AGILENT
EMERGING OMICS RESEARCH TOUR

The Measure of Confidence

INTRODUCING THE HOPKINS CENTER FOR RESOURCES IN INTEGRATED BIOLOGY

WEDNESDAY, SEPTEMBER 24, 2014 — **Johns Hopkins School of Medicine**

Agenda	
12:30 pm	*Science Talk about the CRIB* **David Graham, PhD – Assistant Professor, Molecular and Comparative Pathobiology and joint appointment Department of Medicine, Division of Cardiology, Johns Hopkins University**
1:00 pm	*A Day in the Life of the CRIB* **Robert Harlan – Labratory Manager, Center for Resources in Innovative Biology, Johns Hopkins University**
1:20 pm	*Merging Data for Correlation And Network-based Analysis using GeneSpring 13* **Dipanwita Roy Choudhury – Senior Application Scientist, Agilent**
1:55 pm	*Colon Cancer, Microbiota and Metabolism* **Cynthia L Sears, MD – Professor of Medicine, Oncology and Molecular Microbiology and Immunology : JHU-SOM : Bloomberg School of Public Health : Sidney Kimmel Comprehensive Cancer Center, Johns Hopkins University**
2:15 pm	*Microbial metabolites and host blood pressure regulation* **Jennifer Pluznick – Assistant Professor of Physiology, Johns Hopkins School of Medicine**
2:35 pm	*Heart Failure Metabolomics* **D. Brian Foster M.Sc., Ph.D – Assistant Professor JHU-SOM : Director, Laboratory of Cardiovascular Biochemistry Division of Cardiology, Department of Medicine, Johns Hopkins School of Medicine**
2:55 pm	*Riding on slime: Mass spectrometry of selected novel components of bacterial biofilms* **Egbert Hoiczyk – Division of Cardiology, Department of Medicine, Johns Hopkins Bloomberg School of Public Health**
3:15 pm	Break
3:25 pm	*Metabolic Phenotyping: Integrating Metabolomics with Other Metabolic Signatures* **Susan Aja – Research Associate, Neuroscience, Johns Hopkins School of Medicine**
4:00 pm	*Closing* **David Graham, PhD – Assistant Professor, Molecular and Comparative Pathobiology and joint appointment Department of Medicine, Division of Cardiology, Johns Hopkins University**
5:00 pm	*Life of Reilly-Happy Hour*

The complexity of biology continues to present enormous challenges to understanding even simple systems. Genomics, transcriptomics, proteomics, and metabolomics are widely used throughout industry and academia, and have greatly contributed to the current understanding of many areas of study. However, each omic has its challenges and presents only a partial picture of the organism under study. Agilent is a leader in developing analytical tools, methods, reagents and software for the study of each omic and is at the forefront of developing solutions to integrate multi-omics data.

This seminar series will cover topics of interest to researchers using genomics, transcriptomics, proteomics, and metabolomics. Please join us to learn about analytical developments that can be applied to your research challenges.

Date: September 24, 2014

Location: Johns Hopkins School of Medicine Thomas Turner Auditorium
720 Rutland Ave
Baltimore, MD 21205

Time: 12:30 pm – 5:00 pm
Register Today!

www.agilent.com/chem/jhu

Agilent Technologies

Abstracts & Bios:

A Day in the Life of the CRIB

Robert Harlan

Robert's talk entitled "A Day in the Life of the CRIB" will focus on what has been developed at the CRIB for implementation of high throughput Metabolomic and Lipidomic workflows and will discuss the overall pipeline of sample preparation, quality control, mass spec analysis, and bioinformatics.

Robert Harlan is the current manager of the Center for Resources in Integrative Biology (CRIB) at Johns Hopkins University. His current interests are in Metabolomic and Lipidomic workflows for high throughput applications. He has extensive experience in the development of multiple reaction monitoring (MRM) assays for LC-MS/MS for high-throughput quantification of glycopeptides. Robert earned his master's degree from Michigan State University and began his mass spectrometry research developing clinical LC-MS/MS methods for therapeutic drug monitoring at Johns Hopkins Hospital.

Merging Data for Correlation And Network-based Analysis using GeneSpring 13

Dipanwita Roy Choudhury

Designed specifically for the needs of biologists, GeneSpring offers an interactive visualization and computing environment that promotes investigation and enables understanding of transcriptomics, genomics, metabolomics, and proteomics data within a biological context. New in GeneSpring 13, metadata analysis and visualization tools will allow researchers to analyze phenotypic parameters such as clinical or physiological attributes of the subjects alongside their gene or metabolite expression profiles.

Homologene and BridgeDB are implemented in GeneSpring to facilitate integrative analysis through translation functions, linking probes across data types, array platforms, and organisms that map to the same biological entity. Since GeneSpring can create literature-derived networks, this will allow users to identify NLP derived networks of genes consisting largely of interesting genes from the multi-omic experiment that allow cross-talk between curated pathways.

