【演者】

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【演題】

Spatiotemporal brain transcriptome architecture and application for disease model in marmosets

【講演要旨】

Spatiotemporal transcriptome gene regulations are essential for the construction of brain structure and proper function. Comprehensive analyses of the dynamics and the architecture of transcriptome in the both wild and diseased animal models also lead to understanding the molecular causality of the human neuropsychiatric disease. Here we examine the spatiotemporal transcriptome dynamics using the common marmoset brain to identify the spatiotemporal-specific modulating genes. Currently our team has been doing the following studies, (i) the postnatal developing marmoset brain transcriptome (five postnatal stages) at macro-scale resolution (seven cortex regions of both cerebral hemispheres, thalamus, midbrain, cerebellum), (ii) the adult marmoset brain transcriptome at micro-scale resolution (a single layer of cells from five cortical regions, a single nucleus from three subcortical regions), and (iii) the wild and the autism model marmoset brain transcriptome in prefrontal regions. Through this study, we aim to identify the molecular dynamics and trajectories between proper and atypical brain gene expressional networks.