geXc McMaster Symposium 2025

Unlocking the secret lives of cells using McMaster's multiomics platforms

June 6 2025 | 8:00 am - 6:00 pm

CIBC Hall, McMaster University Student Centre (MUSC), Room 319
1280 Main St W, Hamilton, ON L8S 4S4

Speakers

Christne Mader

Lab Manager, McMaster Genomics Facility

Bio: Christine is the manager of the McMaster Genomics Facility. She is a repeat McMaster graduate, beginning her career in the McMaster Ancient DNA Centre some 20 years ago. While there, she worked on many projects from microbial- to mammoth-scale, ultimately focusing on emerging next-generation sequencing technologies. As a student she supported other labs in adopting technology and was later tasked with setting up NGS services for the university via the Farncombe Institute.

Talk Title: ***"Introduction to the McMaster Genomics Facility's platforms and services "***

Abstract: The McMaster Genomics Facility (MGF) encompasses both the Farncombe Metagenomics Facility and Mobix Lab, providing a variety of next-generation sequencing technologies (Illumina and PacBio) for diverse applications, read lengths, and throughput requirements. Single-cell and spatial profiling assays are available using the 10x Genomics Chromium X and Visium CytAssist systems. Targeted RNA and miRNA expression assays are available using the nanoString nCounter. A full suite of DNA- and RNA processing and QC platforms are also available, as well as traditional Sanger sequencing and fragment analysis instruments. The highly experienced MGF team can provided comprehensive support for project planning, budgeting, experimental design, troubleshooting, data analysis, and pipeline development, as well as general bioinformatics and statistics guidance and training.

Dr. Neil Winegarden

Senior Staff FAS, 10x Genomics

Bio: Neil is a Field Application Scientist supporting researchers from Ontario to Newfoundland. He recently celebrated his 6th anniversary with 10x Genomics. Prior to joining 10x Genomics Neil headed the Princess Margaret Genomics Centre in Toronto, a position he held for nearly 20 years. Neil brings his expertise in transcriptomics and epigenomics to his role, supporting customers with training, experimental planning guidance and troubleshooting support.

Talk Title: ***"Multiplexed Single Cell Transcriptomics - Highest sensitivity, reduced per sample cost"***

Abstract: At every stage of your research, accurate, reliable performance is critical. So is your budget. We're thrilled to be making single cell more accessible than ever before. GEM-X Universal Gene Expression Multiplex and GEM-x FLEX Gene Expression are making it possible to drive down your costs across a wide range of applications. We will discuss how you can maximize your budget without compromising on the highest sensitivity available.

Dr. Josh Koenig

Assistant Professor, Schroeder Allergy and Immunology Research Institute, Department of Medicine, McMaster University

Bio: Dr. Joshua Koenig is an Assistant Professor at McMaster University, within the McMaster Immunology Research Centre and the Shroeder Allergy and Immunology Research Institute. Dr. Koenig's research focuses on understanding the mechanisms by which type 2 immunity causes allergic diseases, with a particular focus on T and B cell memory. Dr. Koenig's research follows a "Systems-to-Mechanism" approach in which he applies next-generation omics analyses to uncover novel immunology in human tissues then uses traditional fundamental research methods and models to uncover mechanisms that govern the novel observations.

Talk Title: ***"Single cell RNA sequencing analysis of human memory B cells in allergy"***

Abstract: Memory B cells perpetuate allergic diseases by regenerating allergen-specific IgE antibodies upon exposure to an allergen. Whether a specific type of memory B cell was responsible for producing IgE was not known. We performed single cell RNA sequencing of human switched memory B cells and identified a novel phenotype of memory B cell with pro-allergic polarization, which we clonally connected to IgE production. Similar efforts in mice revealed unexpected results that speak to the importance of carefully planning scRNAseq experiments.

Alberto Torrez

Research Lab Technician, Han Lab, Centre for Discovery in Cancer Research, Department of Biochemistry and Biomedical Sciences, McMaster University

Bio: Alberto Torrez received his B.Sc. with an Honors Specialization in Biochemistry and Genetics from Western University. He then completed his M.Sc. in Cellular and Molecular Biology from Western University in collaboration with Agriculture and Agri-Food Canada investigating protein-protein interactions with histone deacetylase BdHD1. After completing his graduate studies, Alberto worked at Canopy Growth Corporation as the Genomics

Technician on the Plant Performance Team. Following this, Alberto joined Dr. Hong Han's Lab in 2023 as a Lab Research Technician at the Centre for Discovery and Cancer Research (CDCR) at McMaster University. During his time with the Han Lab, Alberto has helped establish and optimize sci-based single-cell RNA-sequencing and additional omics platforms at McMaster University.

