H94 Determination of Cause of Death in Criminal Cases Using Thanatomicrobiome

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After attending this presentation, attendees will understand how to use 16S rRNA gene amplicon-based sequencing to characterize the thanatomicrobiome of a postmortem liver and spleen from actual criminal casework. Specifically, attendees will learn methods to assess postmortem microbial diversity using cadavers for the determination of cause of death.

This presentation will impact the forensic science community by revealing the thanatomicrobiome succession during putrefaction using high-throughput next-generation sequencing of postmortem microbial communities found in cadaver internal organs to develop a framework for determining cause of death and to establish the Human Postmortem Microbiome Project (HPMP).

Is death the end of life? In some ways, it is; but in relation to the microbial activity on and in cadavers, there are abundant microbes in human death that may potentially assist in criminal investigations. Despite the knowledge of the abundance and activity of microbial decomposers in cadavers, there is a paucity of details on the specific microorganisms involved in the decay of human internal organs. Determinations of the precise cause of death and postmortem interval are critical data for the forensic science community. Modern methods to estimate postmortem interval have the potential to replace traditional methods, such as stages of decomposition, body temperature, and mortis (algor, livor, and rigor). Human microbiome studies have revealed that more than 90% of cells in the body prior to death are microbial; however, information on the human thanatomicrobiome (*thanato*, Greek for death) of the internal organs is in its infancy. It was hypothesized that the thanatomicrobiome exhibits a characteristic microbial diversity that is possibly a function of cause of death. The hypothesis was tested by surveying the thanatomicrobiome of two selected internal organs (liver and spleen) from 50 cadavers with postmortem intervals between 3h-70.5h and known causes of death. To characterize the composition and diversity of thanatomicrobiomic communities, DNA was extracted and Polymerase Chain Reaction (PCR) was performed PCR targeting the V4 region of the 16S rRNA gene using bacterial primers 515F-806R. Standard bioinformatics pipelines (QIIME™), visualization tools (Phyloseq, R), and custom software was used to identify coordinated changes in the thanatomicrobiome that correspond with cause of death. Firmicutes (which includes *Clostridium*) were detected in all liver and spleen samples. In cases of deaths by coronary heart disease and overdose, the order Clostridiales and the genus *Pseudomonas* were the most predominant bacterial decomposers. These results suggest that comprehensive knowledge of the number and abundance of each internal organ's signature microorganisms could be useful to forensic scientists as an innovative source of a biomarker for determining cause of death. Also, this thanatomicrobiome data can aid in the establishment of the HPMP.

Thanatomicrobiome, Cause of Death, Cadaver