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SECTION 1

MEET THE SCIENTIST
Akacia Halliday-Isaac is an Afro-Caribbean woman from St. Thomas, US Virgin Islands currently completing her Ph.D. in Biological Sciences at the University of Mississippi studying microbial ecology, experimental ecology and evolution in the labs of Dr. Peter Zee and Dr. Colin Jackson.

She has her Masters of Marine and Environmental Sciences from the University of the Virgin Islands and a Master’s of Education in Curriculum and Instruction with an emphasis in Secondary Science Education from the University of Mississippi. Her research focuses on marine ecology, studying symbiosis and the roles that various types of microorganisms play in various ecosystems. She has received several awards including the Kenneth J Boss Fellowship in Invertebrate Systematics and the International Coral Reef Society Graduate Fellowship.

She is interested in understanding the microbiology of marine ecosystems and increasing participation in and understanding marine science within communities and is currently a 2024 John A. Knauss Marine Policy Fellow.
Alexis Campbell

Alexis Campbell is a 2nd year doctoral graduate student in the Blind lab located at Vanderbilt University. Her research focuses on ligand regulation of nuclear receptors, mainly SF-1 and its homologue receptor LRH-1. Alexs’s main technique and research interest is with using crystallography to validate protein structures of lipid ligands bound to nuclear receptors.

Publications:
Alexis Riley

Alexis’ research has prioritized the legacy, innovations, and healing of Black women teachers by placing their instinctual and improvisational teaching skills at the center of science education.

She has major publications in journals such as the Journal of Research in Science Teaching, the Journal of Science Teacher Education, Cultural Studies of Science Education, and Race Ethnicity, and Education. She served on the Board of Directors for the ASTE, Alexis has used her position to push the science education field to meet the unique realities of teachers and students of color.

Her research and scholarship are heavily informed by her decades’ worth of experience as a secondary Science and History teacher and curriculum and instruction specialist in public and charter schools in Harlem and Brooklyn.
Ashley Miles

Ashley Miles is originally from Missouri City, TX and currently resides in New Orleans, Louisiana. She holds a Bachelor of Science in Chemistry from the University of Houston and began her career as a lab assistant in 2013 for a chemical supplier company called Polyorganix. Here, she gained foundational skills in chemical synthesis and was encouraged to pursue a higher education. After 3 years with the company, she went to Prairie View A&M University and earned her Master of Science in Chemistry in 2018. She then interned at the National Energy and Technology Laboratory in Pittsburgh, PA to synthesize polymers for carbon capture research.

Ashley is currently a 5th year PhD graduate student at Tulane University in New Orleans, Louisiana and joined the Grayson group in 2019. Her research focuses are polymer chemistry and designing synthetic strategies for linear-dendritic polymers. In her leisure time, she enjoys dancing, festival season in New Orleans, and relaxing.
Breana Turner

Breana Turner is a dynamic advocate for women's empowerment, founding Sisters with Ambition to mentor young women. Proudly affiliated with Alpha Kappa Alpha Sorority, Inc., she emphasizes "Service to All Mankind."

With a Master's in Public Health and certification as a Health Education Specialist from Virginia Tech, Breana focuses on women's health topics, including the impact of exercise and the Superwoman Complex on Black women. Currently pursuing her PhD at Virginia Tech, her research explores Black Feminist Thought Theory and Superwoman Schema's effects on Black women's health.

Breana's diverse background includes a Bachelor's in Kinesiology from George Mason University and a pageant titleholder experience with the Miss Volunteer America Organization, fondly calling this phase of her life "The Princess and the PhD." Her mission remains steadfast: advocating for women's health, advancing health equity, and empowering others.
Camille Smith is an Associate Upstream Process Development Scientist at GSK. She was raised in Bucks County, PA and she studied chemical engineering on a pre-medical track at Villanova University. During her time, she completed her bachelor’s degree with minors in Biochemical engineering and ethics.

She began working at GSK soon after graduation where she’s remained for the past 4 years. During her time, she has been able to learn late-stage process development, technical transfer, and process analytical technology implementation. She has found an interest in optimizing process development ways of working by integrating PAT into late phase projects and implementing them into GMP environments.

Outside of work, she is the founder and CEO of STEM So(ul)cial, a hub for Black aspiring and established STEM professionals and creates content diving deep into the complexities of being a 20-something with multiple interests.
Camry A'Keen

Camry A'Keen, originally from Sunflower, Mississippi, and raised in Albany, Georgia, is a radiochemistry research engineer at NYU Grossman School of Medicine. Her previous research includes stem-cell regeneration at the NSF-funded Center for Genomics and Systems Biology and lung cancer research at Columbia University PET Center. A'Keen studied Biology and Chemistry at Valdosta State University before founding A'Keen Brand and the Tuesday Thing, community-building organizations.

She aims to inspire BIPOC women to pursue their aspirations. A'Keen has worked in various roles in film and collaborated with Nike to design inclusive clothing. She was named 2017's Woman to Watch at the Annual True Beauty Conference and has authored publications like "Think: I am whatever I think" and skincare magazines. She holds a degree in Biology from New York University's Graduate School of Arts and Science and has co-authored publications such as "Carpe M.D." encouraging non-traditional pre-meds to pursue medicine.
Chelsee Holloway

Chelsee Holloway is a Washington D.C native who is a recent graduate of Rutgers the State University of New Jersey where she obtained her doctorate from the Animal Biosciences and Endocrinology graduate program. There she studied under Dr. Loredana Quadro and investigates the regulation of metabolic plasticity in the adult heart and maternal heart growth during pregnancy. Chelsee has been an awardee of numerous fellowships including the prestigious Ruth L.Kirschstein Predoctoral Individual National Research Service Award, F31 Fellowship. She is currently a postdoctoral trainee at the NCI/NIH in the laboratory of Dr. Michael Aregger where she studies the regulation of metabolic processes in renal cell carcinoma. Chelsee's research interests are in metabolic regulation, women's health, and health disparities. She is deeply interested in exploring and promoting awareness for diseases that affect minority populations.

Chelsee has been keenly, consistently and successfully focused on research that impacts diverse populations as well as encouraging and mentoring diverse students in STEM. She is committed to being a researcher who nurtures future trainees and compels the scientific community to be diverse in their research endeavors. She doesn't assume that “one size fits all” in identifying and pursuing the study of disease and preventing disease in diverse communities. She knows she wants to impart the understanding her research uncovers not just to students but to communities of people who can benefit and improve their quality of life.
Chinwe Kamma

Chinwe Kamma, a Chemical Engineering graduate from Nigeria, recently completed her MSc in Sustainable Environment and Energy Systems at Middle East Technical University in Cyprus. During her time in Cyprus, she also served as a teaching assistant, guiding approximately 30 students in fundamental chemical engineering courses. Her dedication to education, particularly for girls in engineering and science, inspired her to mentor and empower young girls aspiring to pursue STEM careers.

Currently pursuing her second master's in chemical engineering at Howard University in Washington, D.C., Chinwe contributes as a research assistant in Dr. Chandran's laboratory and was awarded the prestigious Amgen Program Fellowship for her outstanding achievements. With a focus on addressing global environmental and health challenges, Chinwe aspires to earn a Ph.D. in Chemical Engineering to further enhance her expertise in the field. Beyond academia, she enjoys immersing herself in nature, exploring photography, and experiencing cinema outings.
Dira Melissa "Mel" Delpech is a driven leader in Engineering and STEM education, dedicated to making an impact. As a Diversity, Equity, Inclusion, and Justice advocate, she values thoughtfulness and creativity to empower others. With bachelor's degrees in civil engineering and French from the University of Rhode Island and a master's degree in engineering management from the Ohio State University, Mel is finalizing her Engineering Education Doctoral degree at Ohio State. She collaborates part-time to develop research-backed professional development practices focused on equity.

Mel also serves as the Operations and Students for Energy and Entrepreneurial Development (SEED) Program Coordinator at Chain Reaction Innovations, a climate technology incubator at Argonne National Laboratory. Her responsibilities include managing operations, innovator applications, work projects, and coordinating aspects of the SEED Internship Program. She works closely with the University Student Programs group within Institutional Partnerships to ensure program success.
Dominique Gooden

Dominique is a rising senior at the University of Wisconsin-Madison majoring in Biomedical Engineering and minoring in Health Policy. Throughout her undergraduate years, Dominique has conducted neuroscience and neuro-oncology research at various institutions, including Memorial Sloan Kettering Cancer Center, the University of Wisconsin-Madison, and the Massachusetts Institute of Technology. Dominique has had the privilege to present her research from MIT at various conferences, including the National Diversity in STEM Conference (hosted by the Society for Advancing Chicanos, Hispanics, and Native Americans in STEM) and the Annual Biomedical Research Conference for Minoritized Scientists (ABRCMS). Dominique has been recognized with Outstanding Research Presentation awards at these conferences, which speaks volumes to her strong dedication to her research pursuits.

As a National Academy of Engineering Grand Challenge Scholar, STEM Posse Scholar, and Ronald E. McNair Scholar, Dominique's current research interests focus on nanotechnology, nanomedicine, and therapeutics broadly. But more specifically, she is especially intrigued by engineering drug delivery systems for treating neurological diseases and disorders. After graduating from college, Dominique intends to obtain an M.D/Ph.D and eventually work within the intersections of the clinic, research, and policy as a physician-scientist.
Erica Stephens

Erica S. Stephens (she/her) is a graduate of the University of Virginia where she obtained a Bachelor of Arts in Cognitive Neuroscience and Psychology and a Minor in Health and Well-Being. While at the University of Virginia, she worked under the mentorship of Dr. Seanna Leath to explore Black maternal health, focusing on pathways to motherhood, health disparities, and reproductive justice. Post-graduation, Erica joined the Division of Cancer Epidemiology and Genetics (Infections and Immunoepidemiology Branch–IIB) at the National Cancer Institute within the National Institutes of Health.

Under the mentorship of Dr. Aimée Kreimer, Ph.D., senior investigator, IIB, she has expanded her knowledge of public health and gained experience in clinical and epidemiological research by investigating HPV-related health outcomes and cancers. Dedicated to research, medicine, and advocacy, she plans to attain her Medical Degree and a Master of Public Health to become a physician-scientist who is dedicated to improving healthcare in underserved communities. Her research interests include maternal and child health, health disparities, and oncology.

Beyond academics, Erica Stephens is a poet and spoken word artist. Her passion for poetic storytelling is crafted by her personal experience as a Black woman raised in rural Halifax, Virginia. Erica’s personal interests extend to language learning, global travel, community engagement, and advocacy, particularly focused on equitable education and healthcare.
Gift Nnamdi is currently a post-baccalaureate trainee at the National Institute of Mental Health (NIMH), under the mentorship of Dr. Mario Penzo, investigating the neurocircuitry behind emotional and motivational behaviors. Her research focuses on understanding how paraventricular thalamus (PVT) projections to area postrriata contribute to visual threat detection during hunger, employing a multidisciplinary approach involving behavioral assays and chemogenetic methods.

Previously, Gift completed her undergraduate studies at the University of California, Los Angeles (UCLA), majoring in Neuroscience and minoring in Global Health. Under Dr. Kate Wassum's guidance, she explored amygdalar and striatal circuit mechanisms involved in premature habit formation after stress exposure. Gift's passion extends beyond the lab to public health outreach and healthcare quality improvement. She aims to further enhance her research skills to achieve her goal of establishing a translational neuroscience research laboratory and providing care for patients with neurological and neurobehavioral disorders.
Hamda Said Ali

Hamda Said Ali, a dedicated researcher and advocate from Marsabit, Kenya, currently affiliated with Kenyatta University. Ms. Ali is committed to exploring the medicinal potential of local African herbs, aiming to provide cost-effective healthcare solutions for various ailments, including pain, inflammation, cancer, and wounds.

Beyond her research pursuits, she is driven by a fervent desire to address societal challenges, particularly in STEM fields, aiming to empower teens and contribute to transformative change. With a background in Forensic Science, she leverages her expertise to alleviate health burdens globally. Known for her clarity, diligence, and decisive leadership, Ms. Ali fosters effective communication and teamwork, building trust among colleagues and stakeholders alike.
Jasmine Edwards

Jasmine, a postdoctoral research fellow at the University of North Carolina at Chapel Hill (UNC), collaborates with Dr. Kristina De Paris in the microbiology and immunology department. Her research, a partnership between UNC Global Women’s Health Institute and Zambian pregnancy cohorts, aims to prevent preterm births. She recently spent a month in Zambia training laboratory personnel. Jasmine completed her doctoral dissertation at the University of Miami, focusing on stem cell differentiation’s role in regulating cell-specific antiviral responses in Dr. Emmanuel Thomas’s lab. She co-authored multiple peer-reviewed publications and presented her findings at local conferences. Jasmine has received prestigious awards, including NIH Diversity Supplement and T32 programs, as well as being an Amgen Program Scholar at Stanford University during her undergraduate studies at the Rochester Institute of Technology.

