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A study of differential MiRNAs expression patterns discovered for Alzheimer’s disease

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The superior temporal lobe neocortex and hippocampus of Alzheimer’s disease (AD) patients show signs of significant changes in physiological function that accompany amyloid plaque and neurofibrillary tangle formation, synaptic loss and neuroinflammation which are hallmarks of AD. MiRNA networks control a substantial portion of the post-transcriptional gene regulation and hence an alteration in the expression of micro RNAs (miRNAs) is emerging as a significant contributing factor to AD. It is imperative to discover the biologically significant correlations among co-regulated miRNAs that play a substantial role in the progression of AD. The molecular, genetic and epigenetic evidence indicate that at least 5 miRNAs - including the NF-kB-regulated miRNA-9, miRNA-125b, miRNA-146a, miRNA-34a and miRNA-155 are progressively up-regulated in AD. Our prior investigation has asserted that this quintet of up-regulated miRNAs in turn down-regulate a small brain- and retinal-cell-relevant family of target mRNAs, including that encoding complement factor H (CFH), a major negative regulator of the innate-immune and inflammatory response, and synapsin-II (SYN-2) a critical neurotransmitter release protein. In this study, we are investigating miRNA expression in AD (57 cases) and age-matched controls (29 cases) by specifically concentrating to find discriminatory miRNA-146a, miRNA-9, miRNA-125b, miRNA-34a and miRNA-155 patterns. We have adapted feature selection methods to rank their abundances, which highlight the differentially expressed miRNAs in the diseased as compared to the control. We have further developed a data processing pipeline and classification model, to discriminate between normal and patients with Mild cognitive impairment using Diffusion Tensor Imaging.