Colon Cancer, Microbiota and Metabolism

Cynthia L Sears, MD

Sporadic colorectal cancer (CRC) results from accumulated DNA mutations in colonic epithelial cells. Environmental factors clearly affect CRC incidence with one prime candidate being the colonic microbiota that is known to impact the host tissue microenvironment. We have identified that mucosal microbiota organization, as opposed to its genus-level composition, is a critical factor associated with oncogenic progression in a subset of CRC. We identified invasive polymicrobial bacterial biofilms, structures previously associated with nonmalignant intestinal pathology, nearly universally (89%) on right-sided tumors. Further we have investigated the metabolome associated with bacterial biofilms identifying an association with select polyamine metabolites. Our evidence suggests that both the host and bacterial biofilms contribute to the polyamine metabolite pool. Our results suggest mechanisms by which colonic mucosal biofilms alter cell function and the metabolome to yield cell proliferation required for oncogenic transformation and tumor growth.

Microbial metabolites and host blood pressure regulation

Jennifer Pluznick

Short-chain fatty acids (SCFAs) are metabolites generated by the gut microbiota in the colon. SCFAs are absorbed into the host bloodstream, where they are able to affect several aspects of host physiology, often by interacting with host G-protein coupled receptors (GPCRs). We have identified a novel GPCR for SCFAs, and have shown that microbial SCFAs interact with several host GPCRs to affect host blood pressure. We are currently working to better understand this signaling paradigm, and to explore the consequences of this pathway on host blood pressure control.

Jen Pluznick received her Ph.D. in Renal Physiology from the University of Nebraska Medical Center (Omaha, NE) in 2005. She then spent five years training as a postdoctoral fellow in the laboratory of Michael Caplan at Yale University (New Haven, CT), where she studied both renal physiology and sensory biology systems (in particular, olfaction). Jen's research interests are focused on how the renal and cardiovascular systems employ G-protein coupled receptor "sensory" signaling pathways in order to monitor various substances in the plasma and forming urine, and thus aid in the maintenance of homeostasis.

Heart Failure Metabolomics

D. Brian Foster M.Sc., Ph.D

My primary research interests include the molecular basis of mitochondrial and myofilament dysfunction in heart disease. My PhD and early postdoctoral studies in the labs of Dr. Jennifer Van Eyk and Dr. William Lehman respectively, centered on the biochemical and structural basis of myocardial stunning caused by proteolysis of the myofilament protein, Troponin I. My training at Johns Hopkins under the mentorship Drs. Eduardo Marbán and Brian O'Rourke involved proteomic approaches to discover key proteins associated with ischemic preconditioning (IPC). I have 31 papers spanning diverse aspects of cardiac function, using both reductionist biochemical assays and broader proteomic approaches. My lab currently uses an interdisciplinary systems biology strategy that encompasses proteomics, network modeling as well as cellular and molecular assessments of protein function to understand the role of post-translational modifications in heart failure and IPC. The multi-omic analysis of the guinea pig heart failure model, presented in this grant, testifies to the utility of this approach to uncover novel avenues for therapeutic development.

Riding on slime: Mass spectrometry of selected novel components of bacterial biofilms

Egbert Hoiczyk

Most bacteria in nature do not "float", but attach to surfaces and grow as thin, often-visible films. Within these biofilms, a complex extracellular polymeric matrix that contains carbohydrates, proteins, and nucleic acid surrounds these bacteria. Not only does this matrix define biofilms, but it is also in part responsible for their extraordinary resistance to physical and chemical assault. According to some estimates, up to 80% of all infections are biofilm-related. While biofilms clearly are beneficial to the bacteria, they pose a formidable challenge to bacterial dissemination. Here, we describe the isolation of a polymer that the biofilm model organism Myxococcus xanthus secretes in order to move within the biofilm matrix. Mass spectrometry was used to identify the chemical components of this polymer and electron microscopic data suggest that other important biofilm-forming pathogens such as Pseudomonas aeruginosa appear to secrete similar polymers during biofilm formation.

Since 2002 Assistant Professor, Dept. of Molecular Microbiology and Immunology, Bloomberg School of Public Health. | 1998-2002 1998-2002 Postdoc with Gunter Blobel, Infectious Diseases, Howard Hughes Medical Institute, Rockefeller University, New York, NY. | 1997-1998 1997-1998 Postdoc, Infectious Diseases, Max von Pettenkofer Institute, Munich, Germany | PhD 1996 Technical University Munich, Germany, Microbiology Summa cum laude (The thesis work was conducted at the Max-Planck-Institute for Biochemistry in Munich, Germany in the group of Prof. Wolfgang Baumeister) | M.Sc. 1990 M.Sc. 1990 University Erlangen, Germany, Botany

Metabolic Phenotyping: Integrating Metabolomics with Other Metabolic Signatures

Susan Aja

One goal of metabolomics, as a systems biology discipline, is to better understand how a biological system works by ultimately integrating the data. Elucidating relationships of the metabolome to enzyme/pathway activities, and further to the neurohumoral axis and whole animal physiology, permits identification of comprehensive "metabolic signatures" of physiological states and diseases. This talk will introduce resources at JHU that provide: (1) guidance and assistance in the identification, use, preparation, and phenotyping of rodent models for metabolic and metabolomics studies, (2) shared instrumentation for in vivo metabolic and behavioral evaluations, and for experimental controls, and (3) guidance and assistance in acquisition and extraction of biological specimens for metabolomics research. Highlights from a recent study will demonstrate how metabolomics data help to explain metabolic syndrome in a MeCP2-knockout mouse model of Rett Syndrome autism spectrum disorder, and how a dietary therapy may alleviate the deranged metabolism and other disease symptoms.