Profiling differential expression of miRNA in prefrontal cortices of tobacco smokers vs. non-smokers

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Small non-coding RNAs have gained much attention in recent years for their role in post-transcriptional regulation of gene expression and their potential role as biomarkers of disease states and treatment responses. Of the non-coding RNAs, the ~22 nucleotide microRNAs (miRNAs) regulate gene expression, and a number of disease states show altered miRNA expression profiles, including psychiatric conditions like drug addiction. Along with their utility as biomarkers, profiling differentially expressed miRNAs between case and control populations has the potential to direct attention to novel mechanistic pathways underlying the disease being investigated. The goal of this study was to sequence and profile mature miRNA expression in prefrontal cortices of postmortem human brain samples from smokers and non-smokers. Using Illumina Small RNA-Seq, we profiled miRNA collected from 10 brain samples (5 smokers, 5 non-smokers) and analyzed differentially expressed miRNAs using the Partek suite of tools. A total of ten mature miRNAs were differentially expressed between smokers and non-smokers, and these miRNAs target genes involved in neuroprotection, neurotransmitter release and glutamate uptake by glial cells. These are the first data to show differential expression of miRNA in human brain tissue samples from smokers and suggest that miRNAs may play an important role in neurological processes underlying tobacco/nicotine use.