

DBMR Research Conference

Langhans Hörsaal Pathologie
Murtenstrasse 31, 3008 Bern

Date **February 10, 2020, 5 pm – 6 pm**

Title **Single-cell transcriptome profiling of endothelial cells**

Speaker **Prof. Dr. Yonglun Luo, Executive Director of the Lars Bolund Institute of Regenerative Medicine (LBI), BGI-Research, Aarhus University, Department of Biomedicine, Aarhus, DK**

Bio: Dr. Luo obtained his PhD in Medicine at Aarhus University in 2012, and received postdoctoral trainings at Novo Nordisk A/S (2012-2014), the Roslin Institute (2013) and Harvard Medical School (2015). Since 2015, Yonglun has been leading an independent research group at the Department of Biomedicine, Aarhus University (Link: www.dream.au.dk). He is also PI at the BrainStem – Stem Cell Center of Excellence in Neurology, Copenhagen University. Since 2017, Yonglun was appointed as the executive director of the Lars Bolund Institute of Regenerative Medicine in BGI (www.cris-pratlas.com). Yonglun Luo's research focuses on systematically combining multi-OMICS and NGS technologies, single cell RNA sequencing, CRISPR gene editing, stem cell engineering and animal biotechnology (somatic cell nuclear transfer) to understand and develop regenerative medicine. One of his well-known research focuses is to genetically tailor the pigs for biomedical research. Advanced by the latest high-throughput and automatic single cell RNA sequencing technology, his group is re-visiting the somatic heterogeneity and functions of endothelial cells in various healthy and diseased conditions.

Abstract: The inner layer of blood and lymphatic vessels, also known as the endothelium, is of vital importance, as blood vessels supply every cell in our body with oxygen and nutrients. Not surprising, endothelial cells (ECs) contribute to many prevalent diseases, including conditions characterized excess EC growth (e.g. cancers) and EC dysfunction (e.g. diabetes, cardiovascular diseases). The heterogeneity of ECs has long been aware of and several degrees of EC heterogeneity have been identified, for instance, ECs from different vasculature beds (arterial, microvascular, venous, lymphatic), within and between tissues, and under different diseased conditions. However, the degree of EC heterogeneity at single-cell level and the mechanism by which ECs specify into all these different phenotypes (cell types) remains poorly understood. To systematically characterize and establish the first-in-class atlas of EC heterogeneity in health and disease, we used high-throughput single cell RNA sequencing (scRNA-seq) technology to generate the first mouse scRNA-seq EC atlas (which includes 11 tissues 78 EC subtypes. In press), the first high-resolution renal EC taxonomy (24 renal EC phenotypes) [2] and the first high-resolution lung cancer EC taxonomy (32 EC phenotypes, with 16 previously unrecognized phenotypes) [2]. These findings highlight the extensive EC phenotypic heterogeneity and discover several novel (metabolic) mechanisms leading the diverse EC phenotypes.

Refs:

1. Sébastien J. Dumas et al. Single-Cell RNA Sequencing Reveals Renal Endothelium Heterogeneity and Metabolic Adaptation to Water Deprivation. **JASN**. 2019. doi: <https://doi.org/10.1681/ASN.2019080832>
2. Jermaine Goveia et al. An Integrated Gene Expression Landscape Profiling Approach to Identify Lung Tumor Endothelial Cell Heterogeneity and Angiogenic Candidates. **Cancer Cell**. 2020. 37:21-36

Prof. Dr. Yonglun Luo has been invited by Prof. Dr. Robert Rieben

Next DBMR Research Conference

March 2, 2020

Prof. Dr. Claes Wahlestedt; title to be announced

The DBMR Research Conference takes place from 5 pm – 6 pm and will be followed by an apéro.



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