Originally from Rochester, NY, Jasmine’s passion for science fiction fueled her curiosity for scientific discovery. Despite encountering a lack of Black/African peers and mentors during her studies, she has taken on leadership roles in various organizations, advocating for diversity and mentorship in academia. Jasmine is dedicated to fostering community and mentorship opportunities, particularly for Black/African students, postdoctoral researchers, and faculty, collaborating with local colleges, universities, and HBCUs. Connect with her on LinkedIn (Jasmine S Edwards Ph.D.) and Instagram (Sheria1010).
Jebrail Dempsey

Jebrail Dempsey is a Microbiology, Immunology, and Pathology PhD student at Colorado State University in Fort Collins, CO. Originally hailing from Bowie, MD, Jebrail finished her bachelor’s degree in Biological Sciences from University of Maryland, Baltimore County in 2021.

Her research interests include infectious diseases, vaccine production and manufacturing, public health/epidemiology, and host-microbe interactions. She is passionate about science education and diversity and inclusion efforts. She believes that science cannot exist in a vacuum and is most effective when the general public is involved and educated. Jebrail is a graduate researcher in the lab of Dr. Elizabeth Hemming-Schroeder, investigating the emergence of microhaplotypes in Plasmodium spp.

At her university, she is a member of the Graduate Students of Color Association (GSCA) and is an NIH T32 Initiatives in Maximizing Student Development (IMSD) fellow. She enjoys exploring new cities, girls nights, beach days, and scary movies. In her free time, you can find her at a local cafe, indulging in an oat milk chai latte and reading about emerging infectious diseases.
Jenah Gabby

Jenah Gabby is a recent Biopsychology graduate from Tufts University in Medford, Massachusetts. After graduating in 2022, she went back home to New York to join the Penn laboratory as a research assistant at Columbia University Medical School. She mainly conducts behavioral tests to analyze and determine the efficacy of hormonal treatments on developing mice.

Before joining the Penn lab, Jenah worked as a research assistant in the Maguire Lab at Tufts, studying the effect of stress on interneurons in mice by conducting behavioral tests. Because of this research, she has recently been co-authored on a peer-reviewed publication from the Maguire Lab. Jenah has also been an awardee of an Annual Biomedical Research Conference for Minoritized Scientists (ABRCMS) poster presentation award. She has contributed to research focused on the neural architecture of stress and the developmental side of maternal-fetal health. With this experience, she hopes to learn and be exposed to maternally focused clinical research as she pursues an MD.
Kaela Makins

Born and raised in Miami, FL, Kaela Makins graduated from Hamilton College in 2021 with her B.A in Biology, and found her way over to Los Angeles, CA where she now attends graduate school. She is currently a PhD Student at City of Hope where she studies the mechanisms of DNA double-strand break repair via end joining outcomes in Dr. Stark’s lab. From the very start of her science journey, Kaela has pursued a passion for creating and fostering communities for Black and Brown scientists, hence her passion for serving as a STEMNoire 2024 Planning Council member.
Kenisha Puckett, raised in Southern California, earned her bachelor's in Biological Sciences from the University of California, Riverside (UCR). With over a decade of experience as a Science Educator across various institutions, she focuses on professional development, curriculum design, and diversifying the science workforce. Transitioning to molecular biology and biochemistry research with Dr. Ernest Martinez, she delved into c-myc oncogenesis.

In pursuit of her master's degree in cell and molecular biology at San Francisco State University (SFSU) Bridges to Stem Cell program, Kenisha trained with the California Institute of Regenerative Medicine (CIRM). Her thesis, under Dr. Susan Fisher at the University of California, San Francisco, explored the impact of environmental toxins on human pregnancy. She has received prestigious fellowships and awards, including the NIH Masters to Doctorate Bridge Program Fellowship.

Currently a final-year Ph.D. candidate at Stanford University's Institute for Stem Cell Biology and Regenerative Medicine, under Dr. Vittorio Sebastiano's guidance, Kenisha focuses on trophoblasts, aiming to develop a high-throughput tool for generating trophoblast stem cells in vitro. She advocates for equity in scientific research, serving in leadership roles and balancing her academic pursuits with motherhood and freelance makeup artistry.
Kimora Hudson

Kimora Hudson is a recent graduate from Vanderbilt University with a Master’s degree in Biomedical Sciences. She is from Atlanta, Ga and graduated from the University of West Georgia with a Bachelor’s of Science in Biology (cum laude) at the age of 18. During her time at the University of West Georgia (UWG) she worked in Dr. Farooq Khan's laboratory studying “molecular containers” called Cucurbit[n]urils and their binding properties to alkali metal ions. While at UWG she was a part of the Tri Beta Biological Honor Society, was a UWG Ingram Scholar, and on the President’s List several semesters.

Currently, Kimora works in Dr. Ray Blind’s laboratory at Vanderbilt University with an interest in cell biology and biochemistry. She is investigating whether nuclear receptors such as SF-1 bind to phosphoinositide lipids in vivo.

Outside of research, Kimora volunteers with Youth Science Academy, a non-profit organization, that exposes African American youth to STEM topics. She also has a passion for swimming and has taught many kids in her community essential swimming skills. In the future Kimora wants to pursue a MD degree to become a physician and help underrepresented populations.
Laerissa Reveil is a doctoral student from Orlando, FL in the Department of Pharmaceutics in the School of Pharmacy at Virginia Commonwealth University (VCU). Laerissa is a member of Dr. Matthew Halquist’s lab, where she works on determining age-related differences from exposure to drugs of abuse.

Laerissa previously received a dual Bachelors in Chemistry and Criminology from the University of Florida and a Master’s in Forensic Science at VCU, where she studied the effects of drug mixtures in electronic cigarettes. She published her first, first-author publication on her Master’s research and has also presented her work at numerous national and international conferences. Laerissa is a member of the Society of Forensic Toxicologists (SOFT), the American Academy of Forensic Sciences, and the International Association of Forensic Toxicologists. Within SOFT, Laerissa is a member of the Diversity Task Force, which brings forth initiatives to increase awareness and diversity of the SOFT membership with a focus on students and young professionals. When not working in the lab, she likes to create custom apparel and accessories through her custom design business CreativelyStemmed.
Dr. Lakeisha Lewter was born and raised in Laurel, MD. She received her BS in Biology with a minor in Psychology from Morgan State University in Baltimore, MD.

Keisha obtained her PhD in Neuroscience from The University at Buffalo where she studied the potential utility of GABAA receptor modulators for pain control. Dr. Lewter is currently a postdoctoral fellow in the School of Behavioral and Brain Sciences at The University of Texas at Dallas. Her work mainly focuses on the underlying mechanisms involved in the development of chronic bladder pain. Keisha was awarded a National Research Service Award (NIH) and a Postdoctoral Diversity Enrichment Program Award (Burroughs-Wellcome Fund) to fund her research. Dr. Lewter plans to one day have a lab of her own where her research will focus on pain disorders that disproportionately affects women (e.g., endometriosis and uterine fibroids).

Outside of the lab, Keisha enjoys dancing, attending music/art festivals, and roller skating. She is also a proud member of Alpha Nu Omega Sorority, Inc.
Mazvita Chakawa, a PhD candidate in Biomedical Sciences at Tulane University, arrived in the US from Zimbabwe in 2020 amidst the COVID-19 pandemic to pursue her doctoral studies. Under Dr. Derek Pociask in Pulmonary Medicine, she investigates immune responses to lung injury caused by viruses and chemical toxins, focusing on the IL-22-binding protein’s role in macrophages and dendritic cells. Her research, employing various assays and transgenic mouse models, highlights the protein's impact on lung injury severity and macrophage function crucial for repair.

Mazvita, a recipient of prestigious awards like the Fulbright Foreign Student Award, the OAK Foundation Fellowship, and the Deutscher Akademischer Austauschdienst (DAAD) scholarship, has co-authored publications and presented at international conferences. Now in her fourth year, she aims for a career in pharmaceutical R&D.

She co-founded the Biomedical Science Equity, Diversity, and Inclusion Student board and serves as the International Student’s representative, advocating for streamlined processes and support for international students at Tulane. Connect with her on LinkedIn.
Michaela Allen

Michaela Allen is a PhD candidate at Tulane University School of Medicine. She is originally from Mobile, Alabama. She is a member of Dr. Derek Pociask’s lab, studying the effect of the TWEAK/TWEAKR signaling axis on lung repair in response to respiratory viruses. She has also collaborated on other projects and is a co-author on several publications.

Michaela has mentored a Xavier undergraduate student through the Xavier-Tulane Summer Research Experience along with several Tulane undergraduate students. Michaela is passionate about increasing accessibility to science for the public and plans to work as a science writer once she completes her graduate studies.
Niouma Semega

Niouma Semega is an undergraduate at NYU studying Global Public Health and Sociology as an aspiring public health practitioner with interests in data and environmental health.

She is a CEO of her own founded non-profit SemegaChange, a developing empire of Black and women of color in STEM cultivating change through projects and businesses. She is a past Victoria Secret's PINK GRL PWR Project Winner in the Sustainability Category. A 2023 Emerging Leader at NYU's School of Global Public Health where she delivered a talk on Environmental Health Disparity and investing in LMICs. She recently was awarded 1st Place at the 35th Annual CSTEP Conference for her novel invention that extracts pollutants from bodies of water she has developed in the past 6 years!

She hopes to expand and continue her research in current projects like; "EPA Monitoring Disparity" and "Open Burning in Kphone, Ghana", "Health Effects of Climate Change in Uganda", to continue to improve public health to prevent diseases and illnesses that stem from environmental factors.
Nyna DeWitt, born and raised in Durham, North Carolina, obtained her bachelor’s degree in general engineering with a concentration in biomedical engineering from Wake Forest University. Following her undergraduate degree, she received her master’s degree in biomedical engineering with a focus in immunoengineering from Johns Hopkins University. Currently, Nyna attends The University of Georgia and is a part of the DREAM Research group located within the Engineering Education Transformations Institute. Nyna is working towards her doctoral degree in engineering education. At The University of Georgia, she has been able to contribute to multiple research projects and the engineering education community. As the president of the American Society for Engineering Education at UGA, she works to bring awareness to the department and caters to the needs of students pursuing the field.

In respect to research, Nyna has a strong interest in increasing diversity in biomedical engineering spaces and she intends to explore this by focusing on inclusive classroom spaces and diversifying biomedical engineering research models. In the future, Nyna hopes to work in higher education and rectify engineering education issues in this space. She also has aspirations of increasing biomedical engineering exposure in marginalized populations by engaging with local communities. Nyna has begun working towards this goal by volunteering her time at the University Cancer and Blood Center.
Olivia Joyner is a PhD Candidate in the Molecular, Cellular, & Developmental Biology Department at the University of Colorado, Boulder. She received her BS in Biotechnology from California State University San Marcos. She works in the lab of Dr. Edward Chuong where the lab focuses on how transposons affect genomic evolution and gene regulation. Olivia's thesis work seeks to understand how polymorphisms and structural variants contribute to immune system dysregulation. She is passionate about understanding how genome variants contribute to different phenotypes in underrepresented populations. Her efforts also include extensive outreach and mentorship in her department. She is the Lead Teacher Assistant guiding new graduate students in the department, which includes aiding students looking to earn their Teaching Certificate. Olivia is also a student representative for her department's DEI committee, where she has been instrumental in shaping departmental initiatives aimed at enhancing diversity and ensuring that all student voices are heard and valued.

Olivia is from San Diego, California and when she is not in lab, she enjoys roller skating and painting.
Oluwatoyosi Adaramodu

Oluwatoyosi Adaramodu, commonly known as Lisa, is a 2nd year Biology PhD student at the University of Pennsylvania. Her academic journey commenced with a bachelor’s degree in plant science and biotechnology from the Federal University Oye Ekiti (FUOYE) in Nigeria, focusing on sunflower adaptation in rainforest zones. This foundation led her to a master’s research role at the Institute of Botany, Chinese Academy of Sciences, where she delved into Genome-wide association studies (GWAS) of sorghum under salinity stress.

