



Pathology/Biology Section - 2016

H112 Cadaver Gravesoil Microbial Profiles During Decomposition

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After attending this presentation, attendees will understand how to use high-throughput next generation sequencing analysis to characterize microbial taxa present in gravesoil associated with human bodies decomposing in a natural setting. Specifically, attendees will learn methodologies to use microbial (Bacteria and Archaea) taxa relative abundances to determine predominant community shifts throughout decomposition time.

This presentation will impact the forensic science community by informing practitioners interested in using high-throughput next generation sequencing of the microbial communities found in gravesoils how to develop a framework for determining decomposition time.

The goals of this study were to identify microbial communities associated with cadaver gravesoil and to classify the fluxes in predominant microbes throughout decomposition time. Soil microbial communities associated with decomposition in a natural habitat were characterized using the 16S ribosomal RNA (rRNA) gene from multiple soil samples associated with 18 sets of decomposing human remains at various stages of decomposition. The gravesoil samples were obtained from bodies placed above ground or buried in shallow graves (approximately 45cm) in a natural setting at the Forensic Anthropology Research Facility (FARF) at the Forensic Anthropology Center at Texas State (FACTS) University in San Marcos, TX. The corpse placement/burial times ranged from a three-day placement on the soil to 303 days burial in the soil. Several within-community species diversity indices (i.e., Shannon-Weiner, Simpson, and Whitaker's beta) were evaluated based on the microbial community structure of the cadaver-soil microorganisms as a function of time on or in the soil.

The results of this study demonstrated that the microbial communities differed according to the time that a corpse was placed on or buried in the soil. For surface-placed cadavers, Shannon-Wiener diversity decreased approximately 32% over time, while Whitaker's beta diversity showed that microbes in the soil increased during the process of decomposition; however, the beta diversity of soil microbial communities associated with buried cadavers was U-shaped, suggesting a non-linear relationship with deep soil communities and decomposition. Soil samples collected above buried bodies had more similar community compositions irrespective to the decomposition time. The results also documented that Proteobacteria, Actinobacteria, and Acidobacteria were the most predominant phyla detected in all stages of decomposition in all samples — surface placed, buried, and control. There was also a substantial reduction in acidotrophic bacteria (Acidobacteria) and edaphic bacteria (Verrucomicrobia) over decomposition. These novel outcomes describe microbial compositions across all stages of decomposition and support recent studies advocating that the discovery of succession patterns in microbial communities may be crucial to the advancement of the knowledge of human decomposition with potential applications in the forensic sciences.

This study provides novel microbial metagenomic information that may have the potential to be used to estimate time of death in a natural environment. The study demonstrates a technique that will soon meet the demand for rapid and reproducible methods in investigative forensic science using state-of-the-art genomics techniques to monitor the microbial community signatures in gravesoil.

Microbial Diversity, Cadaver Soil, Next Generation Sequencing