H101 Building a Microbial Model to Estimate the Postmortem Interval (PMI) Using Data Collected During the Spring Season at Three Anthropological Facilities

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Learning Overview: After attending this presentation, attendees will understand the changes to microbial community structure that occur after death in human cadavers and how this information can be applied to create predictive models estimating the PMI.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by proposing a novel tool for criminal investigation in cases of unattended death scenes in active and advanced decay.

PMI is crucial for criminal investigation. When known, this metric allows investigators to identify suspects and validate alibis. However, most tools designed for estimating PMI are no longer useful after 48 hours. In these cases of late discovery, the microbes associated with the remains may serve as physical evidence that can be used to estimate the PMI. The communities of microbes and their associated genes, known as the microbiome, have been shown to change in a repeatable manner on decomposing mammalian tissue, therefore providing a microbial clock that can capture the length of the decomposition period. The objectives of this experiment were to: (1) determine if the microbiome changes similarly in different geographic and environmental regions; and (2) use machine learning techniques to build a predictive model of PMI that can be used as a tool in forensic investigation.

Three anthropological research facilities, located in distinct geographic regions in the United States (Colorado Mesa University (CMU), Sam Houston State University (SHSU), University of Tennessee Knoxville (UTK)) were used for this study. Three donated human cadavers were placed at each facility (*n*=9) in the spring of 2016. Skin and soil swabs were collected daily from each body for 21 days of decomposition. DNA was extracted from these samples, and16S and 18S ribosomal RNA (rRNA) microbial gene amplicons sequenced. Data were then processed to evaluate changes in microbial diversity over time and between locations, and feature information was used to train machine learning models to predict PMI from microbial composition.

Each facility had a distinct microbial signature, primarily driven by the soil composition. As decomposition progressed, the soil came to cluster more closely with the skin samples, likely due to translocation from the cadaver to the soil. The primary phyla found at all sampling points was Proteobacteria, although the relative abundance of Firmicutes increased as decomposition progressed. The changes in microbial diversity and taxonomy that occurred over the 21-day decomposition period differed enough to be included in PMI modeling using machine learning. Overall, in a model built using data from all facilities, the microbiome data could be used to predict the PMI within 3-4 days. Prediction errors from models generated for each facility were similar, with samples predicting PMI within 2-4 days. Each model was also tested across facilities; models trained within a single facility were used to predict PMI at each of the other two facilities. On average, these cross-facility testing errors were within 4.5-6.5 days. The higher error is likely due to temperature ranges in testing sets that were beyond those in the training sets.

Overall, this study confirmed the concept proposed in previous research that the microbiome associated with decomposing mammalian tissue varies in a clock-like pattern. Furthermore, this was then applied to generate predictive models to estimate PMI. These models were accurate, and in future study can be improved by the addition of higher sample numbers and perhaps a longer sampling period. Future work will also include similar results from the summer, fall, and winter seasons to build a fully generalizable model.

Postmortem Interval, Microbiome, Machine Learning