Currently, Lisa’s research is centered on the role of bulliform cells in grasses, specifically Sorghum bicolor, exploring how these cells respond to environmental stressors. Beyond her academic pursuits, Lisa is a passionate STEM advocate and co-founder of Afro in Bio, an initiative aimed at enhancing the presence and support of African scientists in biology. As a black woman in STEM, she is fiercely committed to fostering diversity and inclusion within the field. Her aspirations extend to becoming a professor in plant biology, where she intends to mentor and support underrepresented students. Her dedication to promoting equity in education and research opportunities is a testament to her belief in the transformative power of diversity in science.
Queriah Simpson

Queriah "Que" Simpson, was born and raised in Melbourne, FL, and graduated from Florida A&M University (FAMU) in 2017 and 2020. Having obtained a Bachelors in Pre-professional Biology with a Chemistry minor and a Bachelors in Environmental Science in 2017, and her Masters in Environmental Science concentrated in Marine and Estuarine Environments in August 2020 as a NOAA-CCME Graduate Scholar. During undergrad as a part of NOAA-ECSC, she completed a project titled Evaluating the Eastern Mosquitofish (Gambusia holbrooki) as a Biodiindicator Species for Endocrine Disrupting Chemicals. Proving that chemicals from a paper mill in Perry, FL, have detrimental effects on Mosquitofish and the water quality of the Fenholloway River.

She successfully defended her thesis, the Application of Habitat Suitability Models for Benthic Communities in the Eastern Gulf of Mexico: Linking Bioprospecting and Modeling Research. A project that allowed her to work with scientists from NOAA’s National Centers for Coastal Ocean Science Biogeography Branch in Silver Spring, Maryland, and Florida State University for The Hydrodynamics & Habitat Suitability for Meiofauna And Corals (HydroSMAC) Mission.

Queriah is now a Ph.D. candidate and NOAA-CCME graduate scholar at FAMU, the Program Director for Black in Marine Science (BIMS), on the Executive Board for Little Growers Inc., a member of an NAACP EJ Committee, and a Private Chef.
Rhea Xavier

Rhea Xavier is a Biology and Chemistry graduate of Grambling State University in Grambling, Louisiana. During her time there she began a research project based on this by exploring the correlation between addiction and obesity factors in Drosophila melanogaster and how it may translate in humans.

While actively serving in several clubs including the International Student Organization and Earl Lester Cole Honors College. Following her graduation, she sought the role of a Research Associate at the University of Texas Medical Branch in the laboratory of Dr. Rakez Kayed studying protein aggregates like tau and α-synuclein in neurodegenerative diseases like Alzheimer’s and Parkinson’s Disease.

Eventually she plans on pursuing a PhD to bridge the gap between biomedical development, academia, and low-income communities.
Rhoda Moise

Rhoda Moise, Ph.D., CYT, hails from Philadelphia, PA, with Haitian heritage, embodying resilience, education, and community values. Witnessing the impact of chronic disease on her family and community, she pursued advanced education to promote health. Graduating with honors from Pennsylvania State University with a Bachelor of Science in Biobehavioral Health and minors in Biology and Health Policy and Administration, she earned her Ph.D. in Prevention Science and Community Health from the University of Miami Miller School of Medicine.

Additionally, she holds a 200-hour certification in Ancient Egyptian yoga teaching. Dr. Rho aims to address health system inequities through innovative strategies, engaging stakeholders like patients, providers, and payers. As a health and wellness advocate, she offers speaking, consulting, and training services globally. Dr. Rho has received numerous accolades, including the PRIDE NIH Training Program, Aseemkala Initiative Health Research Choreography Fellowship, and the Barrett Prize for Best Dissertation on a Latin American or Caribbean Topic at the University of Miami.
Sarah Bartley

Sarah Bartley obtained her B.S. in Physics from Agnes Scott College and an M.S. in Physics from the University of Central Florida. She is a Ph.D. student in the Department of Nanoengineering at North Carolina A&T State University. She accepted an IBIEM (Integrative Bioinformatics for Investigating and Engineering Microbiomes) fellowship for the year 2020-2021 to focus on microbiome research. She has accepted the Chancellor Fellowship for the year of 2021-2025. She is also the host of a podcast called Funding is the Matter. For the first series, she is investigating the lack of funds to Historically Black Colleges and Universities (HBCUs).
Savannah Clax is originally from Canton, OH and Louisville, KY. Currently pursuing her master’s at Oregon State University, she focuses on researching the impacts of climate change on fisheries. This academic pursuit stems from her deep-rooted appreciation for animals and the ocean, nurtured during her upbringing traveling to the US south-east coasts with her family. Savannah’s fascination with the ocean extends beyond her academic research. Whether exploring tide pools, reading a good book on the beach, learning to surf, fishing, taking photos of wildlife, or simply going for a swim, she loves all things related to coasts and the ocean. She also indulges in many different artistic pursuits including writing, drawing, photography, and videography.
Sherifa Akinniyi joined the National Institutes of Health Division of Cancer Epidemiology & Genetics (NIH DCEG) as a postbaccalaureate fellow and Undergraduate Scholarship Program (UGSP) Scholar in the Clinical Genetics Branch (CGB) in June 2023. She earned a B.S. in nutritional sciences and minor in biology from the University of Georgia, Athens, in May 2023. She has presented poster and oral presentations at local and national conferences. In CGB, Ms. Akinniyi’s research focuses on estimating the population prevalence of germline variants in genes associated with telomere biology disorders. Using a genome-first approach, she is studying the prevalence and cancer phenotypes of individuals with pathogenic or likely pathogenic germline TERT variants (i.e., mutations) in large biobanks of germline sequencing data linked to electronic health records. Ms. Akinniyi is under the mentorship of Dr. Kelvin C. de Andrade, Dr. Marena R. Niewisch, and Dr. Sharon A. Savage. She recently received acceptance to medical school and is deciding the best career pursuit of her clinical and research interests.

Sherifa is heavily involved in other initiatives to advance diversity and engagement in science, including serving as the co-chair of the Career Development committee in the DCEG Black Cancer Researchers Group, co-chair of the Newsletter committee in UGSP, and an active member of the planning committee for the NCI-DCEG Fellows' Symposium.
Tiffany Hamm

Tiffany Hamm is a doctoral candidate at Syracuse University’s School of Education, Department of Teaching and Leadership. Born and raised in New York City, Tiffany has held a passion for the natural sciences, and pursued a career in Marine Sciences. Her studies came full-circle when she began to teach Earth Science at a high school in her hometown, the Bronx, New York. Since then, Tiffany has been committed to increasing equity and accessibility in science education through the frameworks of holistic engagement, mindfulness, and environmental social justice. Tiffany is completing her doctoral studies in Science Education and is currently a SUNY PRODiG Diversity Fellow at SUNY Cortland where she teaches courses centering the intersections of science education.
Zoe Vaughn recently graduated with her Ph.D. from The University of Pittsburgh Pharmaceutical Science program where she was in the medicinal chemistry track. Zoe was the first African American women to obtain her Ph.D. from the pharmaceutical science program. She is currently working as an ORISE postdoctoral fellow at the US Army Medical Research Institute of Chemical Defense the Department of Defense’s lead laboratory for medical chemical defense research. She is a part of a community of scientists conducting research in medicinal chemistry, with an emphasis on developing countermeasures to combat chemical weapon exposure.

Zoe is originally from Rochester New York where her love for giving back began, her academic journey has been a platform to stand on, from which I can reach young people that look like me. In the Greek, Zoe means “Life” and for the past two years Zoe awarded a high school graduating African American female a scholarship entitled #addlife. The scholarship is an embodiment of her scientific journey and the people that continuously poured into her, that helped her get to where she is today. Zoe's desire is to continue this scholarship to help young girls and boys with a similar background achieve their education dreams.
SECTION 2
POSTER PRESENTATIONS
Host-pathogen evolutionary history drives priority effects in assembled model communities

Akacia K. Halliday-Issac, Peter C. Zee

When new communities assemble, for example in situations such as post-natural disasters, community assembly can result in variable communities even in similar environmental conditions. This is due to priority effects making the final community highly contingent on the order and timing of species immigration. When host-pathogen interactions are involved, the coevolutionary history between hosts and pathogens can lead to complex evolutionary dynamics of resistance and infectivity. As such, the coevolutionary history among pathogens and immigrating species may contribute to the strength and direction of priority effects during community assembly.

In this study, we perform experimental coevolution and ecological assembly experiments using bacterial lineages of Pseudomonas fluorescens and bacteriophage SBW25Φ2 strains to test how host-pathogen coevolution impacts ecological community assembly dynamics.

In the model microcosms, growth rates significantly increased over evolutionary time, and resistance was maintained over evolutionary time indicating that media (environmental) adaptation can overcome growth-resistance tradeoffs. The mean priority effects were inhibitory, however, resistant bacteria in the presence of bacteriophage exhibit neutral or facilitative effects for other lineages. Mismatches within the three-way interaction between the evolutionary history of the focal and competitor bacterial lineages and bacteriophage also resulted in differing priority effects. These altered priority effects may be due to the resistant lineages arriving with the bacteriophage resulting in the reduction of phage populations before the arrival of the second arrivers.

These findings combined indicate that the coevolutionary history between host and parasite has the potential to significantly alter how communities assemble. This study is the first to investigate the effect of these prior coevolutionary histories of hosts and parasites. Understanding the role of bacteriophage evolutionary history, environmental (media) adaptation, and growth resistance tradeoff on priority effects and community assembly dynamics are important in the future understanding and predictions of how these communities may reform and progress following disturbance or when new environments become available.
Sphingolipids and Ligand Dependent Regulation of SF-1

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Steroidogenic Factor-1 (SF-1) is a member of the NR5A DNA binding superfamily of nuclear receptors. SF-1 operates as a DNA-binding transcription factor that is pivotal in regulating the development and adult function of steroidogenic tissues. This nuclear receptor is required for the proper development of adrenals and gonads in mammals and dysfunction of the receptor has been linked to conditions such as adrenocortical carcinoma and endometriosis making the elucidation of SF-1 mechanics a key area of interest for biomedical research.

Current knowledge of SF-1 regulation has been linked to the discovery of phospholipids within the ligand-binding pocket of the nuclear receptor. However, SF-1 is known as an orphan nuclear receptor as no endogenous ligand has been identified. Published SF-1 crystallographic structures have focused on phospholipids as ligands for regulating SF-1, most notably from the Blind lab’s work with phosphoinositide’s PIP2 and PIP3. While structures of phospholipids bound to SF-1 have been published, another potential ligand for SF-1 is sphingolipids. Sphingolipids such as sphingomyelin and sphingosine have been associated with SF-1 by mass spectrometry, however the structure of SF-1 bound to these lipids has not been confirmed.