Talk Title: ***"Integrated single-cell approaches to dissect cancer and other disease"***

Abstract: The Han Lab at McMaster works at the interface of cancer biology, RNA and multilayer gene regulation, and high-throughput technology development. We have pioneered developing and applying several integrated technological platforms for ultra-high-throughput single-cell profiling as well as large-scale genetic and drug screening to dissect the evolution of cancer ecosystems and other diseases. We have established an in-house single-combinatorial indexing (sci-) based single-cell RNA sequencing (RNA-seq) experimental and bioinformatics pipeline to discover disease mechanisms, biomarkers, and therapeutic targets. Our pipeline has the capacity for ultra-high-throughput experiments, significantly reducing costs while maintaining a high degree of flexibility to answer a vast range of biomedical questions. For example, this pipeline has been applied to answer questions regarding glioblastoma, T-cell therapy, and burn injury. We are transitioning to a single-cell multi-omics platform, such as with the addition of sci-based ATAC-seq (epigenomics) and long-read single-cell RNA-seq (full-length mutation-expression-splicing co-analysis) to further expand the tools available to understand complex human diseases at the single cell level. Additionally, Systematic Parallel Analysis of Endogenous RNA Regulation Coupled to Barcode Sequencing (SPAR-seq) is a highly multiplexed and quantitative functional genomics platform we developed to discover multilayer gene regulation, opening the door to large-scale investigations of both genetic and drug modulators in cancer and other diseases.

Liz Balint

PhD Candidate, McMaster Immunology Research Centre

Bio: Liz is a PhD Candidate in the Ashkar Lab at the McMaster Immunology Research Centre. Her research investigates how viral infections, such as Zika virus, can lead to rare but severe neurological complications. Through this work, Liz has identified a novel T cell population that promotes nonspecific tissue damage during viral infection.

Talk Title: ***"High-Dimensional Immune Profiling of Long-COVID Patients Using a 30-Colour Flow Cytometry Panel on the Cytek Aurora"***

Abstract: Understanding the complexity of long-COVID requires robust tools to capture the full spectrum of immune cell diversity and activation states. This talk will highlight our development and application of a 30-colour flow cytometry panel optimized for the Cytek Aurora spectral cytometer. This high-dimensional panel enables comprehensive

phenotyping of peripheral blood mononuclear cells from individuals with long-COVID. Our findings offer new insights into the immunological signatures associated with persistent symptoms post-SARS-CoV-2 infection and highlight the power of spectral flow cytometry in translational research.

Jamie McNicol

Technical Director, Spatial Proteomics and Transcriptomics Laboratory, McMaster University

Bio: Jamie has worked at McMaster for 17 years with a focus on assay development and data science in the single cell space. He lives in the beautiful valley town of Dundas with his wife, son, daughter, dog, and hedgehog.

Talk Title: ***"Spatial Profiling and Multiview Learning"***

Abstract: Our laboratory designs novel data analysis tools and pipelines that leverage machine learning and artificial intelligence to interrogate large spatially resolved single cell datasets.

Dr. Maria Davola

Research Associate – McMaster University

Bio: Dr. Davola is a Research Associate in the Mossman lab (Centre for Discovery in Cancer Research - Department of Medicine - McMaster University) since March 2023. She joined the Mossman lab in 2016 as a postdoctoral fellow. Since then, she has been leading studies on developing oncolytic Bovine Herpesvirus-1 (oBHV-1) as a novel cancer immunotherapy. Since 2019 Dr Davola has been strongly involved in oBHV-1 translational process including patent submission and management of key experiments for pre-clinical development and pre-CTA submission.

Talk Title: ***"MIBI-TOF to characterize changes in the complex tumor microenvironment of pancreatic ductal adenocarcinoma treated with combination immunotherapy in a humanized mouse model"***

Abstract: Pancreatic ductal adenocarcinoma (PDAC) is one of the most lethal diseases. Majority of patients have unresectable, locally advanced, or metastatic disease at the time of diagnosis making them poorly responsive to conventional therapies. Although immune checkpoint inhibitor efficacy in PDAC is limited, combination immunotherapies show promise in clinical studies. Immunotherapies use the patient's immune system to induce anti-tumor responses. Modeling the tumor microenvironment (TME) is particularly important in understanding human tumor immunology and exploring novel immunotherapies. Thus, our aim was to develop a pre-clinical mouse model of human PDAC

capable of recapitulate the complexity in the TME seen in patients' biopsies for validation of new immunotherapies for PDAC. Multiplexed ion beam imaging by time of flight (MIBI-TOF) allowed us to characterize the TME architecture at the single-cell level validating our humanized mouse PDAC model, and to evaluate therapy-induced changes in the TME. In summary, using a novel, clinically relevant PDAC model in humanized mice and MIBI-TOF we were able to recreate the complexity and plasticity in the TME reported in patients' biopsies after treatment success or failure. Accordingly, this model may represent an improved bridge between pre-clinical and clinical studies on human immune responses, accelerating the development of new immunotherapies.

