Understanding the NSF's Rules of Life Program: Scientific Advancements and Future Opportunities - A Workshop Series

EPIGENETICS WORKSHOP

January 26, 2023

11 AM – 2 PM, Eastern Time

MODERATOR AND DISCUSSANT BIOS

Moderators

Alexander Gimelbrant

Alexander Gimelbrant is currently an investigator at the Altius Institute. His research group focuses on developing computational and wet-lab tools to understand how similar cells and individuals can have different fates in development and disease, and how to nudge cells from disease to health. They focus on allele-specific analysis - a powerful approach to map genetic and epigenetic mechanisms that control activity of genes. Before joining the Altius Institute, he was an associate member at the Broad Institute of MIT and Harvard, an associate professor at Dana-Farber Cancer Institute, and an associate professor at Harvard Medical School. In his previous lab he investigated how establishment of cell identity can be determined by the choice of which allele, maternal or paternal, will be expressed in a given cell lineage. The lab's research has shown that this type of allelic choice occurs with many hundreds of human genes, creating an extraordinary epigenetic diversity in cell populations, such as those in the immune and nervous systems.

Connie Mulligan

Connie Mulligan is a professor in the Department of Anthropology and in the Genetics Institute at the University of Florida (UF). Prior to coming to UF, she was a postdoctoral and research associate at the Smithsonian Tropical Research Institute and the National Institute on Alcohol Abuse and Alcoholism. In her research program, she takes a biocultural approach that utilizes molecular genetic data to investigate questions about human evolution and disease, particularly diseases that show racial health disparities. Her research has been funded by National Science Foundation for 20 years. Her current projects focus on the molecular mechanisms, such as epigenetic variation and the microbiome, that mediate the impact of psychosocial stress on health.

Kunal Rai

Kunal Rai is an Associate Professor of Genomic Medicine at MD Anderson Cancer Center. He also serves as Scientific Director of an epigenetics-focused translation research initiative at MDA, named MDACC Epigenomics Therapy Initiative (METI). Dr. Rai's research is focused on understanding contribution of epigenome to cancer progression and identifying new venues for therapy and diagnostic tools. His lab utilizes cutting-edge epigenomic approaches to study chromatin state changes and higher order chromatin structure during evolution of tumor cells. Over the last 20 years, Dr. Rai has developed expertise in studying epigenetic processes by identifying factors that perform epigenetic functions, identifying their roles in cellular events that regulate normal organ development and abnormal cell growth during tumorigenesis.

Discussants

Lydia M. Contreras

Lydia M. Contreras is a Professor (and Jim and Barbara Miller Faculty Fellow) of Chemical Engineering at the University of Texas-Austin; she is also a member of the Institute of Cell and Molecular Biology. She completed her PhD in Chemical Engineering from Cornell University in 2008, focusing on engineering bacterial cells for improved production of therapeutic proteins. As a postdoctoral associate at the Wadsworth Center (New York State Department of Health), she focused on understanding mechanisms of infection in pathogenic bacteria. She began her career at the University of Texas-Austin in 2011, where she leads a research team focused on RNA biochemistry to study gene regulation mechanisms associated with stress-responses for applications in health and biotechnology. Her research team is particularly interested in how environmental stressors influence the transcriptome.

Julie Hotopp

Julie Hotopp has over twenty years of experience in genomics and bioinformatics with a focus on host-microbe genomics and on bacteria-animal lateral gene transfer. This work includes two paradigm-shifting manuscripts on bacteria-animal lateral gene transfer. One of these described widespread lateral gene transfer from Wolbachia endosymbiont to their animal hosts. Her further work on bacteria-animal lateral gene transfer includes sequencing and analysis of numerous microbes, insects, nematode, mouse, and human genomes and transcriptomes as funded over the past decade through an NIH Transformative R01, an NIH New Innovator Award, and other NIH, NSF, and private foundation awards. Her current research profile includes numerous projects pushing the boundaries of genome sequencing technologies to understand and interrogate host-microbe interactions.

Jeffrey Dozier

Jeff Lozier is a Professor in the Department of Biological Sciences at the University of Alabama, where he has held a faculty position since 2011. Dr. Lozier received his PhD in Environmental Science, Policy, and Management from the University of California, Berkeley in 2007 where he worked on the evolutionary genetics of aphids and their parasitoid wasps and was a postdoctoral researcher in the lab of Dr. Sydney Cameron at the University of Illinois Dept. of Entomology from 2008-2011, where he began working on bumble bee conservation and genetics. Dr. Lozier's lab focuses on population genomics of invertebrates, with his main interest being bumble bee evolution, but other projects involve mussel biodiversity genomics and crayfish community ecology. He is especially interested in the mechanisms that allow widespread species to tolerate diverse stressful conditions encountered throughout their geographic ranges.