My research aims to explore the structural and functional consequences of sphingolipids bound to SF-1. Understanding the significance of sphingolipids as regulators of SF-1 will allow for a better understanding of how these regulatory mechanisms can be targeted for the treatment of pathologies such as the previously mentioned adrenocortical carcinoma and endometriosis.
A polymer is a large molecular compound composed of repeating units called monomers. The synthesis of a polymer involves the covalent linkage of monomer molecules to form a macromolecule. Linear polymers, characterized by chain-like structures possess long, flexible chains that can either move past one another or entangle. High molecular weight linear polymers often exhibit limited solubility in most solvents due to increased chain entanglements. On the other hand, dendrimers are globular tree-like structures with branches attached to the core. As an AB2 dendrimer generation increases (G#) the number of branches doubles, leading to a highly branched structure. Due to the globular nature of dendrimers, the structures are much more soluble than their linear counterparts. To combine these properties, linear-dendritic (LD) alternating copolymers can be synthesized. Initially, LD copolymers were just 2 or 3 repeating units, consisting of a monodisperse tadpole or dumbbell architectures. These copolymers consist of a linear polymer with one or two dendritic end groups. However, the Cheng research group (at the University of Buffalo) has reported the only known instance of perfectly alternating linear-dendritic (LD) copolymers, incorporating a poly(ethylene glycol) linear spacers between the dendrimer units though a step-growth copper(I)-catalyzed azide-alkyne cycloaddition (CuAAC) reaction. Our research group is now describing another type of LD copolymer with three generations of 2,2’-bis(hydroxymethyl)propionic acid (bis-MPA) dendrons with two alcohol functional groups. These dendrons, derived from an AB2 monomer through a precise sequence of deprotection and coupling steps, served as the dendritic component for the linear-dendritic (LD) copolymer. The linear component was obtained from poly(ethylene glycol)-dimesylate (PEGMS). To synthesize the LD copolymer, a Williamson reaction was employed with the macromonomers mentioned. The dendron macromonomers and LD copolymers were synthesized and characterized using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-ToF MS) for assessing the structural composition. Nuclear magnetic resonance (NMR) spectroscopy provided detailed information about the chemical structure, confirming the successful synthesis of the designed copolymer. Additionally, size exclusion chromatography (SEC) was utilized to evaluate the molecular weight and purity of the copolymer. In the future, our group and the Cheng research group will determine if these can form well-defined “nanorod” structures because the peripheral dendritic groups will be non-polar but the linear PEG polymer will be polar.
Uncovering Genetic Regulators of Metabolic Plasticity in Renal Cell Carcinoma

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Renal cell carcinoma (RCC) is a term that covers an array of kidney cancer subtypes differing in incidence, histopathology, genetic and molecular alterations, as well as in clinical outcomes and prognoses. RCC is a relatively common disease that affects an estimated 400,000 people worldwide each year with over 100,000 deaths annually, according to the Global Cancer Observatory. A common characteristic of many RCCs is that they are driven by a metabolic change or rewiring, due to a high frequency of mutations in genes that regulate major metabolic processes in the cell. This metabolic rewiring is a hallmark feature of RCC. It was recently discovered that patient overall survival and prognosis has been linked to the expression of certain metabolic signatures in RCC tumor cells. Metabolic plasticity allows cancer cells to survive and adapt to different environments and metabolic stress conditions, such as nutrient deprivation. Therefore, exploring and exploiting metabolic rewiring and plasticity in these cells may reveal genetic vulnerabilities and dependencies. This could lead to discovery of novel biomarkers and molecular targets that can be implicated as future therapeutic interventions for this disease. Here we utilize functional genomic screens to expose genetic dependencies and vulnerabilities under different physiologic and metabolic conditions in patient derived RCC cells, to gain insight into regulation of metabolic plasticity.

CRISPR-based genetic screening is a powerful tool for the systemic characterization of gene function and function regulation. Here we utilized the CHyMERa (Cas hybrid for multiplexed editing and screening applications) system, which applies a co-expression of orthologous nucleases (Cas9 and Cas12a) and the expression of hybrid guide RNAs (hgRNA) for the combinatorial targeting of multiple genes in the same cells in patient derived (PDC) RCCs. Additionally, cells were screened under different media conditions that mimic human physiological conditions and a nutrient deprived of lipids, one of the major metabolic substrates of the cell. High throughput Illumina sequencing and analytic protocols were applied to identify genes that were implicated in cell fitness.

In future studies we will further explore the relationship between different key metabolic regulatory genes in RCC and map for genetic interaction in major metabolic pathways. We aim to provide insights into regulation of metabolic plasticity in RCC and identify novel metabolic regulatory targets that can be used for potential treatment therapies.

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The transportation sector significantly contributes to global GHG emissions through fossil fuel use. Electric vehicles (EVs) are gaining traction globally as a means to reduce environmental impact. In Africa, despite its low share of global GHG emissions, there’s a rising focus on environmentally friendly practices, notably, the growing EV market projected to reach a substantial figure by 2028. Batteries are known to be made of toxic components such as metals and corrosive electrolytes, which can pose a threat to the environment if not properly handled. When not properly disposed of, batteries can cause environmental risks. Higher concentrations of the chemicals used when released into the environment can cause neurological and endocrine problems.

While studies in Africa often emphasize the economic impact of EVs, there’s a lack of attention to the End-of-Life (EOL) phase of electric vehicle batteries. Bridging this gap, a life cycle assessment using the greenhouse gases, regulated emissions, and energy use in transportation (GREET) model was conducted to evaluate the environmental impact of EOL electric vehicle batteries in Africa, with a focus on recycling options. NMC 532, NMC 622, and NMC 811, which are the battery models of the most driven EVs in Africa were studied.

Using the GREET model open-source software, the environmental impact of the EoL of these battery models in the African context was estimated. The study revealed that the generic pyrometallurgy recycling of lithium-nickel-manganese-cobalt (NMC) 532 batteries exhibits the least GHG emissions and energy use compared to other studied battery models, while in the hydrometallurgy category, NMC 811 shows the least potential in energy consumption and GHG emission. It is also important to note that in hydrometallurgy, NMC 532 shows the highest GHG emissions and energy consumption, implying that environmental impacts vary according to battery models and recycling technology. Future studies could incorporate other battery models such as Lithium iron phosphate (LFP), lithium-nickel-aluminium (NCA), lithium-cobalt oxide (LCO), and lithium-manganese oxide (LMO).
Black women in the United States contend with the compounded challenges of racism and sexism, which shapes their unique experiences within society (Collins & Bilge, 2020; Crenshaw, 1991). My dissertation explores the distinct struggles faced by Black women in higher education, specifically in the field of engineering. The study seeks to contribute to the ongoing dialogue on diversity and inclusion in higher education, aligning with the SASR Grants program’s mission to address challenges faced by minoritized student populations.

I employ the asset-based lens of the Community Cultural Wealth (CCW) framework (Yosso, 2005) to broaden the participation of Black women in engineering. This approach recognizes mentorship, navigational skills, and connections to family and community as crucial solutions. One such solution is through participation in student engineering organizations. There is an existing gap in the literature capturing Black women’s participation and perception within such organizations despite increased attention from engineering programs.

Semi-structured interviews with Black women engaged in the National Society of Black Engineers (NSBE) and the Society of Women Engineers (SWE) engineering student organizations will seek to illustrate the unique experiences of interviewees with an intent to inform inclusive practices. The data will shed light on how Black women interpret their participation within organizations like NSBE and SWE, specifically how these women navigate these groups, considering the stratified gendered and racial nature of their experiences.

The project emphasizes the need for an intersectional approach to (1) valorize Black women, (2) capture the narrative of Black women’s experiences, and (3) articulate the unique stories of Black women. The study further intends to understand how NSBE and SWE promote and support Black women’s intersectional identities. Shedding light on the intersectional experiences of Black women in engineering student organizations will guide community leaders and stakeholders in creating more inclusive and supportive environments for Black women in engineering across all of higher education.
Functionalizing Layer-by-Layer Nanoparticles for improved Glioblastoma penetration

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Glioblastoma (GBM) is a lethal brain cancer that recurs after surgical tumor resection. Furthermore, it is highly resistant to radiation and chemotherapy treatments. These factors have, in part, led to a five percent long term survival rate over a five-year period for patients. One main challenge in treating glioblastoma is delivering medication to the tumor. GBM’s dense, solid characteristics pose significant challenges in adequately delivering drugs to the tumor microenvironment because many medicines cannot penetrate the tumor entirely. When vital medication cannot reach GBM, the cancer metastasizes and becomes more difficult to treat. Our project utilizes Layer-by-Layer Nanoparticle (LbL NP) technology to engineer nanoparticles with features that improve their efficiency and effectiveness for drug delivery.

First, we layered multiple ratios of Poly-L-Glutamate (PLE) to Poly-L-Glutamate-PEG-iRGD (PLE-PEG-iRGD) onto LbL NPs containing Poly-L-Arginine (PLR). PLE was used to maximize cellular uptake of our LbL NPs. PLE-PEG-iRGD was used for a variety of reasons; one being that PEG promotes colloidal stability and iRGD demonstrates tumor-penetrating properties. Using a thiol detection assay, we determined the amount of iRGD peptide on our nanoparticles. Then, we also tested our particles’ stability in artificial cerebrospinal fluid at set time points. This was made by mixing various compounds that mimic the biochemical environment of real cerebrospinal fluid. This step was important because cerebrospinal fluid is a biologically relevant fluid that coats and protects the brain and spinal cord. Finally, we utilized flow cytometry to determine the percentage of cells that uptook the LbL NPs.

From this work, we determine that we can control the peptide content of our nanoparticles by co-layering PLE and PLE-PEG-iRGD. Furthermore, we found that increasing the PLE-PEG-iRGD content on our nanoparticles’ outer layer improves colloidal stability. At least 60% of PLE-PEG-iRGD is required for stability in artificial cerebrospinal fluid after 5 hours. This project lays the groundwork for designing efficient nanocarriers for local and systemic drug delivery to GBM tumors in vitro and eventually in vivo.
Elucidating role of paraventricular thalamic projection to area postriata in visual threat detection during hunger

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Animal survival is guided by prioritizing behaviors that address their most pressing needs. In prey species, the need to eat, and to avoid being eaten predominate. When animals are sated, exposure to novel, potentially threatening environments, leads to the prioritization of defensive strategies over foraging to minimize risk of threat exposure. Yet, when animals are food restricted, the deployment of defensive behaviors may be constrained by the competing need of finding food. In such scenarios, delays in defensive responding might increase the likelihood of encountering a predator and/or predatory attack. Surprisingly, the neural mechanisms that govern the arbitration process that shape approach-avoidance behaviors amid competing needs remain unclear.

Prior studies have identified brain regions involved in the regulation of hunger states, which includes the paraventricular thalamus (PVT). Of note, the PVT is also known to participate in guiding defensive behaviors. These collective observations have led to a conceptualization of the PVT as a central hub that shapes behavior choices under motivational conflict. But the precise mechanisms by which the PVT subserves this role on behavior remains unclear. Here, we demonstrate food deprivation suppresses escape behavior in a looming visual threat task, and this is associated with increases in the immediate early gene, cFos, within the anterior portion of the PVT (aPVT). Further, we identify a discrete projection from the anterior PVT to area postriata (APr), a brain region involved in the rapid detection of peripheral stimuli that is critical to the execution of an escape behavior. In preliminary studies, fiber photometry recordings, using a calcium sensor (GCaMP) as a proxy for bulk neuronal activity, show increases in APr activity following visual threat stimuli, and prior to the generation of an escape behavior.

In addition, chemogenetic inhibition of APr or silencing of pituitary adenylate cyclase-activated peptide (PACAP) expressing neurons in APr resulted in delayed escape behavior after loom onset. Our results indicate that escape behavior involves activation of a genetically defined subpopulation of APr neurons, and that mice suppress defensive behaviors to visual threat when metabolic need becomes substantial. Ongoing research is aimed at further testing the hypothesis that hunger-activated PVT projections largely inhibits a distinct subpopulation of APr neurons, suggesting a mechanism where aPVT biases behavioral control away from threat responding towards foraging.
Preterm birth in Zambian Women is correlated with M1 macrophage-driven inflammation exacerbated by HIV and anaerobic vaginal microbiota

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The goal of the Zambian Preterm Birth Prevention Study (ZAPPS) is to discover immunological factors contributing to adverse birth outcomes. HIV infection and vaginal anaerobic bacterial species are associated with promoting inflammation and increased risk of preterm birth. Macrophages are immune cells that regulate immunity during pregnancy. Macrophages have two primary subtypes, M1 and M2. M2 macrophages promote tolerance at the maternal-fetal interface during fetal development. M1 macrophage promotes inflammation in response to viruses/bacteria and facilitate labor. We hypothesize that HIV exposure during pregnancy exacerbates a dominant M1 proinflammatory environment during the fetal development stage of pregnancy that, combined with the more anaerobe vaginal microbiota, will increase the risk of in preterm birth in women with HIV.

PBMCs, from a healthy African American donor, were treated in vitro with vaginal swab elution from pregnant Zambian women with or without HIV who had term birth (TB) or spontaneous preterm birth (sPTB). Two vaginal swabs were collected during either the 1st (weeks 9-12) or 2nd (weeks 13-20) trimester for visit 1 and during the 3rd (weeks 28-29) trimester for visit 2. Flow Cytometry was used to determine the percentage of M1 (CD14+CD68+IL1β+ and/or TNFα+) and M2 (CD14+CD68+TGFβ+ and/or IL10+) macrophages.

