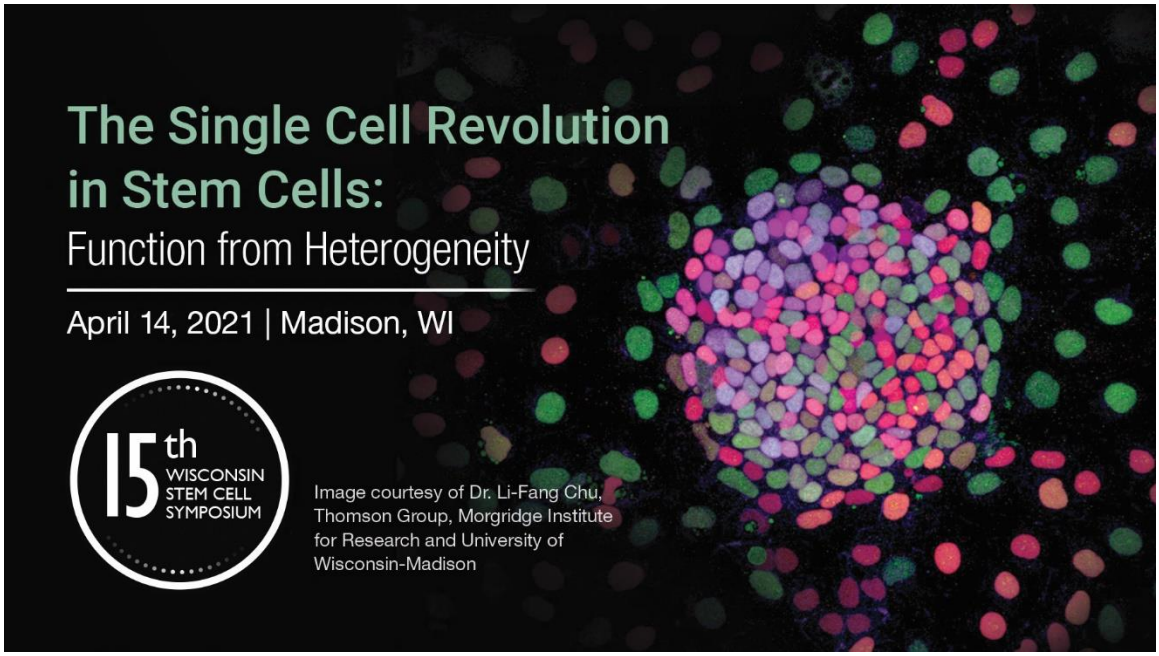

SPEAKER ABSTRACTS

High-resolution Lineage Tracing in Adult Stem Cells
Fernando Camargo

Our group has a strong interest in the study of blood formation, a process known as hematopoiesis. We are particularly focused on dissecting this phenomenon as it occurs in its native microenvironment, without the use of historical tissue disruptive approaches. My lab has developed a number of genetic tools in the mouse to inducibly barcode cells entirely in situ, which has allowed us to follow the lineage and fate of thousands of hematopoietic progenitors simultaneously. We have also developed tools to couple clonal lineage information with molecular single cell transcriptomic measurements. Armed with these tools, we have been able to fully characterize the process of blood production in the native state, and elucidate novel single cell-based lineage maps and identify progenitor populations that drive day-to-day blood production. We have also used these tools to identify novel regulators of stem cell function. Our latest findings and perspectives will be discussed.

Molecular and Functional Heterogeneity of Neural Stem Cells
Sebastian Jessberger
Laboratory of Neural Plasticity, Brain Research Institute, Faculties of Medicine and Science, University of Zurich, 8093 Zurich, Switzerland

Neural stem cells generate new neurons throughout life in distinct regions of the mammalian brain. This process, called adult neurogenesis, is critically involved in certain forms of learning and memory. In addition, failing or altered neurogenesis has been associated with a number of neuro-psychiatric diseases such as major depression and cognitive aging. We aim to characterize the cellular and molecular mechanisms regulating neural stem cell activity and behavior on a single cell level. We present new approaches to

study the cellular principles underlying life-long neurogenesis using imaging-based tools and single cell molecular profiling. Further, we provide evidence for novel molecular mechanisms governing the neurogenic process in the mammalian brain. Thus, the data presented provide new insights into the cellular principles of hippocampal neurogenesis and identify novel mechanisms regulating the behavior of rodent and human neural stem cells.

