcium concentration and the bypass of muscle excitation with direct exposure to calcium-containing (pCa, -log[Ca^{2+}]) solutions, offering a controlled environment to test contractile protein function and regulation. F and M MPS fibers reproduced the sigmoidal force-pCa and hyperbolic force-velocity relationships of human skeletal muscle fibers. Maximum specific force (kN/m^2; F = 28.4 ± 11.7 and M = 31.5 ± 10.8), calcium sensitivity ($[Ca^{2+}]_{50}$, μM; F = 0.90 ± 0.31 and M = 0.67 ± 0.09), peak power (kN/m^2*L_O/s; F = 2.27 ± 0.81 and M = 2.25 ± 0.79), and maximum velocity (L_O/s; F = 2.02 ± 1.16 and M = 1.49 ± 0.26) outcomes did not differ between groups (means ± SD shown, $p > 0.05$). Interestingly, female fibers presented slower rates of force redevelopment (ktr, s^{-1}) compared to male fibers, 2.68 ± 0.97 versus 3.66 ± 0.65 ($p = 0.0044$), which suggests differences in cross-bridge kinetics between sexes. Our study is the first to report contractile protein regulation in donor-derived skeletal muscle MPS. Ultimately, our data further validates the utility of the muscle MPS platform to test mechanisms of contractile dysfunction and therapeutic interventions capable of targeting contractile proteins in muscle disease.
https://www.linkedin.com/in/vini-mariani-ph-d-ms-63b209176

49. **Psychological and Physical Readiness Profiles in Patients after Anterior Cruciate Ligament Reconstruction | *Hana Marmura***

Background: Suboptimal return to sport (RTS) rates continue to be reported for patients after anterior cruciate ligament reconstruction (ACLR) despite established criteria. Psychological factors, in addition to physical factors, are likely to affect RTS and secondary ACL injury rates, yet these factors are traditionally assessed in isolation.
Purpose: To define and examine the agreement between physical and psychological readiness after ACLR by constructing patient profiles (i.e., combinations of both physical *and* psychological readiness outcomes), and investigate whether these distinct profiles are predictive of secondary ACL injury following ACLR.
Study Design: Multi-site retrospective cohort study
Methods: Data was obtained from the ACL Reconstruction Rehabilitation Outcomes Workgroup (ARROW) registry. We constructed "Readiness Profiles" to categorize patients by their physical *and* psychological readiness to RTS based on established criteria. Isokinetic quadricep strength and single leg hop performance were used to assess physical readiness two separate sets of profiles. The ACL Return to Sport after Injury scale (ACL-RSI) scores was used as a psychological measure. Frequencies of all profiles were reported, and logistic regressions were run to investigate the ability of the defined profiles to predict secondary ACL injury.
Results: Physical and psychological readiness aligned for only 52.6% of patients (169/321) when using quadricep strength and 62.5% (255/408) when single leg hop was used. The categorical profiles were not predictive of secondary ACL injury ($p > 0.05$).
Conclusion: There are a variety of distinct profiles of physical and psychological readiness in patients post-ACLR with disagreement between psychological readiness to return to sport criteria. Therefore, interpreting psychological responses to injury and recovery in the context of physical function (i.e., using a biopsychosocial approach) is important to understanding whether physical or psychological factors should be targeted in subsequent treatments.
https://www.linkedin.com/in/hana-marmura

50. Pre-treatment innate inflammation associates with survival after polio virotherapy and can be modulated to sensitize gliomas to in situ vaccination | *Lalita Mazgaeen*

Early-stage clinical trials in glioblastoma (GBM) have tested various virotherapy strategies, yet only a subset of patients appear to benefit. We previously demonstrated that a recombinant poliovirus (PVSRIPO) functions by inducing MDA5-dependent, type I interferon (IFN) dominant innate inflammation in myeloid cells to provoke durable and functional antitumor T cell responses in mice. Long-term survival after intratumoral PVSRIPO infusion was observed in a subset of patients with recurrent GBM (rGBM) in two clinical trials.RNA- and whole exome sequencing of pre-treatment tumor tissue from patients enrolled in phase I and II clinical trials and their blood samples revealed that survival after PVSRIPO was associated with higher pre-treatment intratumoral neutrophil density, MHC-class II gene expression, and higher pre-treatment inflammatory cytokines in blood. Post-treatment induction of type I/III IFNs detected in blood one day after PVSRIPO infusion also associated with survival in patients with rGBM, suggesting that the proficiency of IFN responses to PVSRIPO may dictate therapy outcome. Ex vivo glioma tissue assays of patients showed that only some gliomas mounted type I IFN responses to PVSRIPO and STING agonist treatment, correlating with higher pre-treatment IL-1b levels and lower CXCL10 induction after treatment. Strikingly, in glioma-bearing mice, peripheral vaccination against tumor-irrelevant vaccines in alum adjuvant induced bone marrow, spleen, and intratumoral innate inflammation; rescued the antitumor efficacy of PVSRIPO in an otherwise refractory glioma model; and improved survival after intratumor STING agonist therapy. Notably, peripheral vaccination induced intratumoral neutrophil and CD4+ T cell inflammation and increased MHC-class II expression on myeloid cells. These findings suggest that baseline innate inflammation influences glioma tumors' response to virotherapy, implying a role for systemic innate immune training in the antitumor efficacy of virotherapy. Modulating systemic innate inflammation and/or the inflammatory status of bone marrow myeloid progenitors may sensitize gliomas to virotherapy.

https://www.linkedin.com/in/lalita-mazgaeen-46b2a268/

51. Concerns with Chemogenetics: inhibitory DREADDs in the rat infralimbic cortex | *Julia Mitchell*

Basic neuroscience research investigates changes in brain activity to understand the role specific brain regions have in behavior. Chemogenetics is a technique used by neuroscientists to inhibit or excite neurons using Designer Receptors Exclusively Activated by Designer Drugs (DREADDs), specially engineered G-protein coupled receptors that signal through excitatory (Gq) or inhibitory (Gi) pathways. DREADDs give researchers the ability to precisely manipulate brain activity in a desired region and observe the resulting behavioral outcomes, thereby pairing brain activity with behavior. Historically, many preclinical and basic neuroscience studies have been conducted primarily in male animals, which has led to a gap in knowledge of how tools like DREADDs work in females. My current work is investigating the effectiveness of DREADDs in the infralimbic cortex (IL) in males and females. The IL is an area involved in emotionally regulated behavior, such as responding to fear-inducing or threatening stimuli. In this study, I injected male and female rats with excitatory and inhibitory DREADDs and performed electrophysiology, a technique which allows scientists to directly measure activity in individual neurons, to measure IL activity in response to the DREADD agonist Clozapine-N-Oxide (CNO). We found that in females, CNO application with Gq DREADDs reliably increase excitability of IL neurons, while Gi DREADDs produce a mixture of inhibition, excitation, and no change in activity. These results indicate that Gi DREADDs in female IL might not produce consistent inhibitory effects, which complicates data interpretation. This work emphasizes the importance of validating research tools in both males and females to gain a more complete understanding of neural mechanisms and individual differences in circuit-specific activity that drives behavior. Understanding the mechanisms of these tools in males and females at the basic level sets a stronger foundation for clinical studies built from research using these techniques.