We compared the ratio of M1 to M2 frequencies based on cytokine expression within each clinical group and control condition. For our M0 and M2 controls, the average ratio of M1:M2 frequencies was 1:1, while the average ratio was 3:1 for the M1 control. In the HIV- group, women with TB had an average ratio of 1:1 during the 1st/3rd trimesters. Women with sPTB had an average ratio of 2:1 during the 1st/3rd trimesters. In the HIV+ group, both women with TB and sPTB had an average ratio above 2:1 (2nd trimester), however women with TB had a ratio of 1.5:1 whereas women with sPTB was 1.8:1 by the 3rd trimester. For cytokine frequencies, the percentage of IL1β+ macrophages were significantly greater than IL10+ or TGFβ+ macrophages in women with sPTB during the 2nd and 3rd trimesters. There was no significant difference in TNFα+ macrophages to IL10+ or TGFβ+ macrophages in all clinical groups, despite a significant difference observed for the M1 control.
Elucidating Polymorphisms in Plasmodium falciparum from Asymptomatic Malarial Samples in Homa Bay Residents

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Malaria remains a leading public health threat in sub-Saharan Africa, specifically Kenya and Ethiopia. Intervention techniques, including the use of insecticide-treated bed nets, has decreased malaria transmission; however, these materials cannot stop the emergence of hotspots, or regions where cases remain high as transmission decreases. While there are two WHO-endorsed malaria vaccines, the long-term effects remain to be seen. Detection of low parasitemia infections may provide better chances of treating malaria before it spreads. Genetic variation within malaria infections confers drug resistance, immune evasion and severe disease. We propose investigating infection dynamics and identifying microhaplotypes of *Plasmodium falciparum* the most common malaria parasite, to better detect asymptomatic cases of malaria that fuel these hotspots.

*P. falciparum* the dominant strain of malaria-causing parasites in sub-Saharan Africa, poses a significant health threat. Children younger than 5 years old are a vulnerable population, comprising the majority of malaria deaths. Finding effective strategies in treating and preventing the spread of malaria is difficult due to the variability in the genome. The *Plasmodium* spp. var gene differs among each parasite and its expression is complex. Further, the ability of the parasite to sexually or asexually reproduce begets more genetic variability and confers more parasite fitness advantages, such as antimalarial resistance. Additionally, genotyping *P. falciparum* samples may provide insight into the dynamics of new and old infections as well as co-infections.

Our study uses dried blood spot samples collected from Homa Bay, Kenya to sequence the *P. falciparum* genome. Using selective whole genome amplification (sWGA) and highly-multiplexed amplicon sequencing, we can detect and magnify parasite DNA from infected blood. Then, we will conduct next-generation sequencing (NGS) and identify polymorphisms of interest. Our data will be analyzed using R. Alongside our biological data, we also have qualitative data describing household size, migration, communities with or without irrigation, and numbers of children present. This will allow us to observe transmission trends and their relationship to environmental and lifestyle factors. Previous studies have shown that hotspots with low transmission levels may have higher genetic variation. We expect to see more infections in households with small children, residents living in irrigated communities, and residents moving into hotspots.
Postnatal Treatment with a Neurosteroid Mitigates Autistic-like Behaviors in a Preclinical Model of Placental Hormone Loss

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The placenta is a vital organ for fetal development, especially the fetal brain. Placental pathology or premature placental loss due to preterm delivery is linked to a higher risk of neurodevelopmental disorders such as autism spectrum disorder (ASD) (Lodefalk et al., 2023). In our laboratory, we study the role of placental hormones, particularly allopregnanolone (ALLO), a progesterone-derived neurosteroid that enhances GABAA receptor activity and plays a key role in neurodevelopment.

We have recently developed a mouse model representing placental failure in which the akr1c14 gene encoding the enzyme that synthesizes ALLO, is deleted in the placenta using a Cre-Lox strategy. The resulting placental knockout (plKO) mice were characterized by significantly reduced levels of placental ALLO. Through biological analysis and behavioral testing, we found that the lack of placental ALLO in male plKO’s, was associated with ASD-like behaviors (social interaction deficits, and increased stereotypies) and neuroanatomical alterations (hypermyelination) in the cerebellum.

We found that administration of ALLO (i.p., 10 mg/kg) to Cre-Lox dams at embryonic day (E) 15.5, which coincides with the peak of placental ALLO in control mice, rescued the behavioral and neuroanatomical alterations specifically in male plKOs (Vacher et al., 2021). Male controls however, developed an increased risk of ASD-like behavior, suggesting that excess of prenatal ALLO exposure may be detrimental. Initial rescue experiments with ALLO replacement at E15.5 have been promising; however, early postnatal neuroprotection may also be possible. Here we hypothesize that ALLO treatment at birth has the potential of rescuing ASD-like behaviors in male plKOs and is less detrimental in control animals.

Unlike injections at E15.5, ALLO injections at P0 only partially rescued ASD-like behaviors such as the social preference and the gnawing; however, the lack of digging was exacerbated with an overall risk of developing ASD-like behaviors. Postnatal ALLO injections to male controls were found to be slightly more detrimental in control males.

E15.5 injections have a stronger rescue of ASD-like behaviors compared to P0 injection, however there is still the risk of male controls developing ASD-like behaviors. We have begun to look at alternative hormone replacements such as Ganaxalone, an ALLO analogue with a longer half-life, and THIP, which activates δ-subunit containing extrasynaptic GABAA receptors. We are interested in testing the effectiveness of these drugs in terms of rescue potential and effects of perinatal timing.
Investigating If SF-1 Induces Nuclear Phosphoinositide Lipid, PIP2

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Steroidogenic factor-1 (SF-1, also termed NR5A1) is a nuclear receptor transcription factor that plays a crucial role in the regulation of adrenal and gonadal development, function and maintenance. PI(4,5)P2 (PIP2) is a phosphoinositide lipid that is enriched in the cell membrane, but evidence has found that SF-1 binds PIP2 in vitro. A co-crystal structure of the complex suggests the acyl chains of PIP2 are hidden in the hydrophobic core of the SF-1 protein while the PIP2 headgroup is solvent-exposed. This model explains how this hydrophobic lipid exists within the aqueous nucleoplasm. Cellular evidence that SF-1 expression associates with nuclear PIP2 is still needed. This evidence could provide us with more information to determine if PIP2 could be an endogenous regulatory ligand for SF-1 in human cells. The objective of our experiments is to determine if tetracycline induction of SF-1 expression would associate with nuclear accumulation of PIP2 in HEK cells. We used immunofluorescence techniques to determine if nuclear PIP2 was co-localized with SF-1 in the nuclear compartment. To determine if the nuclear PIP2 signal was dependent on the ability of SF-1 to bind PIP2, we examined a “pocket mutant” of SF-1 (A270W, L345F) shown to be deficient in phospholipid binding by mass spectrometry.

SF-1 expression was induced with tetracycline in a tetracycline-inducible HEK cell line. Antibodies directed against the PIP2 headgroup and FLAG-tagged SF-1 was used to determine is the signals were co-localized in the nuclear compartment. This process was also done in HEK cells with the pocket mutant of SF-1.

We found the nuclear PIP2 signal co-localized with FLAG-tagged SF-1 in the nuclear compartment. Tetracycline induction of this pocket mutant SF-1 in HEK cells failed to induce a detectable PIP2 antibody cross-reactive signal, despite similar Tet-induced expression levels of the wild-type and pocket mutant SF-1 proteins in these cells. Together, these findings indicate that expression of SF-1 induces a PIP2 antibody cross-reactive signal in the nucleus.

We want to do more experiments exploring the role of different enzymes involved with SF-1 to discover how they play a role in PIP2 binding to SF-1.
Development of a Bioanalytical Method to Measure Neurotransmitters Levels following Drug Exposure with Liquid Chromatography Quadrupole Time-of-Flight Mass Spectrometry

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To develop a bioanalytical method to quantify select neurotransmitters (dopamine, serotonin, acetylcholine, gamma-aminobutyric acid (GABA), glutamate, and gamma-hydroxybutyric acid (GHB)) under various drug exposures.

Aging is a predominant factor in neurological changes, and these changes can be greatly exacerbated by drug exposure. Acute exposure to drugs such as opioids, benzodiazepines, and delta-9-tetrahydrocannabinol can contribute to the development of cognitive dysfunction exhibited by neurotransmitter disturbances. Of concern is the gap in current literature on the imbalance in neurotransmitters from drug exposure in vulnerable populations, i.e. adolescent children and older adults, which necessitates an investigation on the age-related effects on neurotransmitter levels. This project aims to develop a sensitive, multiplexed analytical assay to measure key neurotransmitters. This analytical method will be implemented in future studies to measure the selected neurotransmitters from tissues exposed to different drugs across age to determine the impact of acute drug exposure on neurotransmitter levels such that more effective and tailored medical interventions may be identified.

Dopamine, serotonin, acetylcholine, GABA, GHB, and glutamic acid and their deuterated internal standards were optimized for detection and separation on a Sciex LC-QToF X500R. The analytes were tested under various conditions to determine the most optimal separation and peak intensity which consisted of column chemistries; tune solvents; mobile phase compositions; elution method; flow rate; oven temperature; and injection volume.

Five of the selected neurotransmitters were successfully detected in a single assay in positive mode. Gamma hydroxybutyric acid (GHB) was not well ionized in positive mode and thus was more successfully detected with negative ionization. These data suggest this method may be used to analyze and quantify neurotransmitters at low concentrations across various tissues and biological fluids.
Assessing the role of amygdala calcitonin gene-related peptide receptors (CGRP-Rs) on the development of chronic bladder pain

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Visceral pain (i.e., pain from internal organs) is a serious health issue, that disproportionally affects millions of women worldwide. The mechanisms that control and modulate visceral pain (e.g., bladder pain) are poorly understood. Previous work in our lab shows that the neuropeptide, calcitonin gene-related peptide (CGRP), has divergent functions in the left and right amygdala in a mouse model of bladder pain. The amygdala in the right hemisphere of the brain has been shown to increase pain, while the amygdala in the left hemisphere has been shown to reduce bladder pain. In this study, we seek to assess the role of CGRP receptors (CGRP-Rs) on the hemispherical and temporal changes of the amygdala as bladder pain transitions from acute to chronic/persistent pain.

We used a mouse model of bladder pain (100 mg/kg cyclophosphamide, 3 days) to conduct physiology, histology, behavior, and in vivo calcium imaging experiments 2-21 days post-injury (DPI). In the first part of the study, urinary bladder distension and visceromotor responses (UBD-VMR) and bladder histology (hematoxylin and eosin staining) were used to measure bladder pathology progression. In the second study, we administered a CGRP-R blocker - CGRP8-37 (or vehicle) into the right or left amygdala (1 uL of 100 uM) before abdominal von Frey (mechanical sensitivity). In the third study, lenses were implanted into the amygdala to measure the neural activity (via in vivo calcium imaging) of CGRP-R positive cells in the left or right amygdala 2-21 DPI.

Collectively, these data support the study of cell-specific manipulation of the right amygdala to produce bladder pain relief. In particular, this study supports the idea that CGRP-R blockers, which are FDA-approved for migraines, could also be beneficial for attenuating bladder pain. Furthermore, studying hemispherical differences in pain control will lead to the development and advancement of effective therapies for visceral pain.
The Role of the TWEAK/TWEAKR Axis in Viral-Mediated Lung Injury and Repair

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Lung basal cells are airway progenitor cells that become activated during injury and infection. These basal cells are identified by expression of keratin 5 (Krt5). During fibrotic injury and viral infections, Krt5+ progenitor cells migrate from the airway to sites of injury where they form pod-like structures and are thought to be involved in the wound repair process. Our recent cellular and transcriptomic comparisons of early influenza and SARS-CoV-2 infection demonstrated that while Krt5+ progenitor cells were induced during influenza infection, there was a significant lack of Krt5+ progenitor cells during SARS-CoV-2 infection. Single cell sequencing comparison of Krt5+ progenitor cells from each infection showed influenza induced significantly more interferon stimulated genes and the TNF superfamily receptor Tnfrsf12a, the gene encoding the TWEAK receptor (TWEAKR). The only known ligand of TWEAKR is TWEAK, encoded by Tnfsf12, a multifunctional cytokine that is involved in inflammation, tissue injury and repair. In conjunction with TWEAKR, we detected increased TWEAK during influenza but not SARS-CoV-2 infection. Taken together, we hypothesize that TWEAK/TWEAKR signaling promotes the proliferation of Krt5+ progenitor cells in the airways and their migration into the lung parenchyma.

To examine the role of TWEAK/TWEAKR signaling during influenza infection, C57BL/6 mice were treated with an anti-Tweak antibody. Lungs were harvested at 9-days post-infection for quantification of TWEAKR and Krt5 expression by immunofluorescence and RT-qPCR. Lung sections from 6-, 7-, 9-, and 14-days post-infection were also stained for TWEAKR and Krt5 by immunofluorescence.

