H104 Cadavers Show Distinctive Thanatomicrobiome Signatures

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After attending this presentation, attendees will understand the challenges/rewards of sampling the microbiome in human cadaver samples and its potential usefulness for determining the Postmortem Interval (PMI).

This presentation will impact the forensic science community by providing detailed information regarding how to sample the microbiome in order to understand how microorganisms colonize internal organs after human host death.

One of the challenges in forensic science is estimating PMI accurately. PMI is defined as the elapsed time-since-death and it is used in civil and criminal investigations to prove or disprove testimonial evidence (e.g., insurance fraud and homicides, respectively). Although there are many methods to determine PMI, most are susceptible to a range of errors and biases due to an overall poor understanding of how human bodies decompose.

Recent advances in DNA sequencing technologies have resulted in a paradigm shift in the understanding of the microbiome in healthy and diseased humans. For instance, it is now known that 90% of the total cells in a human body are microorganisms; however, what happens to these cells when a human dies is not known. The working hypothesis is that microorganisms involved in decomposing human bodies (i.e., thanato-, Greek definition of death, microbiome) provide an accurate clock for determining the PMI.

The objectives of this study were to survey the thanatomicrobiome of internal organs (the spleen, liver, brain, heart) and blood in human cadavers using two DNA sampling methods to determine which one was optimal for future studies.

The thanatomicrobiome were sampled from human cadavers with PMIs ranging from 20 to 240 hours. Amplifying the 16S rRNA genes and sequencing the amplicons from organ tissues and the blood of five cadavers was used to determine the effectiveness of the DNA sampling methods. Pair comparisons revealed that the conventional DNA extraction method (bead-beating in phenol/chloroform/bead-beating followed by ethanol precipitation) yielded more 16S rRNA amplicons (28 of 30 amplicons) than the second method (repeated cycles of heating/cooling followed by centrifugation to remove cellular debris) (19 of 30 amplicons). Shannon diversity index of the 16S rRNA genes revealed no significant difference by extraction method. DNA sequencing of 19 organ tissue and blood samples yielded a total of 599,268 reads with an average of 31,540 reads per sample (~500bp).

Ordination plots and hierarchical clustering of the annotated data revealed that, in general, the thanatomicrobiome was highly similar among organ tissues from the same cadaver but very different among the cadavers, possibly due to differences in the elapsed time-since-death and/or environmental factors.

Thanatomicrobiome, Cadaver, 16S rRNA

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