Stem Cell Biology and Transcriptomics of Human White Matter Diseases

September 20

Tuesday, 12:30pm

Hybrid: Rosedale Room and Zoom

For Researchers



Speaker:

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Abstract

Multiple sclerosis (MS) is a common, debilitating, progressive and fatal neurological disease that targets myelinating oligodendrocytes. Although most likely driven by an autoimmune response, the effector mechanisms that cause inflammation and that lead to neurodegeneration are incompletely understood. Treatment options

are limited and do not prevent the progressive phase. This talk will cover molecular, temporal and cellular diversity of glial cells in CNS development, and apply this perspective to understand what goes wrong in MS disease progression that: (1) causes inflammation in the brain, (2) death of neurons and brain shrinkage and (3) how to potentially enhance repair of lesions. In an effort to find biomarkers of disease progression and targets for new therapies, we have used transcriptomic approaches, stem cell models of oligodendrocyte disease that have highlighted a role for iron toxicity in cells of the oligodendrocyte lineage.



Figure 3. Human Transcriptomic Marker Genes Characterizing Homeostatic and Reactive Glial Subtypes. Cartoon lists homeostatic (left) versus reactive (right) glial subtype signature genes by means of volcamo plot visualization. Marker genes were selected by their specific enrichment in microglia, oligodendrocyte (OL) precursor, and myelinating cells, as well as astrocytes based on recent single-cell/nucleus RNA-sequencing (sc/nnRNA-seq) studies from human control and multiple selerosis (MS) tissues. See Boxes 2.4 in the main text for details about signature genes and their functional relevance. Note color spectrum on the bottom illustrates dynamic changes in gene expression between homeostatic and reactive glial subtypes according to cell type color code. This figure was created using BioRender (https://biorender.com/).

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