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Single-cell RNA sequencing analysis of human Alzheimer's disease brain samples reveals neuronal and glial specific cells differential expression

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Alzheimer's Disease (AD) is the 2nd most common neurodegenerative disease worldwide with no current early diagnosis or treatment methods. 6-8% of patients are under the age of 65. Several proteins (including RNA binding ones) were detected as related to the disease (e.g. TREM2, APOE, CD33) but there are yet more genes to be detected as related to AD. To identify unique transcriptional networks impacted into distinct neuronal populations in AD, I surveyed gene expression differences in over 25,000 single-nuclei collected from patients post mortem brain hippocampal samples (Braak stage II/III). The single-cell RNA-Seq data analysis of the patient samples and of 2 age- and gender-matched healthy control (HC) volunteers detected involvement of astrocytes and microglia. To conclude, analysis of genomic data from aging and AD samples compared to controls may enable detection of cell type specific gene expression changes and hopefully development of future microglia-based genomic therapeutic approaches (e.g. using Cas9/Crispr system) or early detection methods using blood test on specific marker genes.

Recent Publications

1. Single-cell RNA sequencing analysis of human Alzheimer's disease brain samples reveals neuronal and glial specific cells differential expression
2. Replacement of microglia in the aged brain reverses cognitive, synaptic, and neuronal de cits in mice
3. MicroRNA expression changes in Parkinson's disease (PD) patients' leukocytes prior to and following deep brain stimulation (DBS)
4. Genome-wide analysis of haploinsufficiency in human embryonic stem cells
5. Exon Arrays Reveal Alternative Splicing Aberrations in Parkinson's Disease Leukocytes

Biography

Lilach Soreq have a BSc in computer science (with division in mathematics and in cognitive sciences). MSc in bioinformatics and PhD in neurobiology from the faculty of medicine in Hadassah Jerusalem hospital, Israel. He did all my degrees in the Hebrew university of Jerusalem. He was supervised by Dr. Nissim Ben Arie in my MSc (published a paper on Math1 developmental transcription factor in mice) and my PhD under the supervision of Prof. Hagai Bergman (that developed DBS). During his PhD, I studied Parkinson's disease RNA expression changes in PD patients' blood leukocytes in my PhD prior to and following deep brain stimulation (DBS) on and off stimulus. Published 21 papers a book chapter and 2 patents. He did his post doc in UCL Institute of Neurology (London UK) and Francis Crick Institute studying aging (published in Cell-Reports). I had a Marie-Curie 2 year fellowship, and 3 years Alzheimer's society fellowship.

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