H123 Novel Association Between the Thanatomicrobiome and Postmortem Interval (PMI)

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After attending this presentation, attendees will understand how to use high-throughput next generation sequencing analysis to characterize the thanatomicrobiome of internal organs from actual cadavers in criminal cases (e.g., homicide, suicide, and overdose). Specifically, attendees will learn methods to assess microbial diversity after death using PMI between 3.5 hours and 240 hours.

This presentation will impact the forensic science community by informing attendees interested in using high-throughput next generation sequencing of the microbial communities found in the internal organs, the oral cavity, and blood, if applicable, to develop a framework for determining PMI.

Accurate determination of the time of death, or PMI, is important in suspicious or unnatural deaths, particularly in criminal cases. The PMI provides critical information for crime scene reconstruction and in some cases can mean the difference between courtroom innocence or guilt. Conventional methods of determining PMI include rate (e.g., algor, livor, and rigor mortis) and concurrence methods (e.g., gastric emptying). These methods often do not provide definitive answers, which consequently leads forensic investigators to subjective conclusions. The thanatomicrobiome, or "microbes of death," is the diversity of microorganisms involved in human decomposition.

This study hypothesized that as a human body decays, time-dependent changes in the thanatomicrobiome within different body sites will be more predictive of the time of death. The objectives were to analyze the thanatomicrobiome of internal organs (brain, heart, liver, and spleen), the mouth cavity, and blood of human cadavers. To assess this hypothesis, a cross-sectional study was performed by sampling 28 human corpses with PMIs between 3.5 hours and 240 hours. The samples were obtained from between one to six body sites. 16S ribosomal RNA (rRNA) next-generation sequencing and analysis revealed characteristic time-dependent changes in the thanatomicrobiome community composition that were associated with time of death. Diversity was examined from two perspectives: (1) the overall richness (i.e., the number of distinct microorganisms found within the microbiome); and, (2) the Shannon Diversity (i.e., both richness and evenness, the distribution of abundance among distinct taxa). The diversity was expressed as the number of Operational Taxonomic Units (OTUs) and was quantified using the Chao1 richness estimator. Measures of diversity were screened for group differences using a statistical Analysis of Variance (ANOVA). The thanatomicrobiome results revealed the relative abundance of the 20 most dominant genera in all samples that formulate the diversity of the microorganisms most responsible for decomposition. Remarkably, the obligate anaerobe, *Clostridium*, was predominant in all cadavers in all samples except the oral cavity.

To date, relatively few studies have investigated the microbiome of whole cadavers from actual criminal cases in a forensic context. These results suggest that the thanatomicrobiome could be useful to criminal investigators and forensic scientists as a new source of data for identifying PMI.

Thanatomicrobiome, Cadaver, Postmortem Interval