H96 Internal Microbial Community Translocation Throughout Decomposition in a Controlled Vertebrate Model

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After attending this presentation, attendees will understand the fundamentals of microorganisms associated with decomposition of a vertebrate carcass, the benefit of studying decomposition in a sterile environment, and the microbial community changes in organs during the first seven days after death.

This presentation will impact the forensic community by providing some of the first data to characterize and document the pathways (translocation) of microbially mediated decomposition by commensal microbes without the influence of external environmental microorganisms in a model organism. This baseline is essential to being able to build on the current microbial forensics knowledge for potential estimation of the Postmortem Interval (PMI) range.

Decomposition begins immediately after death and is driven by two forces: autolysis and putrefaction. Putrefaction is the breakdown of the host tissue by microorganisms present in the interior and on the exterior surfaces of the host. These microorganisms may be part of the host's natural microbiota or may be introduced by the environment or manner of death. Although recent studies have detected changes in host-associated microbial communities and show distinct successional patterns during the decomposition process, these studies have included the influence of the environmental microbes present. This presentation describes how the microbiota of a living host changed and translocated within a body after death in a murine model during decomposition in a sterile environment to gain a better understanding of microbial activity solely dependent on the host microbiota after death. This baseline activity can then be built upon with the addition of the variables involved with individuals and multiple manners of death to provide insight on the impacts of these variables to the microbial communities and their relation to a PMI estimate.

This study investigated the postmortem microbial community structure in a murine model that was handled aseptically and allowed to decompose in individual sterile containers allowing only 0.2µm of filtered air to come in contact with the carcass. Immediately after sacrifice, a subset of mice was surface sterilized using a bleach solution to determine the impact of the external microbial communities throughout decomposition process. The mice were dissected at five discrete timepoints (1h, 3h, 5h, 24h, and 7d postmortem) to extract DNA from lung, intestine, heart, and bone marrow organ tissues in preparation for creating high-throughput sequencing libraries for whole genome shotgun sequencing. The 16S rRNA data was analyzed for community structure during the PMI to determine the baseline host microbiota communities associated with decomposition. Results indicate an increase in the relative abundance of *Lactobacillus*, *Clostridium*, and *Staphylococcus* as decomposition progresses through the first seven days. These methods provide original data to uncover how commensal bacterial populations translocate, colonize, and proliferate following death of a host organism, and how successional decomposition of the associated host has the potential be used to estimate the PMI range.

Microbial Translocation, Decomposition, Postmortem Interval