Results: TWEAKR and Krt5 expression was lower in the anti-TWEAK treated mice compared to mice that did not receive the antibody. These mice also formed fewer Krt5+ pods in the lung parenchyma. We also found that Krt5+ progenitor cells in the airways and parenchyma of influenza-infected mice did not express TWEAKR at later infection time points. Instead, TWEAKR expressing cells were mainly confined to the airways and were adjacent to Krt5+ progenitor cells.

These results suggest that the TWEAK/TWEAKR signaling axis is involved early in the activation of Krt5+ progenitor cells during lung repair processes. Future studies will focus on the ability of TWEAK to induce proliferation and migration of airway cells.
A Solar Powered Immersive Heavy Metal & Nitrate Filter for Bodies of Water

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The purpose of this project is to create a device that will extract harmful pollutants from bodies of water using an immersive two-step filtration system.

Water pollution is one of the most dangerous environmental risks resulting in negative health outcomes worldwide. Although there are interventions to reduce pollutants from entering waterways, there aren’t solutions to remove pollution when the damage is already done. It’s been reported that more than 600,000 children in the U.S. alone are born with mercury blood levels at high measurements linked to low IQs and birth defects (Ocean Health Index 2018). Nitrate contamination has been increasing exponentially, in three states, 60% of the communities have elevated levels. Excessive nitrate compounds have been linked to carcinogens that evoke cancer risk and respiratory problems.

The methods used to remove mercury and nitrate from water is through filtration with the sediment filter being the first stage. The methods used to filter mercury and nitrate is through the GAC system, or granular activated carbon is used to remove these chemicals from the water. GAC systems are known for absorbing chemicals in the water like mercury and nitrate (Chemet 2015). Direction of the water would be coming in from the outside into the first chamber then into the sediment pleated sediment filter. Then into the GAC back out, releasing little to no mercury and nitrate in the water. This cycle repeats over and over again, getting more water in, cleaning it, than releasing cleaner water back out.

The amount of mercury, nitrate, and turbidity decreased from the ocean water after being filtered. Renovate the apparatus in a way that it could be submerged into the ocean and still successfully remove mercury, nitrate and turbidity from the ocean water. Include more materials such as a pleated sediment filter, which plays a role in removing nitrate as well as microplastics and plastic. Include turbines that will not allow things that don’t belong in the filter. A buoy will be attached to the device. This will allow the device to be tracked when the filters need to be changed or fixed. Long Term goal is to attach the filter to a tidal energy turbine. This is because it is convenient since the device will be placed in the ocean. Patent my device in order for it to be protected. Be able to use this device in Jamaica Bay and other highly polluted areas such as Arizona’s golden river and more. Use the same components from the device to extract pollution from other factors that evoke water pollution such as air pollution.
Breaking Barriers: A Case Study on the Moderna COVID-19 Vaccine and Cultivating Positive Immunization Perceptions in the Black Community in the United States

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Black Americans have a history of distrust of the American healthcare system, and this has stemmed from instances such as the "Tuskegee Study of Untreated Syphilis in the Negro Male", which have aided in immunization hesitancy [1], [2]. Many Black individuals felt healthcare had ulterior motives because of the massive push to reach herd immunity by getting the COVID-19 vaccine [3]. This has negative implications for the rising field of immunoengineering.

Kizzmekia Corbett-Helaire, Ph.D. is the Black woman virologist who developed the COVID-19 Moderna vaccine [4]. Her development of the messenger RNA (mRNA) vaccine triggers an immune response, helping fight off the virus [5]. The rollout of the vaccine has saved millions of lives, yet there still hesitancy in the Black community.

We seek to explore the methods and strategies used to acquire the trust of Black Americans. This is accomplished by analyzing artifacts from Dr. Corbett-Helaire's recruitment methods and the changes in literature from the beginning of the pandemic to the present day.

Through a review of the literature and relevant artifacts, we found that perceptions towards COVID-19 immunization positively increased over time [6], [7]. We believe that this can set a strong example for improving immunology perceptions in marginalized communities.

We gained strategies to advance immunoengineering research through this case study. Future work seeks to understand how we can implement inclusive practices in the field and better understand the experiences of the affected populations.
Investigating how alternative splicing of Interferon-α Receptor 2 affects innate immune signaling

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Thousands of genes in the genome undergo alternative splicing, generating protein variants with potentially significant biological consequences. Aberrant splicing patterns have been proposed to contribute to many diseases, an idea supported by growing evidence that many disease-associated variants are associated with differential splicing. However, while a few examples have been characterized, the vast majority of disease-associated splicing events have not been experimentally investigated and their causal roles in disease remain largely uncharted. My proposal focuses on the role of alternative splicing using interferon signaling and associated diseases as a model.

The interferon signaling pathway is a crucial innate immune mechanism that functions to defend against viral infection. Upon sensing viral infection, cells secrete Type-I interferons (IFNs), including interferon-α (IFN-α) and β (IFN-β), named after their ability to "interfere" with viruses. IFNs are captured by IFN-α Receptor 2 (IFNAR2) and IFN-α Receptor 1 (IFNAR1), which initiate downstream signaling of IFN-stimulated genes such as antiviral defense and inflammatory response genes. Many IFN-stimulated genes have inflammatory or cytotoxic effects, and dysfunction of the IFN signaling pathway underlies many diseases including pathological responses to infection or autoimmune disorders known as interferonopathies. However, despite the clear importance of tight regulatory control of IFN signaling in innate immunity, we have a poor understanding of how IFN responses become dysregulated in disease.

One underexplored mechanism that can influence IFN regulation is alternative splicing. While most studies of human IFNAR2 focus on the canonical full-length isoform, there are multiple primate-specific alternative isoforms that remain poorly characterized. Preliminary work in our lab indicates that several of these isoforms show robust expression in human cells, suggestive of functional roles in immunity. Furthermore, we have identified over 100 variants that are located in the IFNAR2 locus which are both associated with immune disease and changes in splicing of IFNAR2. This suggests that aberrant splicing of IFNAR2 may be an important yet underappreciated contributor to disease. Here, I will combine experimental and genetic approaches to elucidate the impact of splicing on human immune signaling.
**Hidden in Plain Sight: Decoding the Bulliform Cell's Role in Plant Stress**

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Bulliform cells, the often-overlooked architects of leaf morphology in grasses, play a pivotal role in enabling plants to endure and adapt to drought conditions. These cells, responsible for the critical function of leaf rolling, are key players in plant resilience, especially under water stress scenarios. Despite their significance, the comprehensive understanding of their genetic and functional dynamics remains an intriguing puzzle in plant biology. This study is designed to unravel this mystery, leveraging the cutting-edge technology of single-cell RNA sequencing (scRNA-seq).

Our research approach embraces the power of scRNA-seq to delve deep into the molecular landscape of bulliform cells. This technique offers an unparalleled opportunity to dissect the intricate cellular mechanisms that govern their development and response to water stress. The study will focus on decoding the gene expression profiles of these cells, identifying key molecular pathways that are activated or suppressed during periods of drought. By analyzing these patterns, we aim to construct a detailed map of the genetic networks that underlie the functionality of bulliform cells in different grass species.

Moreover, the study extends beyond the confines of a single species, encompassing a comparative analysis across various grass species. This broader perspective is crucial for understanding the evolutionary adaptation of bulliform cells, offering insights into the diverse strategies employed by different species to combat water stress. Such comparative analysis will enable us to delineate a comprehensive blueprint of bulliform cell adaptation across the grass family.

The implications of this research are far-reaching. By demystifying the genetic underpinnings of bulliform cells, we anticipate uncovering novel strategies for enhancing plant resilience. This knowledge is invaluable in the quest to engineer climate-resilient crops. In an era where climate change poses a significant threat to global food security, our study has the potential to contribute substantially to the development of crops that can withstand environmental challenges, thereby securing agricultural productivity and sustainability.

Ultimately, this research aims to transform our understanding of plant resilience, moving from the microscopic intricacies of cell biology to the macroscopic challenges of global food security. The journey to decode the enigma of bulliform cells is not just a scientific endeavor but a crucial step towards a more resilient agricultural future.
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The microtubule associated protein, Tau, is implicated in a multitude of neurodegenerative disorders that are collectively termed as Tauopathies. These disorders are characterized by the presence of tau aggregates within the brain of afflicted individuals.

Mutations within the tau gene form the genetic backdrop for familial forms of tauopathies, such as frontotemporal dementia (FTD), but the molecular consequences of such alterations and their pathological effects are unclear. We sought to investigate the conformational properties of three mutants of tau 2N4R: A152T, P301L, and R406W, all implicated within FTD, and compare them to the native form (WT). We additionally wanted to probe the interaction between the mutant and WT protein to see if there exists any cross-seeding amongst them.

Our immunochemical analysis reveals that mutant and WT oligomers exhibit similar affinity for conformation-specific antibodies but have distinct morphology and secondary structure. Additionally, these oligomers also possess different dye-binding properties and display varying sensitivity to proteolytic processing. These results point to conformational variety amongst them. We then tested the ability of the mutant oligomers to cross-seed the aggregation of WT-Tau monomer. Using similar array of experiments, we found that cross-seeding with mutant oligomers leads to the formation of conformationally unique WT oligomers compared to unseeded ones.
Molecular dynamics investigation of the TT and TGT mutations of DNA aptamers for lead with variable salinity

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It is widely known that radioactive waste and coal ash pose a significant threat to both human health and the environment. Though they contain multiple components, these pollutants contain varying concentrations of metal ions, such as cadmium, arsenic, mercury, and uranium. However, a major challenge in sensing and detection platforms is the lack of high-specificity receptors to target heavy metal ions. Therefore, to develop new methods to detect metal ions, we look at aptamers, which are short protein or nucleic acid molecules. Aptamers provide a cheap, highly specific, and sensitive method to bind to target analytes, such as metal ions. However, heavy metal ion-specific aptamers lack effective recognition sites. It is challenging for aptamers to specifically bind and recognize metal ions in the same group due to similar structures of different metal ions and the simple structure and single binding site for heavy metal ions. This leads to poor specificity of the aptamer sequence to the target ion. The goal of this work is to develop theoretical approaches for aptamer screening to target lead ions (Pb²⁺) to address this challenge. Two G-quadruplex structures of lead-specific aptamers have been crystalized and shared as Protein Data Bank (PDB) files (7D31 and 7D32). Overall, our objective is to observe the conformational changes of the aptamer sequences for Pb²⁺ to understand the influence of the stability and conformational changes of aptamers with G-quadruplex structures. Our strategy is to (1) mutate 3D aptamers based on the sequences that were unable to be crystalized with a TT or TGT sequence, (2) execute molecular dynamic (MD) simulations to characterize changes of the binding site of aptamers in varying concentrations of salt water, and (3) execute MM/QM simulations to study the interactions of a DNA aptamer with a lead ion. Recent papers have published the sequence of a G-quadruplex structure for a lead-specific aptamer. The TT and TGT sequences are important for the crystallization and stability of the aptamer. This theoretical method provides evidence of the stability and structural changes of aptamer sequences unable to be crystalized without the TT and TGT sequences. These results may play a role in increasing the potential applications of aptamers in new sensing strategies for metal ions.
The effects of climate change on marine ecosystems are becoming increasingly evident, with significant implications for fish populations. Temperature plays a crucial role in these interactions, influencing oxygen solubility in seawater, DO concentration, and metabolic demand for aquatic ectotherms. The alarming decline in dissolved oxygen levels in coastal areas, particularly in eastern boundary currents like the California Current, is exacerbated by natural upwelling processes and organic matter decomposition from phytoplankton blooms. The interactions among these multiple stressors and their potential synergistic or antagonistic effects present significant challenges for effective management strategies. Flatfish, such as the Petrale Sole, are particularly vulnerable to increasing hypoxia and temperature stress. Understanding the impacts of these changing environments on fish growth, recruitment, and maturity is essential for accurate stock assessments and sustainable fisheries management. Otolith analysis, a valuable tool for aging fish, offers insights into growth rates, life history patterns, and population dynamics. Furthermore, otolith chemistry utilizing the ratio of manganese to calcium (Mn:Ca) can serve as a reliable proxy for hypoxia exposure over a fish's lifetime. Analysis of cod fish otoliths has demonstrated the utility of this proxy in tracking responses to changing hypoxic conditions.

