G70 Collecting Microbiological Evidence From Cadavers: Techniques and Implications of Using Bacterial Communities in Decomposition Estimates

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After attending this presentation, attendees will learn how to collect microbiological evidence from decomposing cadavers in order to use previously under-utilized communities of microbes to predict minimum Postmortem Interval (PMI_{min}) estimates and explore phyla-level taxonomic resolution of the microbiological communities sampled from swine carcasses and a human cadaver.

This presentation will impact the forensic science community by providing an approach on how to collect bacterial samples from remains during fresh, bloat, and active decay decomposition stages.

Insects are commonly used for PMI_{min} estimates; however, the potential to use microbiological (bacteria and fungi) samples for forensics has only now began to be explored. The goal of this study was to describe how to collect microbiological communities from decomposing vertebrate remains while identifying the bacterial communities using state-of-the-art metagenomic sequencing techniques.

Sampling for microbiological communities requires minimal equipment such as sterile swabs, microcentrifuge tubes, and, most importantly, aseptic technique in the field to the greatest ability of the forensic investigator. It is recommended that samples be collected from the decedent at various locations of the body including the buccal and anal region, if possible. Samples should be stored individually and shipped to an expert at -20°C (on ice; dry ice is not necessary). To validate these sampling methods in the field, three *Sus scrofa L.* carrion were placed in a temperate forest in the midwest United States for 5 days. Bacteria communities were sampled at initial field placement after one, three, and five days of decomposition using sterile swabs. Additionally, a human cadaver located at The Forensic Anthropology Center at Texas State (FACTS) was sampled daily from field placement until five days of decomposition. Total genomic DNA was extracted using a modified chloroform-phenol protocol and the bacterial community structure was determined by modified bacterial tagged-encoded FLX-amplicon pyrosequencing. Over the course of decomposition, *Proteobacteria* was the dominant phylum with *Firmicutes* being the next most abundant of the community for swine carcasses. Rare phyla accounted for less than 0.5% of the total relative abundance across decomposition. There was a significant negative linear relationship of phylum taxon richness over the course of decomposition. Similarly, in human cadavers, the most dominant phyla throughout decomposition were *Proteobacteria* and *Firmicutes*.

These data are important because of their implications in forensic ecology and PMI_{min} estimates. The results provide basic knowledge of how to use bacteria colonizing and utilizing carrion for forensic investigations and enhance the understanding of microbiological interactions occurring on the cadaver. Further, this work provides empirical data that may be useful to improve PMI_{min} estimations made by forensic practitioners and potentially increase the use of microbiological communities as evidence at crime scenes. Documenting and identifying differences in bacterial communities is key to advancing knowledge of the carrion necrobiome and its applicability in forensic science.

Microbiological Communities, Evidence Collection, Necrobiome

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