Hollie Putnam

Hollie Putnam is an integrative biologist using cross-scale approaches to understand how corals and other marine invertebrates acclimatize and adapt to a changing environment through mechanisms such as parental effects, symbiosis, and (epi)genetics. She received her Ph.D. in Zoology from the University of Hawaiʻi at Mānoa in 2012, and completed subsequent positions as a NSF Ocean Sciences Postdoctoral fellow and Assistant Researcher at the Hawaiʻi Institute of Marine Biology, and as a Research Associate at the University of Washington. Putnam is currently a tenured Associate Professor at the University of Rhode Island in the Department of Biological Sciences. She has published > 85 peer reviewed papers and her work is supported by local, national, and international governmental agencies, as well as private foundations.

Kaushik Ragunathan

Kaushik Ragunathan is an Assistant Professor in the Department of Biology at Brandeis University. Dr. Ragunathan's lab is interested in understanding how dynamic chromatin dependent interactions produce stable, heritable, and adaptive epigenetic states. After completing his undergraduate degree in Biotechnology in India, he joined the Biophysics program at the University of Illinois, Urbana-Champaign. His graduate work was on using single molecule fluorescence microscopy to investigate DNA repair mechanisms. After obtaining his PhD, he served as a post-doctoral researcher at the Department of Cell Biology, Harvard Medical School. He was recruited as an Assistant Professor in Biological Chemistry at the University of Michigan and was also selected to be a part of the Biological Sciences Scholars program that supports promising young researchers early in their career at the University of Michigan. In addition to being deeply invested in mentoring and training graduate students, he also serves as a mentor for the NIH K99 MOSAIC scholars program administered by ASBMB to enable underrepresented scholars to transition successfully to faculty positions.

Keith Slotkin

Keith Slotkin's academic journey has taken him from Michigan (where he was raised), to the University of Arizona (undergraduate), Berkeley (Ph.D.), Cold Spring Harbor (postdoc), The Ohio State University (Assistant and Associate Professor), and now to St. Louis. He currently has a joint position between the Donald Danforth Plant Science Center and the University of Missouri. His lab has four main goals: 1) Investigate how transposable elements and transgenes are selected to undergo epigenetic silencing, 2) Produce next-generation technologies, 3) Work with industry to commercialize our findings and technologies, and 4) Train the next generation of scientists. He is the lead-PI on a Understanding the Rules of Life – Epigenetics project that collaborates with six other labs, including mathematicians and computer scientists, to understand the lasting heritable effects of a higher CO_2 atmosphere on plant chromatin organization and growth.

UROL EPIGENETICS PROJECTS INFORMATION

(Note: to see full abstracts please click on URL provided)

URoL:Epigenetics 1: Collaborative Research: Novel epitransciptomics tools to understand and modulate interactions of modified RNAs with protein readers and erasers (Lydia Contreras, University of Texas at Austin)

An unsolved question is how reader and eraser proteins distinguish one modification from another. This project seeks to address that question by using a combination of biophysical, computational, and protein engineering approaches. The results are expected to provide new insights into how RNA function is controlled by RNA modification, an underexplored frontier in molecular biology. In addition to the scientific impact, the research will provide educational experiences for two graduate students, who will be trained at the interdisciplinary intersection of molecular biophysics and biochemistry, as well as experimental and computational methods. The project will also promote engagement in STEM-related activities by undergraduates and by students in middle and high school, including those from underrepresented groups. Abstract URL: https://www.nsf.gov/awardsearch/showAward?AWD_ID=2022146&HistoricalAwards=false

MTM2: Collaborative Research: Microbially-mediated epigenetic modifications alter host phenotypes (Julie Hotopp, University of Maryland)

The project goal is to understand how and why particular microbes are hosted by invertebrates; whether the diversity of these microorganisms is related to the diversity of their hosts; and how these associations change over evolutionary time. This project is investigating three ecological and evolutionary processes that structure the biodiversity of microbiomes: assembly, diversification, and coevolution. While previous studies have focused on the host-specificity of microbiomes, the project shifts the perspective from host evolution to microbial evolution. The project is developing models of host-symbiont interactions that function across multiple spatial, temporal, and taxonomic scales. The investigators are training graduate, undergraduate, and high school students how to assess microbiome diversity; how to use novel software to search, categorize, and compile data from DNA sequence archives; and how to identify and classify marine invertebrates. They are integrating graduate students and undergraduate students in the development of a high-school-based program to mentor students in the assessment of marine invertebrate biodiversity, training the next generation of scientists in invertebrate biology, host-microbe ecology, and evolutionary data analyses. In addition, research scientists are being trained to use novel data mining and compilation software to address unexplored questions in host-microbe evolution. Abstract URL: https://www.nsf.gov/awardsearch/showAward?AWD_ID=2025384&HistoricalAwards=false

URoL: Epigenetics 2: Collaborative Research: Bumble bee cold tolerance across elevations - From epigenotype to phenotype across space, time, and levels of biological organization (Jeffrey Lozier, University of Alabama)

