Grand Valley State University

Assessment of Parkinson's disease-specific microRNAs in Alzheimer's disease

GRAND VALLEY STATE UNIVERSITY
Department of Cell & Molecular Biology

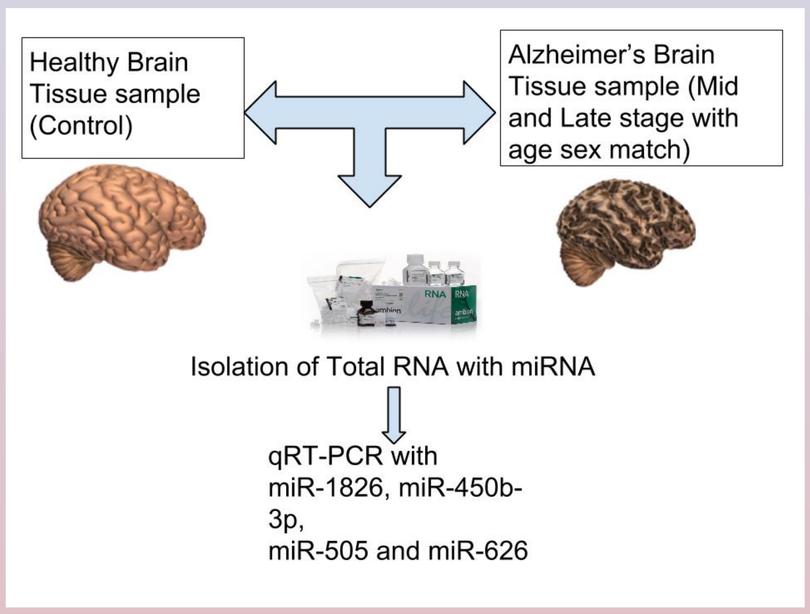
Sayantoni Mukhopadhyay, Stephen Orey, John Beck, Scott Counts, Sok Kean Khoo

Background

Alzheimer's disease (AD) is the 6th leading cause of death in the United States and the 5th leading cause of death for those aged 65 and older [1]. Like Parkinson's disease (PD), the second most common neurodegenerative disorder after AD, there is no cure and final diagnosis of the disease can only be achieved by autopsy. Although AD and PD are distinct pathological conditions, mounting evidence shows possible links between the genetics and brain changes associated with them, such as cognitive impairment and aggregation of misfolded proteins, suggest cross disease association.

MicroRNAs (miRNAs) belong to a class of non-coding regulatory RNA molecules of ~22 nucleotides length which help modify gene expression at the posttranscriptional level by binding to the 3' untranslated region of their target messenger RNAs [2,3,4]. Previous research [5] has identified a panel of PD specific miRNA biomarkers (miR1826, miR450b3p, miR505 and miR626). The pathway analyses of these miRNAs target genes showed enrichment in the neuron differentiation/projection and synaptic pathways, which are also important signaling pathways in AD.

In this study, we plan to evaluate PD-related miRNAs on AD patients to shed light on the similarity between AD and PD.



Experimental Flowchart for the Project

Materials & Methods

Samples: AD brain tissue samples from Counts Laboratory

Sample size: 10 healthy controls, 5 mid-stage AD and 5 late-stage AD (all samples are age and sex matched extracted from both the frontal and temporal lobe)

RNA Extraction: PureLink RNA Mini Kit (Ambion)

Real-time PCR: TaqMan miRNA assay

Data collection: To quantify miRNA expression, the CT (cycle threshold) value of miRNA from an endogenous control (U6) will be used to normalize for variation in the amount and quality of miRNA expression between different samples.

Data Analysis: To calculate the expression of each target miRNA in AD sample relative to the healthy control, the comparative CT(ΔΔCT) method will be used.

Expected Results

We hypothesize that the PD-specific miRNAs show similar miRNA expression patterns in Alzheimer's disease samples, confirming cross disease association. This study is essentially an important first step towards future functional studies of miRNA analytes for potential therapeutic targets for both PD and AD.

Collaborators

Counts Laboratory headed by Dr. Scott Counts, Associate Professor, Department of Translational Science and Molecular Medicine at Michigan State University (Grand Rapids campus) with Lab manager John Beck

Acknowledgements

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