52. Chronic intermittent ethanol exposure in mice elicits heightened mRNA expression of GluA1-containing AMPARs and associated trafficking proteins in the amygdala | *Cassandra Modrak*

Alcohol possesses highly-reinforcing properties in which a subset of individuals are susceptible to escalated alcohol consumption, craving, and progression to alcohol use disorder (AUD). Several neural mechanisms underly the onset and progression of AUD, however an increased focus has been placed on the role of glutamate, and more specifically AMPA receptors within reward regions such as the amygdala. We have previously shown that activation of GluA1-containing AMPARs and associated proteins including TARP γ-8, CaMKII, and PSD-95 in the amygdala are critical for the reinforcing properties of alcohol, as well as dependence and escalation of intake. Despite this, how downstream signaling pathways are altered in this region following alcohol dependence remains to be fully elucidated. Thirty-eight female C57BL/6J mice underwent chronic intermittent ethanol (CIE) vapor exposure 4 days a week for 3 weeks. Sessions were 16 hours in duration with mice receiving exposure either to ethanol vapor (n = 20) or air (n = 18). Mice were then sacrificed 24 or 72 hours following the last CIE session, and changes in gene expression in the amygdala were assessed using real-time polymerase chain reaction (RT-PCR) analyses. mRNA expression for GluA1 and GluA1-associated proteins such as TARP γ-8, PSD-95, and PKC γ were upregulated 24 hours after the last CIE session, while expression for GluA2 was downregulated at this time point. Consequently, at 72 hours, mRNA expression for GluA1, TARP γ-8, and PSD-95 remained upregulated, in addition to upregulation of GluA2, CaMKII, gephryn, and the a-1 $GABA_A$ subunit. This may suggest that the progression of alcohol dependence initially relies on GluA2-lacking AMPAR-mediated mechanisms, before shifting to GluA2-containing, and more inhibitory mechanisms over time. Future research will focus on investigating whether such mechanisms are critical for alcohol craving and relapse.

https://www.linkedin.com/in/cassandra-modrak

53. Progression of post-traumatic osteoarthritis (PTOA) in Long-Evans rats: muscle strength, mechanosensitivity and pain behavior assessments | *Alessandro Molinelli*

Introduction: Osteoarthritis (OA) is a disease of the entire joint, involving synovial inflammation, cartilage/bone damage and damage to other soft tissues leading to pain and disability. OA is characterized by the degeneration of articular cartilage and bone, specifically in osteophytes and subchondral bone sclerosis, as well as decreased joint space. By utilizing surgical induction of post-traumatic osteoarthritis (PTOA) in rodents, we are investigating the affected cartilage, bone, muscle and pain behaviors in efforts to identify potential PTOA treatment strategies.

Methods: Experiments were conducted in male Long Evans rats (16-18 wks old). To induce PTOA, we used surgical anterior cruciate ligament transection (ACLT) and destabilization of the medial meniscus (DMM) model [1-5]. At post-surgical timepoints animals were assessed for mechanosensitivity, pain behavior as well as *in vivo* dorsiflexor muscle strength.

Results: At 8 wks post-surgery, ACLT+DMM group demonstrated greater dorsiflexion torque than sham animals, with a greater twitch torque, whereas no significant differences in muscle contractility measures were detected in later time points. Evoked pain mechanosensitivity was longitudinally assessed in rats. Surgical induction of OA showed an ipsilateral decrease in pain mechanosensitivity of the hindpaw relative to the contralateral hindpaw becoming significant by 16 wks. Weight bearing incapacitance data showed an initial increase in sensitivity and avoidance of weight bearing on the operated side.

Discussion and future directions: Our data supports a minimal influence of ACLT + DMM on hindlimb muscle strength, specifically the primary ankle dorsiflexor muscle group, with some evidence of altered mechanosensitive and increased instances of pain. The progression of OA in rats may require modifications to develop chronic PTOA outcomes. Histological analysis of knee cartilage, hindlimb muscles and bones will strengthen the support of this surgical model of PTOA.

https://www.linkedin.com/in/alemolinelli/

54. GLIS3: A critical regulator of inflammatory gene expression in chondrocytes | *Tanushree Mukherjee*

Loss-of-function of the Krüppel-like zinc finger transcription factor, GLI-similar 3 (GLIS3), causes polycystic kidney disease, neonatal diabetes, and congenital hypothyroidism in both humans and mice. Our *in-situ* hybridization data

show high *Glis3* expression in the chondro-ossification centers and growth plate chondrocytes of the hindlimbs of embryonic mice (e12.5-e18), indicating a possible role of GLIS3 in maintaining chondrocyte functions and skeletal homeostasis. Importantly, *GLIS3* SNPs have been associated with low bone density (osteopenia) and degenerative inflammatory conditions like osteoarthritis (OA). Therefore, to understand its role, we overexpressed GLIS3 in the chondrocyte ATDC5 cells. RNA sequencing analysis of these chondrocytes showed an enrichment of inflammatory pathways, with an elevated expression of OA-associated key cytokines *Il6, Ccl2, Ccl*7. This is consistent with recent studies showing high GLIS3 expression in OA-derived chondrocytes. Further, differentiating GLIS3-overexpressing chondrocytes along the chondro-osteogenic lineage also enhanced inflammation and immune system-related genes together with a significant downregulation of pathways associated with cartilage/skeletal development (*Col1a1, Igf*2). These observations suggest that GLIS3 overexpression induces inflammatory gene expression in chondrocytes, that may in-turn suppress chondro-ossification. This is supported by our data showing reduced expression of *Il6, Ccl2, Ccl7* in primary chondrocytes derived from *Glis3*-KO (knockout) mice during chondro-ossification together with a reduction in the inflammation-driven suppression of differentiation genes (*Sox9*, *Col2a1*, *Runx2*, *Alpl*). In contrast, *Glis3*-KO chondrocytes stimulated with OA-mimicking pathological factors (IL-1B and fragmented fibronectin (FnF)), did not show any differential inflammatory response compared to the WT (*Ccl2*, *Ccl7*, *Col2a1*, *Mmp3* expression); indicating that while GLIS3 may not be essential in response to *in vitro* pathological stimuli; it is critical for regulating inflammation under physiological conditions (differentiation). The use of *in vivo* OA models and chondrocyte-macrophage co-culture systems will provide further mechanistic insights into the role of GLIS3 in chondrocyte-associated inflammation and strengthen the importance of GLIS3 in maintaining chondrocyte homeostasis.
https://www.linkedin.com/in/tanushree-mukherjee-3b44b223b/

55. **Integrated regional dynamic occupancy models inform local predictions of songbird occupancy following landscape-scale disturbance | *Emily Nastase***

Occupancy dynamics, such as rates of local colonization and extinction, vary geographically within a species' range. For example, populations in the periphery of a range typically exhibit greater variation in local colonization and extinction rates compared to those in the range core. Likewise, species' habitat associations may vary by geographic location, latitude, or elevation. Models that integrate occurrence and habitat data benefit avian conservation by partitioning covariation between data sources that are heterogeneous in nature and often hampered by a lack of systematic range-wide survey effort. We use an integrated occupancy model to assess the regional occupancy dynamics of a vulnerable, forest-obligate songbird species. Using a Bayesian framework, we integrate systematic (Breeding Bird Survey) and ancillary (eBird) observational datasets with annual land cover change data from 1997–2023 to estimate avian species' occupancy dynamics and quantify the relative contribution of macroecological covariates (e.g., land use change, climate, location within range) in driving changes. Next, we downscale our framework to model occupancy dynamics following a landscape-scale disturbance. Specifically, we model changes in avian species' occupancy in western North Carolina following the widespread habitat destruction of hurricane Helene in 2024. This assessment will serve as a baseline prediction for managers to make conservation decisions aimed at benefitting songbird populations at local and landscape scales.

https://www.linkedin.com/in/emily-nastase-648b1873/

56. **A Liposomal Carrier to Reduce Leaching of Ionic Nutrient Loads in Agricultural Soils| *Sai Thejaswini Pamuru***

The use of inorganic nutrient fertilizers in crop agriculture is often inefficient due to rapid leaching of nutrients with percolating water in soil. To address this, a liposomal carrier was developed to slow transport and reduce leaching of inorganic nutrient loads within agricultural soils. Liposomes, spherical lipid bilayers, have been widely used in medicine but remain under-characterized for agricultural applications. Their biocompatibility, high loading capacity, and stability under certain compositions and environmental conditions suggest they could effectively deliver agrochemicals to crops.

