H128 Conceptualizing the Gut Thanatomicrobiota in Substance Abuse Disorders

Gulnaz T. Javan, PhD, Alabama State University, Montgomery, AL 36104; Sheree J. Finley, PhD, Alabama State University, Montgomery, AL 36104; LaTia Scott, PhD, Delaware State University, Dover, DE 19901; Silvia D. Visona, MD, University of Pavia, Pavia 21100, ITALY; Antonio M.M. Osculati, MD, University of Pavia, Pavia 27100, ITALY*

Learning Overview: After attending this presentation, attendees will understand how to use 16S ribosomal RNA (rRNA) amplicon sequencing analyses to characterize the thanatomicrobiota of transverse colon samples from Italian cadavers. Specifically, attendees will learn methods to assess the microbial diversity after death using 21 overdose and 19 natural death cases.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by presenting new information on the community composition of postmortem microbial colonizers in drug overdose cases, which could be useful to investigators to devise better methods and improve the accuracy of estimating the cause and time of death using an underutilized molecular method. By probing the relative abundances of specific microbes present in the transverse colon, a comparative analysis was used to identify a possible link between commonly abused drugs and microbes present during the decomposition process.

In this century, drug abuse continues to be a national crisis. Since 1999, the number of opioid-induced overdoses has increased four-fold to more than 500,000 deaths. The microbiota gut-brain-axis is a bidirectional circuit that links the neural, endocrine, and immunological systems with gut microbial communities. Gut microbiota play significant roles in human mind and behavior, specifically pain perception, learning capacity and memory, mood, and emotion, and anxiolytic effects and temperament. Also, disruptions in the gut microbiome have been associated with substance use disorders. While much research still needs to be performed, elucidating the interplay of gut microbiota in substance abuse disorders may produce promising avenues for future forensic development. The goal of the current study was to determine gut microbiome composition in substance abuse disorder cases using transverse colon tissues of 21 overdose criminal cases versus 19 non-overdose-related cases. The hypothesis was that postmortem samples of the same origin will reveal similar taxonomic relationships. Using weighted UniFrac analysis, drug abuse was found to be a significant factor in determining microbiome similarity ($F = 1.93$; $df = 1, 35$; $p < 0.048$; $R2 = 0.05$) indicating that there are detectable differences in composition that are attributable to substance abuse. Using unweighted UniFrac, however, sex was instead found to be a significant predictor of microbiome similarity ($F = 1.88$; $df = 1, 30$; $p = 0.028$; $R2 = 0.05$). A heatmap was generated of the relative abundances of the 30 most prevalent bacteria per case and their associated substance profile. The results revealed that samples of the same origin cluster together, showing a high degree of similarity between samples and a low degree of similarity among samples of different origin. This examination of human transverse colon microflora in decomposing cadavers expands the emerging literature on postmortem microbial communities, which will ultimately contribute to advanced knowledge of putrefaction.

Thanatomicrobiota, Cadaver, Gut

*Presenting Author