Dr. Martin Karam

Account Manager, 10x Genomics

Bio: Martin Karam is an Account Manager at 10x Genomics, supporting researchers across Eastern and Central Canada, as well as Upstate New York. With a background in scientific research and past experience managing research programs at the Research Institute of the McGill University Health Centre, Martin partners with academic labs to help them achieve their research goals. He is passionate about empowering scientists with the right tools, offering strategic guidance on project planning, technology adoption, and funding opportunities.

Talk Title: ***"The Future of Spatial and In Situ Genomics Technology"***

Abstract: Understanding biology's complexity requires precision, context, and scale. That's why we're excited to share the latest spatial and in situ technologies from 10x Genomics. Visium HD enables unbiased whole transcriptome discovery at high resolution, while Xenium In Situ delivers targeted, subcellular gene expression insights with exceptional sensitivity. We'll show you how these platforms are reshaping spatial biology and empowering researchers to uncover the mechanisms that drive health and disease.

Dr. Dongdong Wang

Assistant Professor Centre for Metabolism, Obesity and Diabetes Research, McMaster University. Division of Endocrinology and Metabolism, Department of Medicine, McMaster University.

Bio: Dr. Dongdong Wang is assistant professor at McMaster University, Canada. His research focuses on understanding molecular metabolism of metabolic disease and drug discovery for obesity, diabetes, and cardiovascular diseases, aging and others by using cutting-edge technology such as multi-omics (e.g., single cell spatial transcriptomics) and machine/deep learning (AI). He has published > 70 peer-reviewed articles in high prestigious journals such as Nature, Nature Metabolism, Diabetes et al.

Talk Title: ***"Spatial Transcriptomics: Its application in liver cancer and fibrosis study"***

Abstract: Spatial transcriptomics represents a cutting-edge technique, which provides a comprehensive roadmap of the gene expression profiles of individual cells within intact tissue sections. We recently have established this technology in MODR. We will discuss the workflow by using Visium CytAssist, including sample preparation (H&E or IF), CytAssist, library preparation, sequencing and data analysis through one our study on liver cancer and fibrosis as an example.

Dr. Yongfu Wang

Senior Manager of Field and Sales Support, Complete Genomics

Bio: Yongfu Wang is the Senior Manager of Field and Sales Support at Complete Genomics, where he leads scientific advising, technical support, and customer enabling for the Stereo-seq spatial platform. He joined the company in 2023, following a career in academic research and operations. Before joining Complete Genomics, Yongfu served as Head of Histology at the Stowers Institute for Medical Research and previously held the position of Assistant Research Professor at the University of Kansas. He brings deep scientific expertise and a strong track record in leading support teams to drive customer success.

Talk Title: ***"Introducing Stereo-seq: Redefining What's Possible in Spatial Transcriptomics"***

Abstract: This presentation will focus on Stereo-seq, the highest-resolution spatial transcriptomics platform available today. With 0.5 μm resolution and chip sizes up to 13 cm × 13 cm, Stereo-seq enables full transcriptomic mapping across whole organs or large tissue sections—ideal for developmental biology, oncology, neuroscience, and cross-species studies. This open, species-agnostic platform supports both Fresh Frozen and FFPE samples, integrates transcriptomics with proteomics or histology, and captures total RNA—including noncoding RNAs and microbiome content—from FFPE samples.

Reina Ditta

Academic and Research Development Manager, CRLB-GMEL, Hamilton Health Sciences

Bio: Reina Ditta is the Academic and Research Development Manager of the Genetics and Molecular Epidemiology Laboratory (GMEL) – Clinical Research Laboratory and Biobank (CRLB). Previously, she was the lab manager, GMEL, at PHRI. Reina received her Honours Cell Biology from Western University, her Master's in Forensic Science from King's College London, and has more than 11 years of laboratory experience.

Tara Bryce

Operations Manager, CRLB-GMEL, Hamilton Health Sciences

Bio: Tara Bryce is the Operations Manager for the Clinical Research Laboratory and Biobank (CRLB) and Genetics and Molecular Epidemiology Laboratory (GMEL). A member of the CRLB since 2007, Tara has over 13 years' experience as a laboratory professional, with expertise in biobanking and clinical research. Tara holds an Honours Bachelor of Science from McMaster University, and is a Medical Laboratory Technologist registered with the College of Medical Laboratory Technologists of Ontario (CMLTO).

Talk Title: ***"Facility spotlight:CRLB-GMEL"***

Abstract: Facility spotlight: Clinical Research Laboratory & Biobank – Genetic & Molecular Epidemiology Laboratory (CRLB-GMEL)"

Dr. Lisa Lock

Senior Genomics Specialist, Illumina

Bio: Dr. Lisa Lock is a Sr Genomics Specialist at Illumina, where she has been championing the adoption of advanced genomics technologies for over 14 years. Prior to joining Illumina, Lisa earned her PhD in Molecular Oncology from McGill University, followed by postdoctoral research at the University of Toronto, and as a scientist at Lorus Therapeutics in Toronto.

