Name: Dongmei Li Email: Dongmei_Li@urmc.rochester.edu

Longitudinal changes in expression profile of urine exosomal epigenetic microRNAs in exclusive electronic cigarette adult users

Dongmei Li, Zidian Xie, Irfan Rahman

Univeresity of Rochester Medical Center, Rochester, NY, US

Background: Electronic cigarette (e-cigarette) use in the US has significantly increased in the past few years. Epigenetic-mediated exosomal microRNAs play important regulatory roles in immune regulation and inflammatory response. We aim to investigate the longitudinal changes in exosomal microRNA expression profile when non-users initiate exclusive e-cigarette use and exclusive e-cigarette users quit vaping.

Methods: Using the Population Assessment of Tobacco and Health (PATH) Wave 1 (2013-2014) and Wave 2 (2014-2015) urine samples from 45 subjects, we examined exosomal microRNA expression levels through sequencing when participants initiated exclusive e-cigarette use or quit vaping from Wave 1 to Wave 2 using the generalized linear mixed-effects models. Gene enrichment analyses were conducted on target genes regulated by significant exosomal microRNAs.

Results: We identified two microRNAs (has-miR-181b-5p and hsa-miR-221-3p) that had increased expression levels in subjects who initiated exclusive e-cigarette use in Wave 2 and decreased expression levels in subjects who quit exclusive e-cigarette use in Wave 2. Gene enrichment analyses using the GO and KEGG database showed that the target genes regulate the apoptotic process, cell cycle, gene silencing, small lung cancer cell pathway, p53 signaling pathway, FoxO signaling pathway, and MAPK signaling pathway.

Conclusion: Two urine epigenetic exosomal microRNAs had significant expression level changes during the exclusive e-cigarette use initiation and cessation process. Gene enrichment analyses showed that they regulate genes involved in cancerous pathways, indicating a potentially elevated risk of cancer associated with exclusive e-cigarette use. These findings may have implications for other substance abuse effects on epigenetic alterations.