To assess the impacts of climate change on Petrale Sole, this study utilizes archived otoliths aged, sexed, and measured by the Washington Department of Fish and Wildlife. These collections span from 1998 to 2022 and are complemented by data from the Olympic Coast National Marine Sanctuary and the Northwest Association of Networked Ocean Observing Systems. The integration of these data sources will enable a comprehensive examination of hypoxia and warming thresholds for Petrale Sole and their growth responses.

Preliminary findings will be presented. The mooring data shows frequent levels of hypoxia in all the mooring sites at the Olympic Coast National Marine Sanctuary along with detecting the multiple marine heatwaves that occurred along the Pacific Coast.

Expected results are smaller fish at age. Future research would be to assess changes in habitat use, recruitment, and diet to get the full understanding of the changes to the species.
Developing Teaching Identities through a Curriculum Centered on Environmental Social Justice: A Teaching Experiment

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The climate crisis is an environmental issue that affects people of all walks of life but disproportionately affects historically marginalized communities. The climate crisis therefore is not only an issue of environmental justice, but also social justice. However, incorporating environmental issues within education has been typically left to science classrooms.

Teaching for environmental social justice, however, has the potential to extend itself beyond science content and science classrooms, and instead be incorporated in content across all academic disciplines. This teaching experiment explores the various influences that shaped 6 preservice teachers’ emerging teaching identities and the pedagogical practices they aim to implement in their classrooms, after engaging in a curriculum that centered environmental social justice. This study revealed influences that shaped preservice teachers’ emerging teaching identities including their personal experiences as a student, experiences with teachers, family influences, and experiences in their teacher preparation program.

As part of this teaching experiment, this study further explored the ways preservice teachers enact their teaching identities within their pedagogical practices. This teaching experiment revealed that while some preservice teachers’ teaching identities were consistent with their pedagogical practices, other preservice teachers’ teaching identities were inconsistent with their pedagogical practices. Inconsistencies between preservice teachers’ teaching identities and their pedagogical practices were attributed to the expectation to reproduce and implement traditional methods of instruction that preservice teachers’ have observed throughout their academic journey. Overall, this teaching experiment suggests that preservice science teachers are more inclined to incorporate transformative methods of instruction that uphold values of environmental social justice, than preservice teachers of other disciplines.

Additional findings within this teaching experiment demonstrates areas of growth for preservice teachers, including a shift in perspectives, further aspirations as a teacher, and developing an orientation towards environmental sustainability.
SECTION 3

ORAL PRESENTATIONS
Making Sense of Historically Relevant Science Pedagogy: Building Black Women Science Teachers Anti-Racist Work

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As a Black women science education researcher, my work focuses on the legacy, innovation, and healing of Black women science teachers for the purpose of retaining healthy and restored practitioners through Sista Circles and to further inspire these women to enact liberatory, anti-racist science curriculum so that our students see themselves as scientists and science-knowledge producers. As a part of my research, I center the legacy of Black teachers in America as a way to cultivate and connect with the genius of Black teachers today who use their science content expertise to help students better connect with the content and the potential of using the content for social change. This proposed study will further my doctoral research which helped develop an anti-racist, liberatory framework for teaching science entitled Historically Relevant Science Pedagogy (Riley, 2021).

This is a workshop where participants will learn about an emerging K-16 liberatory and anti-racist framework for teaching science that was inspired by Sista Circles with Black women science teachers (Riley & Mensah, 2023). This framework is called Historically Relevant Science Pedagogy (HRSP), a framework that merges and distinguishes three frameworks from Black women education scholars [Culturally Relevant Pedagogy (Ladson-Billings, 1994/2015), Historically Responsive Literacy (Muhammad, 2020), and Liberatory Pedagogy (hooks, 1994)] into the context of teaching and learning science. Historically Relevant Science Pedagogy is theoretical contribution that merges and distinguishes three differential anti-racist educational frameworks: Culturally Relevant Pedagogy (Ladson-Billings, 1994), Liberatory Pedagogy (hooks, 2015), and Historically Responsive Literacy (Muhammed, 2020) and uses them in the context of science teaching and learning. Historically Relevant Science Pedagogy is a framework that results from my work with learning about legacy, healing and innovations of Black women science teachers. Specifically using a Black Feminist intersectional lens to make sense of how we engage in curriculum redesign and liberatory practices for the uplift of all students and to aid in the fight for science teaching and learning with a social justice lens.

In this workshop, participants will engage in a quick lecture about the framework, observe examples of teaching science and provide feedback on the concepts and practices. Participants will be asked to consider their K-12 younger selves, identifying the ways they would have liked to have been seen wholly. We will discuss ways to honor the gendered, classed, and racialized (and other) aspects of their identity and how a framework like HRSP could support the future generations of young girls and gender-expansive folks to see themselves as scientists AND use science to the benefit of themselves and their community.
Black Feminist Theory argues that Black women have a different lived experience as compared to white women due to the pervasiveness of racism and sexism in society. Furthermore, the Superwoman Schema Framework, posits that there are five distinct characteristics that Black women have embodied to combat negative stereotypes and tropes, which led to the creation of the Superwoman or the Strong Black Woman Narrative. However, the Superwomen and Strong Black Women mentalities and personas that were created out of necessity beginning with the enslavement of Black women have also proven to be a liability for Black women’s mental, physical, and overall health.

The sociocultural complexities of the lived experience of the Black woman have also contributed to how Black women navigate their personal health and wellness journeys, and how public health approaches Black women’s health and wellness. During the presentation or poster session, Sis Throw Your Cape Away, audience members will learn about the poignant historical factors contributing to the Superwoman and Strong Black Woman narrative and its impact on Black women’s health.

Further, utilizing data from focus group discussions with Black women from Virginia, we will facilitate an enriching discussion regarding the factors that have led to this narrative. Emergent themes from preliminary data suggest that Black women’s lived experiences are not monolithic. Thus, underscoring the need for further research and discussion to comprehend the nuances of this group. Creating culturally responsive programming and interventions is imperative for positively impacting this community. Preliminary themes indicate that the role of BBL culture, religion/spirituality, and the influence of familial examples of the Strong Black Woman significantly impact Black women’s health and wellness.

Attendees will gain a deeper understanding of how social and cultural narratives and history affect Black women’s health and well-being. Furthermore, they will leave empowered with actionable strategies to shed the burdensome cape of societal expectations, fostering a healthier and authentic sense of empowerment. The session aims to equip participants with tangible steps to discard their proverbial capes.
Implementing Raman-Based Glucose Control for Large-Scale CHO Cell Culture Processes

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Purpose
In biopharmaceutical manufacturing, Chinese hamster ovary (CHO) cells are commonly employed to produce various therapeutic monoclonal antibodies. Glucose serves as the primary carbon source for CHO cells and when limited during processing can result in cell health decline. An emerging trend within biopharmaceutical development has been the implementation and industrialization of process analytical technologies (PAT). Using PAT tools enable real-time monitoring of cell culture processes and feedback control of nutrient levels. Specifically, Raman spectroscopy is used to monitor and control glucose concentration in bioreactors. The objective of this work is to develop and implement a Raman-based glucose control system for large-scale CHO cell culture processes.

Background
The absence of glucose leads to cell starvation, resulting in cell apoptosis and death. Hence, it is crucial to maintain an optimal glucose concentration during processing of a batch and create a reproducible glucose strategy that can be run at various scales. Raman probes function as glucose sensors within bioreactors and can be interfacing with a feedback controller to regulate glucose levels at a defined setpoint.

Methods
A series of cell culture experiments were conducted in small-scale 3-L bioreactors to generate Raman spectra and offline measurement data for developing a robust Raman model for glucose control. These cell culture experiments explored various glucose setpoints to determine impact on the overall process and determine feasibility of implementing the technology.

Results
A glucose Raman model was developed after concluding the small-scale experiments. This model was successfully deployed in a final demonstration run to showcase glucose control in a 1000-L bioreactor.

Conclusion
Achieving this milestone of glucose control in a 1000-L bioreactor serves as a starting point of industrializing Raman-based feedback control to reduce manual feeding and to maintain nutrient levels automatically. The implementation of Raman-based control would allow for less batch to batch variability, reliable product quality, and more ambitious outcomes for the patients that we serve.
The OMNI, Omniscient Methodology for Novel (pharmaceutical) Injections, method is primarily used to analyze PET radiotracers with short half-lives. This method was developed using automatic injections to identify and quantify residual solvents in samples of fluorine-18 (half-life 109 minutes) and carbon-11 (half-life 20.4 minutes) radiopharmaceuticals. This approach evaluates 8 analytes in less than 5 minutes of acquisition time. The method additionally includes a 3 min bakeout to aid in the removal and carry-over of higher-boiling impurities. Chromatographic parameters such as column temperature, hold time, column pressure, flow rate, and split ratios were adjusted and optimized to analyze radioactive drug samples including methanol, ethanol, acetone, acetonitrile, triethylamine, N,N-dimethylformamide, and dimethyl sulfoxide. The relative standard deviation for each solvent was determined to be no greater than 1.6%. The method limit of detection (LOD) and limit of quantification (LOQ) were between 0.053 and 0.163 and 0.000 (5.791 × 10−6) and 0.520 mg/mL, respectively.

This technique, using flame ionization detection (FID), was validated and is currently employed for the routine quality control of all approved IND and RDRC PET radiopharmaceuticals at NYU Radiochemistry Laboratory. The original methods (a total of six) were produced separately and run on Shimadzu's GC-2014, with the longest method lasting 23 min. Individual OMNI method is analyte-focused and only requires this method to be performed daily for system suitability quality control checks. This study validates the application of the OMNI method in a clinical research setting, adhering to the guidelines set forth by the FDA and ICH.
Changes in Cancer Care and Perceived Quality of Care Among Cancer Survivors During the COVID-19 Pandemic

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The COVID-19 pandemic changed delivery and access to healthcare in the U.S., which may have impacted quality of care (QoC). We described changes in cancer-related appointments, perceived QoC, and characteristics associated with QoC during the early onset of the COVID-19 pandemic among U.S. cancer survivors.

We used data from the Health Information National Trends Survey-Surveillance, Epidemiology, and End Results pilot study, collected January-August 2021, which oversampled cancer survivors from Iowa, the Greater Bay Area, and New Mexico cancer registries. Among 1,130 cancer survivors aged ≥18 years who visited a provider in the past 12-months, we calculated weighted prevalence of changes in cancer screening and follow-up appointments, and perceived QoC. Characteristics associated with suboptimal (less than very good) QoC were assessed using logistic regression, adjusting for sex and age. Due to differences across registries, analyses were stratified by registry site (Iowa, Greater Bay Area, New Mexico).

Among cancer survivors, 25.0% (Iowa) to 39.6% (Greater Bay Area) reported their cancer screening or routine preventative care appointments were affected (canceled and/or changed to telehealth) by the COVID-19 pandemic. Among those who had treatment or follow-up appointments related to their cancer diagnosis, 16.6% (Iowa) to 33.9% (Greater Bay Area) reported these appointments were affected. Perceived suboptimal QoC ranged from 12.5% (Iowa) to 22.5% (New Mexico). Characteristics of perceiving suboptimal QoC included affected preventative care appointments (New Mexico), less education (Greater Bay and New Mexico), and waiting for test results longer than expected (Iowa).

The early stages of COVID-19 changed cancer care delivery. Up to 23% of cancer survivors perceived suboptimal QoC, which was associated with having changes in routine preventative care appointments, delayed test results, and less education, representing potential modifiable points of intervention for QoC improvement.
Antinociceptive And Anti-Inflammatory Effects Of Alkaloid-Rich Fraction Of Moringa Stenopetala Stem Bark And Leaves Extract In Animal Model

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Pain is a significant symptom of many different diseases. It is the sensation specifically evoked by potential or actual noxious (i.e., tissue-damaging) stimuli or tissue injury. Analgesics are the primary pharmaceutical treatment method for chronic pain, especially opioids (Han et al., 2016). However, prescription opioid misuse and abuse have become increasingly prevalent and concerning, and the side effects of these drugs can also contribute to substantial declines in health and quality of life (Kaye et al., 2017). There is a need for research into alternative treatment methods that avoid the side effects of conventional treatments (Kaye et al., 2017). Hence the need to embrace medicinal herbs.

Moringa stenopetala is commonly used in folk medicine to treat various ailments like hypertension, headache, stomach disorders, diabetes, and malaria. According to the practice of the local people, Moringa stenopetala leaves are boiled and used to cure stomach pain, hypertension, and malaria. Despite its use for the treatment of pain and inflammation management, these effects have not been scientifically investigated. Hence this study aimed to evaluate the antinociceptive and inflammatory effect of extract from this plant material in the animal models.

