



Physical Anthropology Section - 2013

H108 Microbial Community Change Associated With Decomposing Corpses

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After attending this presentation, attendees will understand the basics about microbiome research (study of the genes of microbes) and how recent advances in sequence technology have allowed microbial ecologists to characterize the vast, but measurable, microbial diversity present in animal hosts (e.g., humans) and environmental habitats (e.g., soil). Attendees will be presented with results from recent experiments in which microbial community change was assessed in and on corpses and in their associated gravesoil over the time course of decomposition.

This presentation will impact the forensic science community by revealing the potential of microbial succession during the decomposition process to help: (1) determine the time since death; and, (2) locate clandestine graves.

Biotic signatures of corpse decomposition, such as chemicals or the succession of insects, are commonly used to determine the postmortem interval and to detect gravesoil, but no method is successful in every scenario. Therefore, the development of new forensic tools is important. Microbes are ubiquitous in the environment and they play a key role in regulating the speed of decomposition. However, microbial communities are not currently utilized to their full potential as a forensic tool. Testing whether changes in microbial communities are predictable over the timeline of decomposition is crucial for assessing whether microbes can be used as a “clock” to assess time since death.

Powered by advances in culture-independent microbial community analysis methods and sequencing technologies, recent research has revealed that microbial communities are quantifiable and predictable across habitats such as human skin and soil. In the research presented here, a laboratory experiment was conducted to characterize temporal changes in the microbial communities associated with mouse corpses as they decomposed on soil at ambient temperature for more than a month. Samples from the abdominal cavity, skin, and gravesoil were collected at regular intervals from five corpses. Partial 16S and 18S ribosomal RNA genes were sequenced using Illumina HiSeq deep sequencing technology. Computational pipelines were used to characterize the succession of bacterial and eukaryotic communities during the decomposition process.

Microbial community change was significant and fairly consistent across replicates within each sample site (skin, abdominal, or soil) through the decomposition process. For each corpse-associated site, Proteobacteria increased over time, but most notably in the abdominal cavity—a site in which bacteria of the family Enterobacteriaceae dominated at late stages of decomposition. Furthermore, the decrease in abundance of genera such as Bacteroides and Lactobacillus in the abdominal cavity over time lends support to the long-held hypothesis that decomposition in the abdomen shifts from anaerobes to aerobes or facultative anaerobes after corpse rupture occurs. Importantly, the microbial diversity of gravesoil was significantly modified by corpse decomposition. Several genera from the families Enterobacteriaceae and Rhizobiaceae may be important indicators of gravesoil. Eukaryotic sequence data revealed that nematodes of the family Rhabditidae dominate the meiofauna of both the corpse and soil during late stages of decomposition. Nematodes of the family Rhabditidae may also serve as an indicator of gravesoil. Results demonstrate that microbial communities hold great promise as a forensic tool as there is a predictable succession over time and taxa are detected.

Microbiology, Decomposition, Ribosomal RNA Genes