We present soil column experiments to evaluate the ability of a liposomal carrier to reduce the transport of an ionic tracer load, sodium bromide, under varying soil and water saturation conditions. Results from saturated column experiments demonstrate that encapsulation in liposomes slowed tracer transport and reduced leachate concentrations in sand and silty clay loam soils. Reduction in tracer leachate was also observed for unsaturated column experiments in silty clay loam soil. Subsequent experiments suggested a combination of processes (i.e., attachment, aggregation, physical exclusion, and biogenic immobilization) were responsible for the observed behavior of liposome encapsulated tracer in the soil column experiments. These findings support the use of liposomes as an effective carrier of inorganic nutrients to reduce leaching.

57. **Molecular Insights into the Influence of Tail Architecture on Self-Assembly of Peptide-Polymer Amphiphile | *Sabila Kader Pinky***

Peptide-polymer amphiphiles (PPAs) combine functional peptides with a hydrophobic tail that drives self-assembly in aqueous environment. Their ability to form well-defined nanostructures with tunable physical properties makes them ideal candidates for a wide range of applications. However, predicting and tuning these features remains challenging due to the complex interplay of molecular interactions. Here, we systematically investigated the self-assembly of a random coil peptide (XTEN2)-based PPAs by varying the side chains of alkyl acrylate tail (ethyl, n-butyl, tert-butyl, hexyl, and cyclohexyl). We used all-atom molecular dynamics (AMD) simulations to examine how molecular interactions influence the formation, structure, and stability of micellar assemblies. The simulations reveal the formation of a range of core morphologies, including worm-like, perforated, spherical, and multi-core structures. Our findings indicate that the balance between tail-to-tail versus tail-to-water non-bonded interactions primarily determines the micellar morphology. Additionally, the extent of core hydration also impacts the structural stability. Furthermore, the comparison between experimentally obtained particle sizes and simulation-obtained particle sizes shows good agreement, validating the computational approach. We anticipate that the insight from this study will collectively provide a comprehensive understanding of how molecular properties and interactions drive the self-assembly and structural diversity of PPAs, offering insights into designing nanostructures with tailored morphologies for specific applications.
https://www.linkedin.com/in/sabila-kader/

58. **Just Not Sound: A Brain Circuit For Socially Meaningful Vocal Communication| *Thomas Pomberger***

Social communication is central to how humans and animals build relationships, express needs, and respond to others. Yet, we still know little about how the brain supports the ability to both speak and listen in dynamic, real-world settings. In this study, we investigated a brain region called the posterior insula and its role in vocal communication during social interactions in mice. Using a newly developed behavioral setup and miniature brain imaging tools, we recorded activity in this brain region while mice rapidly switched between making vocal sounds and hearing them during social encounters. We discovered that largely distinct sets of brain cells were involved in vocalizing versus listening. Activity in the posterior insula often ramped up before a mouse made a sound and was still present in congenitally deaf mice, suggesting this signal reflects preparation to speak rather than hearing oneself. We also found that the way the brain responded to vocal sounds varied depending on the social context, pointing to a flexible, situation-aware communication system. Finally, we showed that neurons in the posterior insula are directly connected to both the auditory thalamus, which processes sound, and a brainstem region that controls vocal output. Together, these findings suggest that the posterior insula helps coordinate when to speak and when to listen, adapting to social context to support effective communication. Understanding how the brain manages this balance could provide valuable insights into speech and social disorders, such as autism or aphasia, where this coordination is often disrupted.

59. **Electrochemical precipitation of Ca^{2+} and Mg^{2+} from seawater using oxygen reduction reactions on activated carbon electrodes | *Luz Quispe Cardenas***

Electrochemical precipitation can remove divalent ions such as calcium (Ca^{2+}) and magnesium (Mg^{2+}) from high ionic strength solutions, but its practical application is often hindered by high-energy demands associated with water electrolysis. This study investigated an electrochemical process that combines oxygen reduction reaction (ORR)-induced pH elevation with activated carbon cloth (AC) electrodes to enhance precipitation of Ca^{2+} and Mg^{2+} from synthetic seawater. Using a flow-through cell operated with a whole-cell applied voltage of 1.2 - 1.8 V, we evaluated the effects of electrode configuration, charging duration, bicarbonate concentration, and oxygen concentration on mineral precipitation and selectivity. Traditional capacitive deionization cycling (repeated charge/discharge cycles), did not improve precipitation or decrease energy demands compared to applying a constant voltage, suggesting that capacitive current was not beneficial for precipitation. Under optimized conditions (two cathodes, one anode, constant 1.8 V, single-pass mode, and supplemental oxygen), Ca^{2+} and Mg^{2+} removal reached 39% and 5%, respectively, recovered primarily as $CaCO_3$ and $Mg(OH)_2$ phases. Equilibrium modeling using Visual MINTEQ predicted the formation of these mineral phases, but it did not align quantitatively with experimental results. The system achieved a specific electrical energy consumption of 16 kWh per gram of combined Ca^{2+} and Mg^{2+} removed, offering decreased energy demand. Under recirculation mode, total Ca^{2+} and Mg^{2} removals reached 65% and 16%, respectively, further enhancing the permanent removal of these ions. This study provides new insights into the use of AC electrodes and ORR-induced pH changes to precipitate metals from saline waters.

60. **BB0298 is a tetratricopeptide domain-containing protein crucial for the periplasmic flagellar collar assembly, morphology, and motility of the Lyme disease spirochete | *Md Khalesur Rahman***

Lyme disease is the most reported vector-borne illness in the United States, increasing the burden on public health. The organelles essential for the distinctive spiral morphology and corkscrew-like motility of the Lyme disease spirochete *Borrelia burgdorferi* are periplasmic flagella, which are distinct from the external flagella found in many bacteria, such as *Escherichia coli* and *Salmonella enterica*. Importantly, flagellar motility is critical for virulence in all pathogenic spirochetes. The unique structure of the periplasmic flagella, termed collar, is a multi-protein complex required to assemble the flagellar stator, the spirochete's distinctive morphology, and motility. Five collar proteins are already identified and are only responsible for part of the periplasmic collar, with the rest of the complex formed by novel unidentified proteins in *B. burgdorferi*. Using various comprehensive strategies, we discovered multiple proteins annotated as "proteins of unknown function" in *B. burgdorferi*. One is BB0298, which possesses tetratricopeptide repeat domains crucial for protein-protein interactions. The deletion mutant of *bb0298* exhibits motility-defective and altered morphology phenotype. Cryo-electron tomography reveals that the Δ*bb0298* mutant assembled a motor structure lacking the peripheral part of the collar structure, suggesting that BB0298 is a collar protein. Furthermore, protein-protein interaction assays show that BB0298 interacts with another collar protein, FlcA, located near BB0298. To determine the key residues that form the BB0298-FlcA interface, we took advantage of the structural modeling tool AlphaFold multimer to predict a co-fold structure of the BB0298 and FlcA complex and subsequently analyzed it with PDBsum. These analyses indicated top-ranked interactions between BB0298-Tyr194 and FlcA-Phe10, -Lys11, -Ileu14 residues. Further protein-protein interaction assays demonstrate that Tyr194 of BB0298 is indeed involved in interacting with FlcA. Guided by the protein-protein interaction assays described above and having identified the binding-deficient residues in BB0298 (and FlcA), we will construct corresponding *B. burgdorferi* mutants, such as *bb0298*-Y194A, to determine the impact of BB0298 on the flagellar collar assembly and spirochetal motility.

