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Poster Submissions

Poster Title

Novel brain-specific miRNAdiscovery using small RNA sequencing in post-mortem human brain

Authors and their Affiliation

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Please describe the extent of your work in this research

All of this project's associated computational/statistical analyses were completed by Chris Wake over the past year, guided by members of Rick Myers' and Anita DeStefano's labs.

Abstract Submission

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Would you like your abstract to be considered for an oral presentation (students and post docs only)?

No

Novel brain-specific miRNA discovery using small RNA sequencing in post-mortem human brain

Chris Wake1,2, Adam Labadorf1,2, Alexandra Dumitriu1, Andrew Hoss1,3, Richard Myers1-4
1) Department of Neurology, Boston University School of Medicine; 2) Bioinformatics Program, Boston University; 3) Graduate Program in Genetics and Genomics, Boston University School of Medicine; 4) Genome Science Institute, Boston University School of Medicine

MicroRNAs (miRNAs) are short, non-coding RNAs that regulate gene expression mainly through translational repression of target mRNA molecules. More than 2,700 human miRNAs have been identified and some are known to be associated with disease phenotypes and to display tissue-specific patterns of expression. Here, we use high-throughput small RNA sequencing to discover novel and possibly brain-specific miRNAs in 94 human post-mortem prefrontal cortex samples from patients with Huntington's disease, patients with Parkinson's disease and from neurologically healthy controls. Using a custom analysis pipeline which utilizes miRDeep* miRNA identification and result filtering based on false positive rate estimates, we identified 99 novel miRNA candidates that originate from both intergenic and intragenic regions of the genome. Forty-two of the candidate miRNAs show sequence similarity with known mature miRNA sequences and may be novel members of known miRNA families, while the remaining 57 may constitute previously undiscovered families of miRNAs that are specific to the brain. Twenty of the 99 candidate miRNA were replicated using independent, publically-available, human brain RNA-sequencing samples. In a small number of the novel miRNAs, differential expression analysis between neurodegenerative disease and normal samples identified significant differences in expression. These results suggest that a portion of these novel miRNAs may not only be unique to brain, but may also have a role in the neurodegenerative disease processes.