H162 Understanding the Role of the Thanatomicrobiota in the Decay of “Reproductive Organs” in Human Decomposition

Gulnaz T. Javan, PhD, Alabama State University, Montgomery, AL 36104; Holly L. Lutz, University of Chicago, Chicago, IL 60637-1508; Sheree J. Finley, PhD, Alabama State University, Montgomery, AL 36104; Silvia D. Visona, MD, University of Pavia, Pavia 21100, ITALY; Antonio M.M. Osculati, MD, University of Pavia, Pavia 27100, ITALY; Jack A. Gilbert, PhD, University of California San Diego, La Jolla, CA 92093*

Learning Overview: After attending this presentation, attendees will understand how to use 16S ribosomal RNA (rRNA) amplicon sequencing analyses to characterize the thanatomicrobiota of reproductive organs from actual cadavers in criminal cases (e.g., homicide, suicide, and overdose). Specifically, attendees will learn methods to assess the microbial diversity after death using cases with Postmortem Intervals (PMIs) between 3.5 and 240 hours.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by revealing the specific bacterial signatures associated with the uterus and prostate of cadavers with different manners of death. These signatures could help to improve trace evidence regarding characteristics of manner of death for criminal cases.

Human organs decompose at different rates and in different ways. For example, human prostate glands and uteri are the last internal organs to deteriorate during putrefaction. However, the reason for this phenomenon has not been elucidated. To determine whether the bacteria associated with these organs differ from other organs, and to determine whether the taxonomic signature is associated with the PMI, this study applied 16S rRNA amplicon sequencing to tissues associated with 21 prostate glands and 13 uteri collected at autopsy from criminal casework cadavers. The 16S rRNA V4 region was amplified and sequenced from each sample, and non-parametric statistics were used to determine the resulting microbiota profile and its association with cadaver characteristics. Both the uterus and prostate had a significantly greater alpha diversity compared to other organs, as well as maintaining a significantly different microbial composition (beta diversity) as determined by unweighted UniFrac. The prostate was significantly enriched for two 16S rRNA Absolute Sequence Variants (ASVs) associated with the Bacteroidia, one in the family Comamonadaceae (genus *Limnohabitans*) and another in the family Oxalobacteraceae. Uterine tissues were enriched for only two ASVs, including a single ASV in the class Bacilli (family Lactobacillaceae, genus *Lactobacillus*) and a single ASV in the class Gammaproteobacteria (family Enterobacteriaceae, unknown genus). Prostate tissues had a significant underrepresentation of 4C0d-2 ASV (order MLE1-12) and a single Clostridia ASV (family Lachnospiraceae, unknown genus). It is possible that these organisms may associate with differential decay rates. Natural deaths were enriched for class 4C0d-2 (order MLE1-12) and ASVs in the classes Bacilli (family Lactobacillaceae, *Lactobacillus zeae*), Gammaproteobacteria (family Enterobacteriaceae, unknown genus), and Saprospirae (family Chitinophagaceae, genus *Sediminibacterium*). Among victims of accidental death, a single Bacilli ASV (order Lactobacillales, unknown family) and Gammaproteobacteria (family Enterobacteriaceae, unknown genus) were enriched. Homicide victims did not exhibit enrichment of any bacterial taxa. Currently, none of these signals was a significant predictor of manner of death.

Thanatomicrobiota, Reproductive Organs, 16S rRNA

---

*Presenting Author