Talk Title: ***"From Sequence to Solution: Empowering Multiomic Breakthroughs"***

Abstract: Discover how Illumina is accelerating multiomic research with innovations in single-cell, constellation mapped read technology, 5-base, protein prep, and spatial workflows.

Dr. Nazia Pathan

Post Doctoral Fellow, McMaster University

Bio: Dr. Nazia Pathan holds a PhD in Medical Sciences from McMaster University, specializing in genetic epidemiology, under the supervision of Dr. Guillaume Paré. She has received international awards and published in Nature Communications for developing a novel genetic algorithm, RARity (Rare variant heritability estimator), to measure the contributions of rare genetic mutations to complex trait heritability. She is currently a postdoctoral researcher collaborating with multiple departments and the Population Health Research Institute at McMaster University. Her research focuses on leveraging data from large biobanks to investigate the relationships between genes, proteins, and diseases, while harnessing multi-omics platforms to identify and validate lipid-lowering therapeutic targets in mice, humans, and cell lines.

Talk Title: ***"Whole exome sequencing to measure the influence of rare coding variants on complex traits"***

Abstract: Many human traits, like height, cholesterol levels, and diseases status differs between individuals, due to differences in genetics and environmental exposures. One possible source of genetic differences are rare mutations, which are found in fewer than 1 in 100 people and detected through whole exome sequences (WES).

Heritability is a way of measuring how much of the differences we see in a trait can be explained by genetic differences between people. We developed a genetic tool called RARity (Rare variant heritability estimator) to estimate how much the rare mutations influence complex traits, using 49 traits from over 167,000 individuals in the UK Biobank. Using this approach, we showed that rare mutations have significant influence on measurable traits and diseases, with height being the most affected, as reflected with a heritability of 21.9%. With RARity, we were able to estimate the influence of individual genes, helping to identify potential genetic targets for therapeutic or diagnostic use. RARity also allowed evaluation of existing predictive tools used to decide which mutations are detrimental to health and illustrated a need for better predictive tools.

In conclusion, RARity is a versatile tool that can measure the influence of mutations on traits, identify genetic targets, and help evaluate genetic predictive tools for complex traits. Overall, our findings suggest that rare genetic mutations, as detected through WES, play a crucial role in human health, and emphasizes the need for better predictive tools to identify harmful mutations.

Dr. Joe Mellor

Chief Scientific Officer and Co-Founder, SeqWell

Bio: Joe Mellor is an entrepreneur and scientist with expertise in genomics technologies and bioinformatics. He is a founder and Chief Scientific Officer at seqWell, a genomics technology and product company focused on creating scalable multiplexing solutions for today's demanding genomics applications.

Talk Title: ***"Transposase-based Tools for Scalable Sequencing Workflows"***

Abstract: As the capacity sequencing instruments continue to rapidly grow, bottlenecks still arise in library workflows needed to cost-effectively take full advantage of these expanding platforms. seqWell has developed a portfolio of transposase-based products and library tools to simplify and scale a wide range of sequencing applications. Recent innovations in transposase technology, including the newly engineered TnX™ transposase, are highlighted in applications to high-throughput plasmid sequencing, long-read sequencing, and population-scale WGS/WES assays.

Dr. Shahrokh Shekarriz

Postdoctoral Fellow, Surette Laboratory,Farncombe Institute, McMaster University; Mitacs Fellow, Taylored Biotherapeutics; Senior Bioinformatician, eDNAtech

Bio: Dr. Sharok completed his B.Sc. in Molecular Biology in Iran, followed by an M.Sc. in the Department of Biology at McMaster University. He then completed his Ph.D. in Biochemistry and Biomedical Sciences, also at McMaster. He is currently a Mitacs Postdoctoral Fellow in a joint project between the University of Calgary and the Surette Lab at McMaster, where he develops microbiome-based therapies for mental health. In addition to his academic work, Sharok provides bioinformatics consulting to industry partners, including environmental and biotech startups.

Talk Title: ***"Detecting microbial engraftment after FMT using placebo sequencing and culture enriched metagenomics"***

Abstract: We developed a framework to improve detection of microbial engraftment following fecal microbiota transplantation (FMT) by leveraging data from multiple recipients of a single donor. Combining amplicon sequencing, shotgun metagenomics, and culture-enriched metagenomics, we showed that cross-patient analysis reduces false positives, especially when placebo samples are used to estimate background noise. Our method identified uniquely engrafted genes in FMT responders, supporting strain displacement as a key mechanism.