This project will focus on thermal tolerance across elevations in wild and laboratory reared bumble bees, an important group of pollinators that are threatened by environmental pressures. The project will provide valuable tools to understand how bee populations overcome environmental stress that will help predict the stability of bee populations. The major research goal of the project is to address the question: How does information flow from genetic and epigenetic variation through expression of this information to produce intraspecific phenotypes adapted to abiotic extremes? Post-doctoral fellows, graduate students and undergraduates at the University of Alabama, Tuscaloosa and University of Wyoming will be broadly trained in molecular biology, physiology, and computational modeling approaches. A strategy game app to demonstrate how molecular changes can affect populations and ecosystems under different thermal conditions will be developed for K-12 students. Results of the study will be disseminated through an exhibit at a native bee garden within the Stokes Nature Center in Utah to increase awareness of wild pollinators. Abstract URL: https://www.nsf.gov/awardsearch/showAward?AWD_ID=1921585&HistoricalAwards=false

URoL : Epigenetics 2: Predicting phenotypic and eco-evolutionary consequences of environmental-energetic-epigenetic linkages (Hollie Putnam, University of Rhode Island)

This project uses symbiotic, metabolically complex reef building corals as a model system to test the connections between physiological, epigenetic, and metabolic states, and predict how population and community dynamics are influenced by epigenetically modulated phenotypes. This work will advance biological knowledge by delineating fundamental links (Rules of Life) between ubiquitous organismal energetic processes, epigenetics, and eco-evolutionary outcomes. This project examines how nutrient metabolism in the mitochondria generates cofactors and energy that will instruct the epigenetic machinery in the cell nucleus to modulate genome function to appropriately respond to environmental conditions. The Broader Impacts activities parallel the project's integrative approach, linking insights from Environment x Energetics x Epigenetics x Ecology for Education into an E5 platform. The E5 platform will provide i) early career STEM training, ii) local and global community education, and iii) educational resources for open science, quantitative approaches, and research reproducibility. Further, this E5 platform will train and inform the next generation of diverse scientists and public by combining local and global initiatives focusing on groups underrepresented in STEM. The proposal is highly interdisciplinary, incorporating methods and perspectives from molecular biology, anthropology, neuroscience, and psychology, and will advance fundamental knowledge about mechanistic processes underlying gene-environment interactions in the brains of highly social species. In addition to offering interdisciplinary training for graduate and undergraduate students during the proposed research, the PIs will integrate research opportunities with outreach efforts for high school students, high school teachers, and also for broader public audiences, including children. Abstract URL: https://www.nsf.gov/awardsearch/showAward?AWD_ID=1921465&HistoricalAwards=false

URoL: Epigenetics 2: Robustness and Adaptability of the Dynamic Epigenome: A Multiscale Approach (Kaushik Ragunathan, Brandeis University)

This NSF-funded research program aims to understand the fundamental rules that shape the inner workings of the cell. This research program captures the chaotic collisions between molecules within a cell which can work in unison to help cells make accurate, adaptive decisions. This research uses high-resolution imaging to visualize single molecules in cells, microfluidic platforms to reveal decision making events within individual cells, and automated continuous culture methods to investigate the dynamics of cell populations. The synthesis and integration of these multi-dimensional viewpoints will enable the development of mathematical models with the potential to predict emergent properties of these complex regulatory networks. Ultimately, the outcome of these studies will be a set of rules that define how adaptive epigenetic states, much like genetic mutations, represent evolvable traits in eukaryotic genomes. This project also seeks to broadly impact high school and undergraduate education in Michigan through a unique emphasis on interdisciplinary research and learning. Abstract URL: https://www.nsf.gov/awardsearch/showAward?AWD_ID=1921677&HistoricalAwards=false

URoL: Epigenetics 2- Collaborative Research: Revealing how epigenetic inheritance governs the environmental challenge response with transformative 3D genomics and machine learning (Keith Slotkin, Donald Danforth Plant Science Center)

This project seeks to define how plants respond to environmental challenge. This project will advance the understanding of how elevated carbon dioxide alters plant form on both the molecular scale of DNA organization, as well on the scale of plant growth. This proposal asks whether these plant responses will last generations, and if so, tests the mechanism of inheritance. This proposal establishes a team with expertise in genomics, phenomics, data visualization, image analysis, machine learning, modeling, and analysis of three dimensional (3D) shapes for the common goal to bridge the environment/genotype/phenotype gap. By utilizing diverse plant species, well-characterized mutants, and machine learning, the researchers will deliver a computational algorithm to predict and model across the plant kingdom how environmental challenge regulates plant form, and which of these aspects are epigenetically inherited to the next generation. Additionally, this project promotes the training and development of a diverse future science-enabled workforce. The product of this research will be a predictive model for the lasting consequences of environmental challenge on growth patterns across the plant kingdom. Abstract URL: https://www.nsf.gov/awardsearch/showAward?AWD_ID=1921724