H103   The First Use of Postmortem Microbiomes in Human Death Investigations

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After attending this presentation, attendees will understand that in recent years several research groups have recognized the potential use of postmortem microbiomes in forensic investigations. Several of these studies have demonstrated that the process of describing changes in microbial communities during the decomposition process of vertebrate remains has the potential for use in estimating the minimum Postmortem Interval (PMI_{min}) range. Specifically, these studies have employed metagenomic techniques, such as Illumina® MiSeq® and 454 pyrosequencing, to identify microorganisms present throughout the decomposition of model organisms (e.g., swine and mouse carcasses) or donated human remains placed in facilities dedicated to cadaver decomposition research; however, there has yet to be a study to survey the postmortem microbiome associated with human cadavers from real-world cases and evaluate the potential use of these bacterial communities in death scene investigations.

This presentation will impact the forensic science community by providing the first baseline database of the human postmortem bacterial communities found on human cadavers during routine death investigations of a medical examiner's office. Determination of the PMI_{min} range is a critical measure following events such as homicide or unwitnessed deaths, and resolving the precise window of time and location of both the decedent and witness(es) is essential for excluding or including witness accounts and for defining the circumstances of death. Microorganisms are ubiquitous in the environment and associated with humans both antemortem and postmortem and are often overlooked and underutilized biological indicators of circumstances and length of time since death. Little is known about this postmortem microbiology and biodiversity in human cadavers, particularly the microbial succession of indigenous microflora residing on or in the human body throughout decomposition; however, recent work suggests that bacterial communities are quite dynamic during the postmortem interval on model organisms. While there are several research groups developing predictive models based on the changes in microbial communities to estimate PMI_{min} ranges on these surrogates for human cadavers (e.g., swine and mouse), none to date have applied these statistical approaches to PMI_{min} estimates for human remains; the first step toward developing models to be used in human death investigations is to establish a baseline database of known bacterial taxa found on human cadavers resulting from various manners of death and in differing progressions of the decomposition process. The goal of this presentation is to describe the human bacterial communities on different areas of cadavers in relation to manner of death and autopsy-estimated PMIs from human remains discovered in a major metropolitan city — Detroit, MI. Here, the first baseline database of the postmortem microbiome developed from human remains investigated by a medical examiner's office is presented.

Bacterial samples were collected from human remains received into the Wayne County Medical Examiner's Office in Detroit, MI; each cadaver represented different circumstances of death and progression of decomposition. Individual DNA-free sterile cotton-tipped swabs were used to aseptically collect individual bacterial communities from six areas: the external auditory canal, nose, mouth, umbilicus, rectum, and the trabecular space between the inner and outer tables of the occipital bone. DNA extractions were performed according to the manufacturer's instructions using the Invitrogen™ PureLink® Genomic DNA Mini Kit. DNA was quantified using a Qubit® 2.0. All bacterial DNA samples were sequenced using Illumina® MiSeq® (2x250bp paired-end). Library construction and sequencing of the 16S rRNA V4 gene region was performed by the Michigan State University Genomics Core Facility using a modified version of the protocol adapted for the Illumina® HiSeq® 2000 and MiSeq®. Samples were collected from 50 cadavers representing four manners of death: homicide, suicide, accident, and natural. There were distinct bacterial community assemblages found on individuals based on body region and related to manner of death. Additionally, there was increased variation of bacterial community composition within an individual (across all sampled body regions) compared to communities among individuals.

This project greatly expands on earlier studies of the postmortem microbiome by partnering with a medical examiner's office to characterize bacterial communities associated with a large number of human cadavers during routine death investigations. These data offer a transformative way to rectify common practical issues associated with studying human decomposition while moving the science of postmortem microbial communities in a direction that addresses the importance of replication and real-world cases.

Postmortem Microbiome, Medical Examiners, PMI Estimates