61. **Soil microbial composition responds to diverse long-term management systems in coastal region of North Carolina | *Dipti Rai***

Soil microbial communities play a crucial role in influencing nutrient inputs and soil biogeochemical processes. However, the long-term responses of soil microbes to changes in input under various farming systems remains a critical and unresolved question. The objective of this study is to examine the responses of soil microbial communities, in terms of activity, diversity, composition, and predicted functionality to shifts in long-term (24 years) farming systems. Here, we collected soil from two depths (0-10 cm and 10-20 cm) across six distinct long-term plots established at the Center of Environmental Farming Systems in Goldsboro, North Carolina, US. The experimental plots included (i)

conventional tillage with mineral fertilizer (CTCC), (ii) no-tillage with mineral fertilizer (NTCC), (iii) organic system with conventional tillage (ORGC), (iv) organic system with reduced tillage (ORGR), (v) integrated crop-livestock system using pasture-crop rotation (PSTR), and (vi) agricultural abandonment with successional plant development (SUCC). Long-term organic inputs in ORGC and ORGR systems significantly enhanced potential enzyme activities related to soil C, N, and P cycling at both depths, and altered bacterial and fungal community composition. Our findings highlight that microbial shift were not limited to surface soils but extended into the 10–20 cm layer, emphasizing the deeper influence of sustained management practices. Structural equation modeling revealed that the quality of nutrient inputs is the primary driver influencing soil microbial community composition and their functional potential rather than tillage practices. Adopting organic farming practices can significantly enhance soil enzymatic activity and reshape microbial composition and functional potential at multiple depths, demonstrating the importance of sustainable agricultural management for long-term ecological benefits.
https://www.linkedin.com/in/dipti-rai

62. **Engineering a Clean Future: Designing of Self-Cleaning Photocatalytic Membrane for | *Chhabilal Regmi***

Membrane fouling remains a critical limitation in water treatment technologies, leading to decreased permeability, reduced operational efficiency, and frequent cleaning or replacement. While photocatalytic nanoparticles such as TiO_2 have demonstrated effective pollutant degradation under UV light, their use in dispersed form is hindered by drawbacks like leaching, agglomeration, and limited light accessibility. This study addresses these challenges by developing self-cleaning photocatalytic membranes designed to resist fouling while maintaining high treatment performance. TiO_2 was immobilized onto anodic aluminum oxide (AAO) membranes using Atomic Layer Deposition (ALD), enabling conformal, strongly adhered coatings. For polymeric membranes, TiO_2 was applied through dip-coating, ensuring good surface coverage without compromising membrane flexibility. These immobilization strategies effectively prevented nanoparticle leaching and preserved light accessibility for photocatalytic activation. Even with 40% surface coverage on the AAO membrane, up to 80% degradation efficiency of methylene blue was achieved under UV irradiation. Both membrane types demonstrated excellent antifouling properties, maintaining over 90% of initial water flux after repeated fouling-cleaning cycles. SEM and EDX analyses confirmed uniform TiO_2 distribution and coating stability. These results highlight that TiO_2 surface functionalization via ALD and dip-coating provides an effective route for fabricating fouling-resistant, self-cleaning membranes suitable for sustainable water treatment applications.

63. **ISG15-Mediated Suppression of Type I Interferon Signaling Leads to Susceptibility to Epstein-Barr Virus Infection | *Nicolas Reinoso***

Epstein-Barr Virus (EBV) latently infects over 90% of people worldwide. While infections are typically asymptomatic, in some individuals, EBV can drive the development of serious diseases, including several cancers like lymphoma and gastric cancer, as well as autoimmune disorders such as multiple sclerosis (MS). Despite its global prevalence and lifelong presence in the body, we still don't fully understand why EBV triggers disease in only a subset of people. Our research focuses on uncovering how human B cells -the antibody producing cells- naturally resist or support EBV's ability to transform them into cancer-like cells. We developed a new platform using cutting-edge gene-editing tools in human B cells to identify genes that either help or hinder EBV capacity to transform. One key gene we identified is *ISG15*, an interferon-stimulated gene typically activated during viral infections. ISG15 exists either as a free molecule or conjugated to other proteins. Surprisingly, we found that EBV-infected cells initially rely on the ISG15 to support their grow— highlighting how the virus can hijack immune-related molecules for its benefit. Free ISG15 plays a critical role in modulating interferon responses, which normally act as the first barrier against viral infections. We also discovered rare mutations in a gene called *UBA7* in patients with severe EBV-related diseases. UBA7 is essential for conjugating ISG15 to target proteins. When *UBA7* is mutated, conjugation is impaired, leading to higher levels of free ISG15, creating a more favorable environment for EBV-driven transformation. By uncovering how host genetic variation influences EBV susceptibility, our findings provide a potential explanation for why some people are more vulnerable to EBV-associated diseases. This

approach opens new avenues for bench-to-bedside studies, improving strategies for predicting, preventing, and treating EBV-linked cancers.

64. **Body mass index as a modifier of visio-vestibular deficits in children and adolescents with concussion | *Sicong Ren***

PURPOSE: To characterize the relationship between body mass index (BMI) and visio-vestibular examination (VVE) outcomes in children and adolescents with concussion.
METHODS: This observational study included patients presenting to a specialty care concussion setting within 28 days post-injury and non-concussed participants from a local high school. BMI was classified into four categories (i.e., underweight, healthy weight, overweight, and obese) based on CDC growth charts. The VVE consists of assessments of smooth pursuit, saccades, vestibular-ocular reflex (VOR), binocular convergence, monocular accommodation, and tandem gait. Kruskal-Wallis and chi-square tests were performed to analyze group differences. Post hoc tests with Bonferroni-adjusted *p*-values were conducted for pairwise comparisons.
RESULTS: A total of 5,534 participants were included: 5,439 pediatric patients with concussion and 95 non-concussed participants. More obese patients demonstrated abnormality in horizontal saccades than underweight patients (54.1% vs 36.5%, $p = 0.032$). For VOR, fewer underweight patients demonstrated abnormality than patients with healthy weight (H) or obesity (OB) (horizontal: 33.3% vs H: 49.6%, OB: 52.4%, $p \leq 0.045$; vertical: 31.1% vs H: 48.0%, OB: 49.1%, $p \leq 0.035$). More obese patients showed abnormal tandem gait compared with patients with healthy weight or overweight (OV) (32.2% vs H: 26.1%, OV: 24.1%, $p \leq 0.006$). There were no significant differences in pursuit, binocular convergence, or monocular accommodation across BMI categories in pediatric patients. Additionally, there were no significant differences in all VVE metrics by BMI in non-concussed participants.
CONCLUSION: Among concussed pediatric patients, obese children showed more abnormality in saccades, VOR, and tandem gait compared with others. Although a greater proportion of abnormality in pursuit, binocular convergence, and accommodation were observed in obese children, differences did not reach statistical significance. This study may identify the potential role of BMI as a modifier for visio-vestibular deficits and functional impairment in pediatric concussion.
https://www.linkedin.com/in/sicong-ren

65. **Quantum-AI Enabled Framework for Multi-Omics Biomarker Diagnostics in Lung Cancer Subtypes: MQML-LungSC | *Mandeep Saggi***

The integration of multi-omics data presents a promising frontier in cancer diagnosis and biomarker discovery, especially for complex diseases like lung cancer. However, challenges such as high dimensionality, low sample sizes, and inherent data noise hinder traditional machine-learning approaches. Quantum Machine Learning (QML) is a cutting-edge field that bridges quantum computing and ML to address computational challenges more effectively. We have developed a two-phase approach to address these limitations, offering a novel framework- Multi-Omic QML Lung Subtype Classification **(MQML-LungSC)-**for classifying lung cancer subtypes: Lung adenocarcinoma (LUAD) and Lung squamous cell carcinoma (LUSC) from (TCGA): Phase I focused on diagnostic biomarker identification using classical ML. This phase leveraged integrated multi-omics modalities, including (i) (RNA-Seq), (ii) (DNA methylation), (iii) (miRNA-Seq), alongside clinical phenotype data to distinguish between subtypes. Statistical analysis and ML methods were applied to multi-omics data for initial feature extraction, identifying significant and insignificant subset, thereby enabling the discovery of subtype-specific molecular signatures. Phase II advanced this work by implementing Quantum Neural Network classifier within a hybrid workflow. QNN's models using various feature dimensions (256, 64, and 32) were applied to combine tumor and normal samples, achieving accurate subtype classification. The approach identified clinically relevant molecular and demonstrated scalability via classical simulations of quantum circuits (up to 8 qubits) on real cancer datasets. The model not only achieves high classification accuracy (training: 0.95; testing: 0.90) using 256 encoded features but also demonstrates enhanced efficiency by outperforming ML methods and

quantum models with a significantly reduced architectural complexity. This work highlights the potential of QML to enhance early diagnosis, enable biomarker discovery, and support precision oncology through prognostic modelling and risk stratification.