In the study, both male and female mice distributed equitably were divided into six groups, each group with five mice each was used in the study. Animals were then induced on both pain and inflammation using a 5% formalin solution. The animals were given an intraperitoneal injection of the alkaloid-rich fraction at doses of 2.5, 5, 10, and 20 mg/kg. They were injected with 50mg of 5% formalin to induce pain in the left hind paw. The time spent in pain behaviour, biting, shaking, flinching the paw, and jumping, was measured and quantified as the latency of nociception. Observation of nociception is done under two phases (early and late), representing acute and chronic pain, followed by inflammatory response recording of paw thickness (diameter) using digital vernier calipers at an interval of 30mins for 2 hours period (0, 30, 60, 90, 120 mins). The data were analysed using the one-way ANOVA of Scheffe as the post hoc test. All the doses of the extract except 5 mg/kg exhibited a significant (p<0.05) antinociceptive effect but NO significant anti-inflammatory effect.

The results showed that the plant might possess alkaloids with both analgesic properties to support the traditional use of the plant in pain management.
Defining the Interplay Between DNAPKcs and Shieldin During Chromosomal Break Repair

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Chromosomal DNA double strand breaks (DSBs) are the effective lesion of cancer radiotherapy and other cancer therapeutics, such as topoisomerase 2 poisons. Understanding how cancer cells repair DSBs can provide insight into cancer cell resistance to these therapeutics, as well as inform development approaches to improve cancer sensitivity. DSB repair is also significant for cancer biology because aberrant repair of DSBs can cause mutations and chromosomal rearrangements that drive cancer. Repair of DSBs occurs through several pathways, including non-homologous end joining (NHEJ). DNA-PKcs (DNA-dependent protein kinase) promotes NHEJ, inhibits HDR, and is an emerging drug target with kinase inhibitors in oncology clinical trials. DNA-PKcs phosphorylates itself and other DNA damage response proteins, and promotes long-range DSB end synapsis to facilitate NHEJ. Another protein complex implicated in long-range DSB end synapsis is Shieldin, which includes the proteins 53BP1, RIF1 (Rap1-interacting factor 1), and other factors. Shieldin is critical for NHEJ to promote class switch recombination, which is a programmed DSB repair event during antibody maturation. However, the role of Sheildin in NHEJ repair outside this context remains poorly understood. Indeed, a specific gap in knowledge is the functional interplay between how DNA-PKcs and Shieldin promote synapsis of DSB ends to favor NHEJ.

To study end joining outcomes, I use Cas9 reporter assays to measure end joining frequencies via flow cytometry. These reporter assays are chromosomally integrated into human HEK293 cells. Additionally, I examine end joining junctions using deep sequencing to compare parental HEK293 cell junctions between wild-type and 53BP1-knockout or RIF1-knockout cell lines. This PCR-based approach allows me to categorize junction types into four categories: No Indels, Insertions, Deletions, and Complex Indels.

My preliminary studies indicate that RIF1 and 53BP1 are genetic modifiers of DNAPKcs function during DSB repair. I will present our current efforts to address this gap in knowledge.
Deciphering the Genetic Landscape: Unveiling Trophoblast Stem Cells in Early Human Embryos through Transcriptomic Profiling and Wnt Signaling

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The human placenta is the first organ formed in development and the site of nutrient exchange during pregnancy. A specialized population of stem cells called trophoblasts establishes the architecture of the placenta. The distinct molecular features of trophoblast stem cells (TSC) during development from a biologically relevant context remain undefined. A recent spatial transcriptomic study highlighted the inability of current trophoblast markers (i.e., GATA3, TP63, TFAP2C) to identify trophoblast stem cells. Current methods for culturing human trophoblast stem cells (TSC) in vitro have limited reproducibility and create heterogeneous trophoblast populations, causing any TSC to senesce. This study aims to produce a biologically relevant human trophoblast stem cell (TSC) in vitro tool to determine critical components of early placentation. Trophoblast stem cells require specific cues to maintain stemness consistent with the TSC of the early human blastocyst.

Here, we identify TSC in human development by utilizing publicly available single-cell transcriptomic sequencing data of three-dimensional human embryos from post-fertilization days six to fourteen. We analyzed biologically relevant stem cell pathway Wingless-integrated (Wnt), which is required for placenta organogenesis, to evaluate transcriptomic signatures of known pathway stem cell markers (i.e., TBX3, FOXM1, AXIN2) to identify TSC. Next, we used our in-silico examination to optimize a protocol for chemical induction of TSC from naïve pluripotent stem cells in vitro and develop a novel purification protocol via fluorescent activated cell sorting.

Our results show a population of FOXM1+AXIN2+ TSC arises post-fertilization day seven. We examined five distinct clusters of trophoblast subtypes, including trophoblast progenitors. After generating a list of novel TSC surface proteins (i.e., GREM2, S1PR2, NRPI) and trophoblast subtypes, we validate a new set of TSC markers.

A high-throughput bioengineering tool of TSC in vitro is vital for disease models to uncover potential mechanisms of placenta dysfunction. This research contributes to future therapies in Maternal-Fetal Medicine to improve pregnancy outcomes.
IL-22 Binding Protein Promotes Macrophage Phagocytosis During Lung Injury

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Interleukin 22 binding protein (IL-22BP) is a soluble receptor that is produced by myeloid and epithelial cells. While the only documented function of IL-22BP is regulation of IL-22 activity, our new data suggests IL-22BP is involved in macrophage function and phagocytosis independent of IL-22. Specifically, we hypothesize that IL-22BP promotes lipid uptake during toxic acute lung injury.

Using a bleomycin model of acute lung injury and acute respiratory distress syndrome (ARDS), we found that IL-22BP knock out mice (IL-22BPKO) had severe lung injury and inflammation compared to wildtype mice. The inflammation in the IL-22BPKO mice consisted of significantly increased numbers of inflammatory macrophages (CD68+ CD11B+ Ly6C +). To investigate the contribution of these macrophages in the inflammatory process, we treated mice (IL-22BPKO and wildtype) with clodronate, which ablates macrophages. We performed flow cytometry analysis to assess lung macrophage populations after clodronate ablation. To determine if IL-22BP has a role in phagocytosis, we performed phagocytic assays using in-vitro phagocytic fluorescent beads assays. To evaluate if there is a global phagocytic pathway deficiency in IL-22BPKO mice, we assessed phagocytic capacity using an Aspergillus fumigatus infection model. We performed reverse transcription polymerase chain (RT-qPCR) to compare fungal burden in wildtype and IL-22BPKO mice. Using Oil Red O staining, we assessed the proportions of foamy macrophages in wildtype and IL-22BPKO mice. Foamy macrophages are important in clearance of cellular debris during lung injury. We assessed expression of lipid recognition receptors using RT-qPCR.

Taken together, these data suggest lipid uptake is compromised in IL-22BPKO-derived macrophages and demonstrates that IL-22BP may have a novel role in lipid recognition and macrophage function. IL-22BP may be used as a therapeutic tool to improve protective macrophage responses during lung injury. Our future experiments interrogate the mechanism by which IL-22BP influences phagocytosis of lipid antigens.
Black in Marine Science (BIMS) has been a powerful force in amplifying the voices of those silenced for far too long. Their exceptional efforts empower and inspire the next generation of scientific thought leaders while creating a space for them to express themselves freely without any inhibitions. BIMS has relentlessly raised environmental awareness in marginalized communities historically excluded from social and environmental protections. Their dedicated work has resulted in trustworthy partnerships between diverse groups of stakeholders that center underrepresented Black communities. From a tweet, Black in Marine Science has proliferated into a community of over 400 members across 33 countries and a social media footprint of over 35,000 people and counting. Since 2020, BIMS has strategically developed and implemented programs that promote workforce development, ocean literacy, and inclusion. Through BIMSTV, Black in Marine Science has provided thousands with accessible educational marine science content made by Black Marine Scientists. The BIMS Immersion Program (BIP) has provided 33 free SCUBA certifications to Black marine scientists since 2021. BIMS is also dedicated to increasing aquatic safety amongst Black people by offering free swimming lessons as part of the BIMS Swims program. To provide mentorship to Black marine science professionals and students, BIMS created the Tidal Wave program. BIMS also hosts its annual BIMS Week at the end of the year to ensure that Black marine scientists can focus on their holistic well-being without interruption.

Dr. Tiara Moore's vision and dedication drive BIMS to make the marine science field safe for Black people. Their unwavering commitment to their mission has led to the development of a blueprint that raises diversity, equity, and inclusion standards in marine science. The BIMS Blueprint creates a nexus between marine science, inclusivity, and well-being. This presentation explores how BIMS has been making waves in marine science by offering accessible programming to enhance diversity, equity, inclusion, and accessibility in Science, Technology, Engineering, the Arts, and Mathematics (STEAM) fields. It will also introduce the groundbreaking framework responsible for the exponential growth of this premier, Black-led grassroots organization. BIMS is proud to lead the charge toward a more equitable and inclusive future for all in marine science.
**Genome-First Approach to Understanding the Phenotypes of Individuals with Germline TERT Variants**

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Rare, pathogenic germline TERT variants are associated with telomere biology disorders (TBD) and an increased risk of cancer, bone marrow failure, as well as pulmonary and liver diseases. Studies suggest variable phenotype, penetrance and expressivity in individuals and families with pathogenic/likely pathogenic (P/LP) germline TERT variants. The prevalence of disease due to TERT variants is not known. We sought to estimate the population prevalence of TERT-related TBDs by using a genome-first approach, which is a way to avoid ascertainment bias resulting from only studying highly affected families.

In this study, we estimated the prevalence of P/LP TERT variants and assessed the associated clinical manifestations using sequencing data linked with electronic health records (EHR) from 469,802 participants from the UK Biobank (UKB). Variant filters applied were minor allele frequency < 1% in the gnomAD v2.1.1 non-cancer subset, genotype quality ≥ 30, allele depth ≥ 20X, and variant allele fraction > 20%. ClinVar was used to collect variant classifications reported by clinical laboratories. TERT variants never reported to ClinVar, or with conflicting interpretations, were internally reviewed using adapted ACMG-AMP criteria with TERT-specific recommendations. Data outcomes obtained from EHR included cancer types, other diseases of interest, and cause of death.

Our preliminary genome-first approach identified individuals with P/LP germline TERT variants with a more variable phenotype than previously appreciated in TBDs, such as colorectal cancer and bone-related disorders. This analysis, although limited as it is comprised of older, White individuals from the UK, suggests that disease due to P/LP germline TERT variants is rare in this population and provide a starting point for understanding the true prevalence and disease penetrance of these variants in other populations.
Design, Synthesis and Biological Evaluation of Small Molecule HDAC8 Inhibitors for use in Acute Kidney Injury (AKI)

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Acute Kidney Injury (AKI) is the most common cause of organ dysfunction in critically ill patients. 2 million deaths throughout the world can be attributed to AKI and in the United States, AKI can account for up to 24 billion dollars in healthcare costs. AKI is also a major risk factor for developing chronic kidney disease (CKD), which can ultimately lead to end stage kidney disease, the need of dialysis, or even kidney transplant. Despite this sobering statistic there are no direct therapeutics to treat AKI.

Studies have linked class I histone deacetylase (HDAC) inhibition to recovery from kidney injury. In a recent publication, we evaluated multiple inhibitors with a variety of scaffold that ranged in potencies and selectivity’s in a series of increasingly stringent AKI assays. PCI-34051, a potent and selective HDAC8 inhibitor was shown to be effective in increasingly stringent models of AKI. Classical HDAC inhibitors (HDACi) such as PCI-34051 rely on a three-part pharmacophore, the cap, linker, and zinc binding group (ZBG) with hydroxamic acids often being utilized as the ZBG because of high metal binding affinity.

However, hydroxamic acid ZBG can lead to limitations of efficacy and toxicity, thus emphasizing the need for the development of novel HDAC inhibitors. In the HDAC active site there is a pocket deep within the enzyme responsible for generating the next catalytic cycle that is known as the “foot pocket” or acetate release channel. Herein we describe inhibitors that were developed to mitigate the negative effects of hydroxamic acids and improve potency and selectivity by extending the HDACi pharmacophore deeper into the pocket as well as relying on novel zinc chelation moiety.

The biological results show a first in class HDAC8 inhibitor design that displays efficacy in multiple AKI models and overall provide a promising starting point for use in AKI.