“Nature and Nurture of Microglia Identity and Function”

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Abstract

Dr. Glass’ primary interests are to understand the mechanisms by which sequence-specific transcription factors, co-activators and co-repressors regulate the development and function of macrophages. A major direction of his laboratory has been to define the genome-wide locations and functions of these proteins through the use of assays that are based on massively parallel DNA sequencing. The combination of these technologies with molecular, genetic and cell-based approaches is providing new insights into mechanisms that regulate macrophage gene expression and function that are relevant to human diseases that include cancer, diabetes, atherosclerosis and neurodegenerative diseases. A relatively new direction of the laboratory is to investigate gene expression and epigenetic landscapes in macrophages resident within different tissue environments in normal and disease contexts. Major progress has been made in methods to isolate and characterize mouse and human microglia and to assess their transcriptomes and epigenetic landscapes ex vivo and following transition to an in vitro environment. These studies indicate significant effects of the brain environment in shaping microglia identity and are facilitating interpretation of non-coding risk alleles identified by genome-wide association studies.

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