https://www.linkedin.com/in/mandeepkaursaggi/

66. **A tale of two proteins: how cancer-causing herpesviruses usurp cellular proteins, DDX5 and DDX17, to promote viral infection | *Praneet Kaur Sandhu***

Herpesviruses cause widespread infections in humans. Upon infection, these viruses persist for life and are never cleared from the body. Gammaherpesviruses, namely Kaposi's sarcoma-associated herpesvirus (KSHV) and Epstein-Barr virus (EBV), can cause various types of cancers as well as other diseases. These oncogenic viruses utilize cellular proteins for infection and producing copies of themselves. As there is no cure or vaccine available to prevent infection or eliminate gammaherpesviruses from the human body, studying the viral infection cycle will enable the development of novel strategies to target these viruses, and prevent or cure diseases caused by them. Our objective was to identify cellular proteins that are indispensable for viral infection in order to find ways to block infection and mitigate gammaherpesvirus-associated diseases such as cancer. In this study, we found that two cellular proteins, DDX5 and DDX17, are required by KSHV and EBV for optimal infection. We observed that the DDX proteins promote virus infection by boosting the presence of Brg1, a member of the cellular machinery that organizes and opens DNA for gene expression, near viral genes. As such, the DDX proteins are used by the viruses to enhance the expression of viral genes, and are required for virus production. Importantly, we show that reducing the levels of the DDX proteins or inhibiting Brg1 effectively reduces infection of both KSHV and EBV. This study identifies DDX5 and DDX17 as key regulators of gammaherpesviral infection due to their ability to control viral gene expression and ensure optimal virus production. Importantly, these findings can pave the way to design interventions to target these cancer-causing viruses and curb their associated diseases.

67. **Elucidating the mechanism of RNA G-quadruplex mediated RNA polymerase pausing | *Uma Shankar***

This study employs structural analysis of nascent RNA folding to gain mechanistic insight into the regulation of transcription by the mitochondrial RNA polymerase (POLRMT). Guanine quadruplexes (G4s) are nucleic acid structures that play key roles in gene expression regulation. While their role in Pol II-mediated transcription is well studied, less is known about the role of G4s in the regulation of mitochondrial transcription. Previously, we found that POLRMT pauses at multiple sites during transcription, and these pauses occur after G4 forming sequences. In the *MT-CO1* gene, we identified a sequence (CO1-G4) that is associated with paused POLRMT. This sequence forms a G4 in RNA, but not in DNA, and using an *in vitro* transcription assay we showed that the CO1-G4 is sufficient to pause the POLRMT. This finding suggests a novel regulatory role for RNA G4s in mitochondrial transcription. While DNA G4s ahead of the polymerase are known to impede elongation, how RNA G4s positioned behind POLRMT contribute to pausing is still unknown.

Firstly, we cloned and purified four truncated versions of the POLRMT protein. Among these, we selected PORLMTΔ150 to confirm its functional ability to undergo G4-mediated pausing through *in vitro* transcription. To model the POLRMT elongation complex, we designed a scaffold containing the CO1-G4 sequence hybridized to a duplex DNA and validated its quadruplex folding using gel-based and NMR spectroscopic assays. Additionally, we designed mutant RNA sequences which are unable to form G4 structures by replacing guanine residues with poly-U repeats. We assembled the transcription complexes with POLRMT and the RNA-DNA scaffolds and are using Cryo-EM to study the interaction between RNA-G4 and POLRMT. We successfully solved the apo structure of POLRMT and have begun analyzing the 2D classes of both CO1-G4 and mutant G4 in our Cryo-EM studies. In the CO1-G4 Cryo-EM 2D dataset, we observed a density structure outside POLRMT, which is absent in the mutant, strongly suggesting that this density corresponds to the G4 structure. So, our findings will provide insights into how nascent RNA G4s paused transcription, their role in cis-regulation of mitochondrial gene expression under physiological conditions, and how this mechanism may serve as a model for an overlooked mode of transcription regulation in the nucleus.

https://www.linkedin.com/in/umashankariiti/

68. **Impact of CYP2C19 and CYP3A Inhibitors on Clopidogrel Clinical Effectiveness in CYP2C19 Genotyped Patients Undergoing Percutaneous Coronary Intervention (PCI) in a Real-world Setting | *Danwei Shao***

Background: Clopidogrel requires CYP2C19 and CYP3A4/5 for bioactivation. *CYP2C19* no function alleles diminish clopidogrel's antiplatelet effects and clinical effectiveness. Co-administration of CYP2C19 and CYP3A4/5 inhibitors can also diminish clopidogrel's antiplatelet effects and may lead to phenoconversion (a mismatch between the genotype-predicted and actual metabolic phenotype). However, the impact of CYP2C19/CYP3A inhibitor use on clinical outcomes in clopidogrel-treated patients with and without a *CYP2C19* no function allele remains unclear.

Methods: A single-center retrospective cohort study included 848 clopidogrel-treated PCI patients who were clinically genotyped for *CYP2C19*. Data were abstracted from electronic health records. Moderate and strong CYP2C19 or CYP3A4/5 inhibitors defined by the FDA Examples of Drugs that Interact with CYP Enzymes and/or the Indiana University Drug Interactions Flockhart Table™ were considered. Major atherothrombotic event (MAE: death, acute coronary syndrome, stent thrombosis, or ischemic stroke) incidence was compared across patients receiving vs. not receiving a CYP2C19/CYP3A inhibitor over 1-year post-PCI after stratifying by *CYP2C19* genotype.

Results/Conclusion: Ten moderate/strong CYP2C19/CYP3A inhibitors were co-prescribed with clopidogrel. Overall, 340 (40.1%) patients received inhibitors. Commonly prescribed inhibitors were omeprazole (19.1%), amlodipine (18.2%), esomeprazole (4.0%), diltiazem (2.6%), and fluoxetine (2.0%). Across clopidogrel-treated patients receiving vs. not receiving an inhibitor, there was no significant difference in MAE rates in *CYP2C19* no function allele carriers (20.8 vs. 25.6 events/100-pt-yrs; aHR = 0.87, 95%CI: 0.38 – 2.02, p = 0.75). MAE rates were numerically higher but not significantly different in non-carriers receiving vs. not receiving an inhibitor (17.7 vs. 11.6 events/100-pt-yrs; aHR = 1.45, 95%CI: 0.87 – 2.42, p = 0.15); a sensitivity analysis considering only moderate/strong inhibitors defined by FDA shows significantly higher MAE rates in non-carriers receiving vs. not receiving an inhibitor (24.5 vs. 13.4 events/100-pt-yrs; aHR = 2.54, 95%CI: 1.04 – 6.16, p = 0.04). CYP2C19 and CYP3A inhibitor use may diminish clopidogrel clinical effectiveness in CYP2C19 no function allele non-carriers.

69. **Claims-based definitions achieved similar gestational age distributions for prenatal care initiation as birth certificate data | *Elizabeth Simmons***

Background: Insurance claims data provide longitudinal, real-world insights into healthcare use during pregnancy. Identifying prenatal care encounters within these data is essential but challenging due to the lack of validated algorithms. This study compares claims-based methods for identifying the timing of prenatal care initiation with estimates from birth certificate data.

Methods: We analyzed data from live births recorded in the Merative™ MarketScan® Commercial Claims and Encounters Database and publicly available birth certificates from January 2011 to September 2015. Prenatal care initiation in MarketScan was defined using four claims-based approaches relying on ICD-9 codes: (1) prenatal or pregnancy outcome codes; (2) definition #1 excluding lab codes; (3) only prenatal codes; and (4) pregnancy supervision codes. Each approach was tested with three restrictions: (a) limited to specific provider types; (b) care starting at ≥4 weeks' gestation; and (c) both a and b. We then compared the gestational month of prenatal care initiation in MarketScan to birth certificate data.

