



Spatial Transcriptomics-correlated Electron Microscopy maps morphological and transcriptional responses to brain injury

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A hallmark of nervous system aging is a decline in white matter volume and function, but the underlying mechanisms leading to white matter pathology are unknown. In a series of studies, the Gokce group used single-cell RNA sequencing (scRNA-seq) to study white matter aging. These scRNA-seq studies showed that CD8+ T cell-induced interferon-responsive oligodendrocytes and microglia are important modifiers of white matter aging. To accelerate progress in aging research, they also developed Spatial Transcriptomics-correlated Electron Microscopy (STcEM) which correlates large-area scanning EM and multiplexed error-robust fluorescence in situ hybridization (MERFISH) and links transcriptional identities of single cells with ultrastructural data. They applied STcEM to characterize the damage-associated microglial identities in the mouse brain, allowing, for the first time, to link the morphology of foamy microglia and interferon-response microglia with their transcriptional signatures.

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