Detecting Structure and Patterns in Developmental Data
Smita Krishnaswamy

[TBA]

Stem Cell Signals in Cancer Progression and Therapy Resistance
Tannishtha Reya
Departments of Pharmacology and Medicine, Sanford Consortium for Regenerative Medicine and Moores Comprehensive Cancer Center, University of California San Diego School of Medicine, La Jolla, CA 92093

Our research focuses on the signals that control stem cell self-renewal and how these signals are hijacked in cancer. Using a series of genetic models, we have studied how classic developmental signaling pathways such as Wnt, Hedgehog and Notch play key roles in hematopoietic stem cell growth and regeneration and are dysregulated during leukemia development. In addition, using real-time imaging strategies we have found that hematopoietic stem cells have the capacity to undergo both symmetric and asymmetric division, and that shifts in the balance between these modes of division are subverted by oncogenes. Further, regulators of this process, including the cell fate determinant Musashi, are critical players in driving progression of solid and liquid cancers and could serve as targets for diagnostics and therapy. Ongoing work is focused on understanding the mechanisms that drive therapy resistance after drug delivery, as well as developing high resolution in vivo imaging approaches to map normal stem cell behavior and interactions within living animals, and to define how these change during cancer formation.

Blastoids: Modeling Blastocyst Development and Implantation
Nicolas Rivron

[TBA]

Deciphering Gene Reugulatory Network Dynamics from Single Cell and Bulk Omic Data
Sushmita Roy

Gene regulatory networks are molecular networks that control which genes must be expressed when and where in a living cell, translating the information encoded in an organism's genome to context-specific responses. Identification of these networks is important to advance our understanding of many biological processes such as development, disease, response to stress, and evolution. Technological advances in genomics are enabling us to measure the transcriptome, epigenome, proteome for populations and single cells, which is revolutionizing our understanding of cell type

identity. However, there are numerous computational challenges that arise to effectively integrate these data to gain insight into the gene regulation machinery that determine the type and identify of cells. In this talk I will present some recent computational tools from our group towards mapping genome-scale regulatory networks and their dynamics using multi-omic datasets measured at the population and single cell level. Using our tools we have prioritized and validated important regulatory connections during early human hind-brain development and mouse cellular reprogramming from differentiated cells to pluripotent cells, uncovering key components of the molecular machinery important for establishing cell-type specific programs.

Label-free Metabolic Imaging of Stem Cell-derived Cardiomyocytes

Melissa Skala

(Tongcheng Qian, Tiffany M.Heaster, Angela R. Houghtaling, Kexin Sun, Kayvan Samimi, Melissa C. Skala)

Investigator, Morgridge Institute for Research, Madison, WI

Professor of Biomedical Engineering, University of Wisconsin, Madison, WI

Human pluripotent stem cell (hPSC)-derived cardiomyocytes provide a promising regenerative cell therapy for cardiovascular patients and an important model system to accelerate drug discovery. However, cost-effective and time-efficient platforms must be developed to evaluate the quality of hPSC-derived cardiomyocytes during biomanufacturing. Here, we developed a non-invasive and label-free live cell imaging platform to predict the efficiency of hPSC differentiation into cardiomyocytes. Autofluorescence imaging of metabolic co-enzymes NAD(P)H and FAD was performed under varying differentiation conditions (cell density, concentration of Wnt signaling activator) across multiple hPSC lines. Live cell autofluorescence imaging of single cells and multivariate classification models provided high accuracy to separate low (< 50%) and high (≥ 50%) differentiation efficiency groups (quantified by cTnT expression on day 12) within 1 day after initiating differentiation (area under the receiver operating characteristic curve, 0.98). Autofluorescence imaging of single cells also quantified changes in metabolism during cardiomyocyte maturation. This non-invasive and label-free method could be used to avoid batch-to-batch and line-to-line variability in cell manufacturing from hPSCs.

Radia Glia in Glioblastoma

Viviane Tabar

[TBA]