Results: Our analysis included 1.5 million MarketScan births and over 8 million privately-insured births from birth certificates. In the birth certificate cohort, 44% and 36% initiated care in gestational months 2 and 3, while 3.2% had no recorded prenatal care. The pregnancy supervision code algorithm in MarketScan most closely matched this distribution (45% and 29% in months 2 and 3) but had a higher rate of "no prenatal care" (11.8%). Restricting by provider type had minimal impact, while gestational age restrictions slightly delayed initiation estimates.

Conclusions: Among the definitions tested, pregnancy supervision codes yielded a gestational distribution most similar to birth certificate data. However, this method also resulted in the most missing data. Claims-based definitions must balance accuracy with completeness when identifying prenatal care initiation.

www.linkedin.com/in/lizzysim

70. **Patterns of Social Difficulties and Anxiety in Autism | *Grace Lee Simmons***

As many as 40% of autistic youth exhibit clinically significant anxiety, through measurement of anxiety is complex as parents and youth often fo not agree. In non-autistic youth, anxiety is related to difficulties with social/emotional reciprocity and parent-reported social difficulties. Research examining this model in autistic youth is inconsistent. We examined autistic youth, caregiver, and teacher ratings to examine the impact of social difficulties on anxiety in autistic youth.
https://www.linkedin.com/in/grace-lee-simmons/

73. **Unlocking the Potential of 15dPMJ2: Pluronic F127 Micelles as a Non-Toxic, Efficient Delivery System for Melanoma Therapy | *Berwin Singh Swami Vetha***

Introduction/Objectives: The development of efficient drug delivery systems is critical for improving cancer treatment outcomes. Pluronic F127 micelles offer a promising platform due to their unique properties and biocompatibility. 15d-deoxy, Δ12,14-prostaglandin J_2-ethanolamide (15dPMJ_2) is an investigational small molecule therapeutic with potent anti-cancer activity. However, its therapeutic efficacy is limited by neutralization by glutathione and sequestration in adipose tissue. The current study seeks to optimize and evaluate Pluronic F127 micelles to enhance the delivery and effectiveness of 15dPMJ_2 in cancer treatment.
Methods: To examine whether Pluronic F127 formed micelles efficiently, the critical micelle concentration (CMC) was determined by performing fluorescence spectroscopy. To examine if Pluronic F127 was cytotoxic against cancer cells, its biocompatibility was assessed in cytotoxicity assays.
Results: Our findings demonstrate that the CMC of Pluronic F127 was 0.9 mg/mL, a value indicative of efficient micelle formation. We also observed that Pluronic F127 was not cytotoxic against B16F10 melanoma cells at concentrations up to 20 mg/mL, suggesting its favorable biocompatibility.**Conclusions**: This study highlights the potential of Pluronic F127 micelles as a delivery system for 15dPMJ_2 in cancer treatment. Future research will assess the efficiency of 15dPMJ_2 drug loading and encapsulation to determine the feasibility of utilizing 15dPMJ_2-loaded Pluronic F127 in animal tumor studies.

75. **Management of western flower thrips (Frankliniella occidentalis) in tomatoes with cultural and chemical methods | *Mandeep Tayal***

Insect pests cause severe damage to agricultural crops, including grains, fruits, vegetables and ornamentals. One of the most problematic pests is the western flower thrips (*Frankliniella occidentalis*, "WFT"), which is responsible for >$1 billion in crop losses annually worldwide. In tomatoes, it causes direct damage by feeding on leaves, flowers and fruits, and indirect damage by transmitting tomato spotted wilt virus (TSWV). Insecticides are widely used to manage thrips, but on tomatoes, they are primarily effective on leaves, as thrips hide within flowers and remain protected from sprays. This challenge, combined with the limited availability of effective insecticides, highlights the need for integrated management strategies. We conducted multi-year field trials to evaluate new insecticide products (Plinazolin, Lannate, Beleaf, and Verimark) and mulch types (white, black, and reflective) for their impacts on thrips populations and tomato yield. We found that Plinazolin was the most effective in reducing thrips on leaves, followed by Beleaf and Lannate. Soil-applied Verimark was also effective in lowering thrips populations compared with the untreated control. However, none of the insecticide treatments were effective in controlling thrips populations within flowers over the three-year period. Among the mulch types, reflective mulch significantly reduced thrips populations on both leaves and flowers, followed by black mulch. Importantly, higher marketable fruit yields were observed in those treatments most effective in lowering thrips on leaves and flowers. These findings support integrating selective insecticides with cultural practices like reflective mulch to improve WFT management and reduce crop losses in tomato production.
https://www.linkedin.com/in/mandeep-tayal-phd-73671013b

76. **Insights Into the Binding Affinity of PFAS Towards Human Lactoferrin via Differential Scanning Fluorimetry | *Mallory Thomas***

Per- and polyfluoroalkyl substances (PFAS) constitute a wide variety of man made chemicals that are utilized for their many advantageous industrial properties such as heat, oil, and water resistance. Due to their ubiquity in manufacturing, these chemicals are persistent in the environment with no successful methodology of degradation. Their longevity highlights the necessity for experimental toxicity data with respect to human exposure from contaminated waterways and other systems. Here, studies turn to the affinity of PFAS to bind to proteins to determine the toxicity and bioaccumulation in the human body. A protein of interest is human lactoferrin for its presence in bodily fluids such as milk and saliva, as well as its primary function as a component of the immune system. Due to a protein's fluctuation in stability when bound to various substances, changes in melting temperature measured using Differential Scanning Fluorimetry (DSF) can be utilized to provide valuable insight into potential destabilization of proteins at biological temperatures. In addition, these changes in temperature can reveal relative binding affinities to PFAS to determine the strength of binding in biological systems. Our study aims to discuss these relative binding affinities, and overall destabilization of human lactoferrin when exposed to a variety of PFAS covering a range of functional groups and carbon chain length. Preliminary studies reveal a mass destabilization to all PFAS investigated leading to profound questions on how the immune system would be severely affected by the binding of PFAS to human lactoferrin.
https://www.linkedin.com/in/mallory-thomas-phd-15295b148/

77. **Salivary miRNA as a diagnostic biomarker for periodontitis-induced neurologic disorders | *Chukwudi Ubah***

Background: Periodontitis, a chronic inflammatory condition affecting tooth-supporting tissues, has recently been implicated in neurodegenerative disorders such as dementia and mild cognitive impairment (MCI). Emerging evidence suggests a potential mechanistic link through systemic inflammation and microbial dysbiosis. Despite increasing recognition, there is a scarcity of studies exploring non-invasive diagnostic tools for early detection of periodontitis-induced cognitive disorders. MicroRNAs (miRNAs), detectable in saliva, offer promise as next-generation biomarkers due to their gene regulatory roles and stability in biofluids.
Objective: This study aims to identify salivary miRNA signatures in patients with periodontitis-associated dementia or MCI and evaluate their diagnostic potential through bioinformatic and molecular validation.
Hypothesis: Distinct salivary miRNA profiles can serve as predictive biomarkers for periodontitis-induced neurologic disorders, including dementia and MCI.
Study Design: Twenty age-matched (55-70) participants will be divided into four groups based on periodontal and cognitive status. Saliva and blood samples will be collected for miRNA extraction. miRNA profiling will be conducted using the HTG EdgeSeq Whole Transcriptome Assay (2,083 miRNAs), followed by validation via RT-qPCR and Western blotting for target gene expression.
Expected Results and Implications: We anticipate discovering salivary miRNA signatures specific to periodontitis-linked cognitive decline. These biomarkers could enable earlier, non-invasive diagnosis of neurocognitive disorders, paving the way for targeted therapeutic strategies involving miRNA modulation.
Conclusion: This pioneering study will lay the foundation for the use of salivary miRNAs as diagnostic tools in the intersection of oral and neurodegenerative diseases, with significant implications for public health and personalized medicine.
www.linkedin.com/in/chuks-ubah-b72447257

