

Transcriptomic profiling and integrated bioinformatic analyses of glial cell types of the brain

Speaker:

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Funding period:

Since 2014

Project description:

Increasing evidence suggest that glial cell type heterogeneity contributes to higher order brain functions. Astroglial cells, for example, are essential in modulate in synaptogenesis during development and maintaining the metabolic integrity of neurons in the mature brain. In the proposed project and with several partners, we aim at applying deep sequencing of MACS, FACS and RiboTag purified glial cell populations from different brain regions and developmental stages to generate a comprehensive molecular catalogue of glia. In depth bioinformatic analyses and visualizations will be used to setup a database for follow up queries and public accessibility. By analyzing the transcriptomes of cortical astrocytes harvested at early postnatal developmental stages, we identified several astrocyte expressed genes which have been implicated in synaptogenesis and metabolic support. For most of these developmentally regulated genes, however, the function is not known. We will apply a combined bioinformatic guided selection and experimental validation screen to identify novel astrocyte expressed genes and mechanisms which modulate neuronal activity during development and in the adult brain.

Quelle:

<https://gepris.dfg.de/gepris/projekt/254896936?language=en>