



Pathology/Biology Section - 2014

G77 The Living Dead: An Investigation Into the Internal Microbiome of Human Decomposition

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The goal of this presentation is to demonstrate the unique biodiversity of the bacteria inhabiting corpses at the onset and the end of the bloat stage of decomposition. It will conclude by making comparisons between the internal microbiome and external microbiome of cadavers. It will also demonstrate how abiotic and biotic forces can be influential and can be assessed via remote sensing technologies such as Light Detection and Ranging (LiDAR).

This presentation will impact the forensic science community by progressing the field of forensics by presenting the first data set of bacteria associated with the bloat stage of decomposition. These data represent part of the initial effort to catalog the biodiversity of bacteria associated with decomposition and will add to emerging data sets which will eventually paint a larger picture of the utility of bacteria in forensic research.

Despite the integral role of bacteria in decomposition, few studies have catalogued internal bacterial biodiversity for terrestrial scenarios. To explore this biodiversity, two cadavers were placed at the Southeast Texas Applied Forensic Science (STAFS) facility and allowed to decompose under natural conditions. Each cadaver was sampled at two time points, at the onset and end of the bloat stage, from various body sites including internal locations. This study was conducted at the STAFS facility located at the Center for Biological Field Studies of Sam Houston State University. STAFS 2011-006 was sampled from September 8 to September 15, 2011, and STAFS 2011-016 was sampled from November 3 to November 17, 2011. Cadavers were Caucasian male, not autopsied, and determined to be in early stages of decomposition according to the Megyesi *et al.* Body scoring system.¹ They were placed supine without clothing. Bacteria were collected from 18 locations, three locations during pre-bloat time points (mouth swab, mouth scrape, and rectal scrape) and six locations during end-bloat points (mouth scrape, small intestine swab, transverse colon swab, sigmoidal colon swab, general body cavity swab, and stomach scrape). Several of the body sites sampled in this study have not previously been sampled from living human beings and are the first of their kind. Bacterial samples were analyzed by pyrosequencing of the 16S rRNA gene following protocols benchmarked as part of the Human Microbiome Project.^{2,3} 16S data was processed and analyzed using QIIME version 1.7.0.⁴ This data also show a shift from aerobic bacteria to anaerobic bacteria in all body sites sampled and demonstrate variation in community structure between bodies, between sample sites within a body, and between initial and end points of the bloat stage within a sample site. The microbiome richness varies widely across cadaver body sites with the most prevalent phyla being the *Firmicutes* and *Proteobacteria*. These data represent the initial cataloging of bacterial species associated with both the pre-bloat and end-bloat stages of human decomposition.

References:

1. Megyesi MS, Nawrocki SP, Haskell NH (2005) Using accumulated degree-day to estimate the postmortem interval from decomposed human remains. *J Forensic Sci* 50(3): 1-9
2. Consortium, T.H.M.P. (2012) A framework for human microbiome research. *Nature* 486(7402): 215-21.
3. Consortium, T.H.M.P. (2012) Structure, function and diversity of the healthy human microbiome. *Nature* 486(7402): 207-14.
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Bacteria, Cadaver, Bloat