78. **Epigenetic Changes Seen in Baby Girls Prenatally Exposed to Maternal Smoking are Still | *Vaishnavi Venkat***

Epigenetic Changes Seen in Baby Girls Prenatally Exposed to Maternal Smoking are Still Present in Middle Age and May Mediate an Increase in Propensity to Miscarriage A recent study showed that maternal smoking during pregnancy alters DNA methylation at thousands of CpG sites in newborns. If these changes persist into adulthood, they could be markers for long-term health effects. In this study, I examine whether these epigenetic changes persist into middle age and influence miscarriage risk in daughters. Based on data from a large cohort of women (median age 56) providing detailed reproductive histories (the Sister Study), prenatal exposure to maternal smoking was associated with propensity to miscarriage. Women exposed *in utero* were 6.18% more likely to miscarry, even after accounting for their

own smoking. In contrast, there was no evidence of early passive smoking effects, hence no evidence of effects due to exposure to smokers during childhood. To explore potential epigenetic mechanisms, I analyzed the DNA methylation profiles of a random sample from the same cohort, comparing those with confirmed prenatal maternal smoking exposure to an unexposed comparison group. Differential methylation analysis identified 285 CpG sites that remained differentially methylated in exposed women, with all showing the same directional changes as had been observed in newborns. Notably, one CpG sites were linked to both prenatal maternal smoking exposure and miscarriage propensity, suggesting a shared epigenetic signature. These enduring modifications could indicate long-lasting epigenetic mediation for this effect. These findings highlight a lasting impact of prenatal maternal smoking exposure on DNA methylation and reproductive health. Understanding these pathways may inform strategies to mitigate the long-term reproductive risks associated with maternal smoking and may have implications for vaping.
https://www.linkedin.com/in/vaishnavi-venkat-9b580378/

79. **Unraveling the role of exogenous autoinducers and quorum quenching in enhanced nitrification for wastewater treatment systems | *Hira Waheed***

Microbial signaling-based quorum sensing (QS) manipulations have emerged as a promising strategy to enhance nitrification in wastewater treatment by overcoming rate-limiting steps. This study investigated the impact of QS signals, also termed as autoinducers, on nitrogen transformation rates and their correlation with ammonia monooxygenase (*amoA*) expression of ammonia oxidizing bacteria (AOB) in sequencing batch reactors (SBRs). Two identical SBRs were operated over 250 days with synthetic wastewater fed with 200 mg/L NH_4^+-N. Enriched sludge with AOB enhanced NH_4^+-N oxidation by 2-fold and reduced the hydraulic retention time (HRT) from 60h to 36h, despite biomass reduction from 4.5 to 1.0 g/L. After satisfactory enrichment, various signals including autoinducer-2 (AI-2) and nine different acyl-homoserine lactones (AHLs) were tested and correlated with NH_4^+-N oxidation rates. AI-2 dosed experiments exhibited fastest ammonia oxidation, achieving a removal rate $0.214h^{-1}$, significantly outperforming other groups for early-stage enrichment attributed to effective proliferation of ammonia oxidizing *N. europaea* in fresh sludge. Enhanced NH_4^+-N oxidation by 4-folds was observed with AHLs containing longer side chains and an oxoacyl functional group with respect to control group, i.e. correlated well with *amoA* abundance of *N. europaea* up to 21298.9 and 12587.7 copies/mg-biomass, compared to control (7031.4 copies/mg-biomass), and *N. eutropha* up to 426405.5 and 1447887.1 copies/mg-biomass, compared to control (1264.2 copies/mg-biomass), respectively. Quorum quenching enzymes (acylase and quercetin) liable to cellular disruption were spiked to observe the anti-QS impact on nitrification rates. Wherein, the AOB proliferation mitigated the negative effects of cellular disruption during quenching in the sludge, while reduced cellular agglomeration favored nitrification by 2-folds. Our findings offer insights into future strategies to focus on optimizing QS-mediated nitrogen metabolism aligned with microbial communities to enhance nitrification in pilot-scale wastewater treatment systems.
https://www.linkedin.com/in/hira-waheed-521782277/

80. **Structural determinants of inverted Alu-mediated backsplicing revealed by -MaP and -JuMP | *Justin Waldern***

Biogenesis of circular RNA usually involves a backsplicing reaction where the downstream donor site is ligated to the upstream acceptor site by the spliceosome. For this reaction to occur, these sites must be in proximity. Inverted repeat sequences, such as Alu elements, if positioned in the upstream and downstream introns, can base-pair and represent one mechanism for inducing proximity. Here, we investigate the pre-mRNA structure of the human HIPK3 gene at exon 2, which forms a circular RNA via backsplicing. We leverage multiple chemical probing approaches, including the recently developed SHAPE-JuMP strategy, to characterize secondary and tertiary interactions in the pre-mRNA that govern backsplicing. Our data confirm that the antisense Alu elements AluSz(-) and AluSq2(+), in the upstream and downstream introns, form a highly-paired interaction. Circularization requires formation of long-range Alu-mediated base pairs but does not require the full-length AluSq2(+). In addition to confirming long-range base pairs, our SHAPE-JuMP data identified multiple long-range interactions between non-pairing nucleotides. Genome-wide analysis of inverted repeats flanking circular RNAs confirm that the presence of these elements favors circularization, but with

modest predictive power. Together our study suggests that secondary structure considerations alone do not fully explain backsplicing and that additional interactions are involved.
https://www.linkedin.com/in/justinwaldern/

81. **Exploring Feasibility of Stochastic Storm Transposition (SST) at Multiple Spatial Scales | *Marissa Webber***

Flood maps are often used to assess flood hazard and risk to homes and businesses, and to make decisions regarding insurance based on the likelihood of flooding. However, conventional floodplain mapping applies rainfall uniformly in space and restricts rainfall to a characteristic temporal pattern. The Federal Emergency Management Agency (FEMA) plans to move towards a more probabilistic approach, using Stochastic Storm Transposition (SST), a data-driven approach that allows storms to vary in space and time. This approach has been used to simulate hydrologic responses in small watersheds, but it remains unclear whether SST can be applied to large-scale watersheds and their smaller watershed subunits. This project aims to address critical questions related to the feasibility of the application of SST, including whether rainfall statistics can be accurately captured at multiple watershed scales. We used the Neuse River Basin in eastern North Carolina as a test basin and used SST to generate rainfall frequency curves for nested watersheds of different sizes. We found that rainfall depths over small, nested watersheds were larger than rainfall depths over large watersheds for the same storm duration (24-hour). This indicates that rainfall events necessary to simulate flood hazard in larger watersheds are unlikely to represent rainfall events and intensities needed to simulate flood hazard in smaller, nested watersheds. These results motivate the development of alternative processes in the SST framework to better account for variability at multiple scales and therefore inform the development of more reliable national flood maps. This work will support FEMA's Future of Flood Risk Data (FFRD) initiative, which aims to provide a more comprehensive picture of the United States flood hazard and risk by leveraging new technologies to include more efficient, accurate, and consistent flood risk information.

82. **More than Accessibility Loss: Barrier Effect of Highways on Greenspace Use in Phoenix, AZ | *Youngjae Won***

Transport infrastructure can create a "barrier effect," or community severance, that divides communities by isolating residents from essential services, facilities, and one another. This study examines the highway-induced barrier effect on parks within walking distance through spatial accessibility measures and observed visitation data. Focusing on the rapidly growing Phoenix-Mesa Urbanized Area, the study constructs an origin-destination matrix that links Census Block Groups (origins) to nearby parks (destinations). Leveraging geospatial datasets for highways and parks, the analysis distinguishes between origin-destination links that are interrupted by highways and those that are not. Mobile phone data from SafeGraph collected in 2019 is used to measure per capita visitation and travel distances are obtained via the Google Maps API and then compared between the two link types. Fixed effects regression models are employed to control for community and park characteristics. Findings show that highways increase the travel distance by an average of 315 meters and reduce per capita park visitation by 56% when routes are interrupted by highways. Notably, the reduction in visitation remains statistically significant even after controlling for the increased travel distance. By extending the barrier effect analysis beyond traditional spatial accessibility measures, this study demonstrates that spatial separation alone cannot fully capture highway barrier effects. Integrating behavioral data provides a more comprehensive understanding of highway-induced barriers. Consequently, an effective evaluation of infrastructural barriers should combine spatial and behavioral approaches to more accurately reflect the multifaceted nature of community severance.

83. **Improving the texture and structure of high protein yogurt alternative using pea protein hydrolysate as functional ingredient | *Qihui Wu***

Non-dairy yogurt alternatives have become increasingly popular in the market but the impact of enzymatic hydrolysis on the textural and structural properties of Greek-style protein yogurt alternative is not well understood. In this study, commercial pea protein isolate was hydrolyzed with trypsin to obtain a degree of hydrolysis approximately at 1% using the pH-stat method. The trypsin-treated pea proteins yogurt alternatives were produced subsequently at both bench- and pilot-scale with a protein content at 10% (w/w) and compared with their non-enzyme treated counterparts. Trypsin hydrolysis led to significant degradation of the major pea proteins including convicilin, vicilin and legumin. The hydrolysis of proteins prior to yogurt production reduced gel particle size and gel strength, resulting in a less viscous yogurt product with better lubrication properties. The improvement in the texture and structure was consistent with visual and microscopical observations, where the yogurt gels made from pea protein hydrolysates featured smoother surface characteristics and finer microstructure. Pea protein yogurt gels produced at pilot-scale exhibited a similar trend in functional properties to those produced at the bench-scale, demonstrating the feasibility and potential for scale-up production. The study provides a route to produce pea protein yogurt alternatives with increased protein content and optimized functional properties using enzymatic treatment.
https://www.linkedin.com/in/qihui-wu-117512311

84. **Fanconi anemia protein FANCJ regulates the repair of DNA-protein crosslink â€“ stalled replication forks | *Akbar Zainu***

DNA protein crosslinks (DPC) are toxic lesions that form when a protein becomes covalently linked to DNA due to exposure to various endogenous, environmental or chemotherapeutic agents. DPCs impair DNA unwinding and synthesis during replication and transcription. Failure to repair such DPCs is associated with human diseases such as Ruijs-Aalfs syndrome. However, the precise mechanism of DPC repair is poorly understood. Recently we showed that Fanconi anemia (FA) pathway is involved in replication-coupled DPC repair. However, the mechanism of repair of DPCs by the FA pathway is unknown.
FANCJ is a key downstream effector in the FA pathway, where germline mutations in FANCJ leads to diseases like Fanconi anemia, hereditary breast and ovarian cancer and other cancers. FANCJ is a 5' to 3' helicase and interacts with BRCA1. After BRCA-1/2, FANCJ is the third highest cancer susceptibility gene in ovarian cancer. FANCJ is shown to be involved in repair of DPCs *in vitro*, however its exact contribution to pathogenesis remains unknown. Here I examine the precise role of FANCJ in the repair of DPCs in mammalian cells.
Using CRISPR/Cas9, I generated different *Fancj* mutant mouse embryonic stem cell lines – (i) I biallelically deleted the ATPase/helicase and BRCA1 interaction domains, and (ii) generated an ATPase/helicase dead mutant. My preliminary results suggest that the FANCJ ATPase/helicase domain is dispensable for the repair of DPCs generated by the chemotherapeutic drug 5-aza-2' deoxycytidine. However, the BRCA1 interaction domain is essential for DPC repair. Using a site-specific DPC barrier reporter system (Tus/*Ter*), I observed that both FANCJ mutants display increased repair of stalled forks, which is discordant with the viability assays. Further experiments are required to determine whether DNA repair arising at DPCs in FANCJ mutants is aberrant/deleterious. Altogether our data suggest FANCJ plays a critical role in regulating the repair of DPC-stalled replication forks.
https://www.linkedin.com/in/akbar-zainu-ph-d-6a1575a8/

85. **An Ex Vivo Platform based on Organotypic Brain Slice Culture for Informing Personalized Brain Cancer Therapy | *Xiaopei Zhang***

While the improved classification of CNS tumors is already enhancing the scientific rigor of clinical brain cancer treatment guidelines, the impact of these integrated diagnoses based on histopathological features or molecular insight on precision oncology medicine has yet to demonstrate widespread clinical benefit. Patient tumor-derived cancer models (PTDCMs), including patient tumor-derived cell lines, patient tumor-derived organoids, patient tumor-derived explants, and patient tumor-derived xenografts, provide practical models based on a patient's individual tumor that can be used to *ex vivo* or *in vivo* screen for effective therapeutic drugs. Moreover, several studies have shown that patient tumor-derived organoids have the potential to guide personalized care and optimize clinical outcomes by functionally predicting patient response to antitumor drugs prior to treatment. Our team has built an organotypic brain slice culture (OBSC)-based platform and multi-parametric algorithm that allows for the *ex vivo* engraftment, rapid treatment, and

systemic analysis of resected patient brain tumor tissue. This OBSC platform has successfully supported engraftment of each patient tumor tested to this point, including high- and low-grade adult and pediatric tumor tissue. More interesting, the established patient tumor-derived organoids show the ability to activate the brain slice endogenous astrocytes, which have been reported in brain tumor. Whole exome sequencing analysis showed that patient tumor tissue engrafted onto OBSCs maintained a significant genetic resemblance to their parent tumor, while tumor tissue expanded *in vitro* displayed a distinctly different DNA profile. Additionally, our algorithm calculates dose-response relationships of both tumor kill and normal brain tissue toxicity, generating summarized drug sensitivity scores based on therapeutic window and allowing us to normalize response profiles across a panel of FDA-approved and exploratory agents. Summarized patient tumor scores after OBSC treatment revealed positive associations to clinical outcomes, suggesting the OBSC platform can provide rapid, accurate, functional testing to ultimately guide patient care.

86. Genome-Wide Molecular Data Reveal Complex Phylogeography with Conservation Implications for the Endangered Venus Flytrap (Dionaea muscipula J. Ellis) | *Wenbin Zhou*

The Venus flytrap (*Dionaea muscipula*) is an iconic carnivorous plant endemic to the Carolinas in the southeastern United States. Its distinctive morphology and unique survival strategies have fascinated biologists for decades. However, the species' population genetic structure has remained largely unknown. Given its restricted distribution and ongoing population decline, assessing genetic diversity across natural populations is essential to guide effective conservation strategies. In this study, we collected 624 individuals from 43 natural populations and generated a genome-wide SNP dataset using RAD-seq. We applied admixture analyses, population structure inference, and coalescent modeling to investigate genetic patterns. Our analyses identified four distinct ancestral gene pools. All Coastal North populations formed a monophyletic group, whereas Coastal South populations were paraphyletic. Surprisingly, Piedmont populations were polyphyletic, comprising two distinct lineages derived from Coastal South ancestors. Analysis of nuclear genetic diversity, measured as nucleotide diversity (π), revealed considerable variation among populations. Most populations maintained moderate to high levels of nuclear diversity, suggesting they still retain a substantial portion of ancestral genetic variation. However, three populations—CIR (Piedmont), SOC (Coastal North), and HIB (Coastal North)—exhibited extremely low nucleotide diversity (π = 0.012–0.015), indicating genetic erosion, likely due to small population sizes, historical bottlenecks, or isolation. Species distribution modeling predicted a potential northward shift in suitable habitats under future climate scenarios. Together with evidence from isolation-by-distance patterns, these results suggest that Venus flytrap has limited natural dispersal capacity, making localized populations more vulnerable to environmental change. These findings underscore the importance of in situ conservation, particularly for the Piedmont populations, which are not only small and isolated but also harbor unique genetic lineages, making them especially susceptible to extinction.