H131 Analyses of Necrobiome Structure and Function for Utility in Forensic Science

Heather R. Jordan, PhD, Mississippi State University, PO Box GY, Mississippi State, MS 39762; Zachary M. Burcham, BS, Mississippi State University, 75 B S Hood Road, Mississippi State University, MS 39762; Jeffrey L. Bose, PhD, University of Kansas Medical Center, 4003 Wahl Hall, W, Kansas City, KS 66160; Jennifer L. Pechal, PhD, Michigan State University, 243 Natural Science Bldg, Dept of Entomology, East Lansing, MI 48824; Jason Rosch, PhD, 262 Danny Thomas Place, Memphis, TN 38105; Carl J. Schmidt, MD, Wayne County MEO, 1300 Warren, Detroit, MI 48207; and M. Eric Benbow, PhD, Michigan State University, Depts of Entomology & Osteopathic Med Specialties, 288 Farm Lane, East Lansing, MI 48824*

After attending this presentation, attendees will have a better understanding of how host-associated microbial communities respond following host death.

This presentation will impact the forensic science community by discussing the ways in which the methods outlined and data obtained determine how commensal bacterial populations in host remains translocate, proliferate, and modulate gene expression following death. These data may allow identification of specific microbial taxa or proteins for the potential use in quantifiable measurements of Postmortem Interval (PMI) used in forensic science.

Estimating minimum PMI relies on multiple factors, such as detecting chemical signatures and measuring insect colonization, but a widely used method relies on assessing physical changes a body undergoes during decomposition: fresh (including pallor, algor, rigor, and livor mortis), bloat, active decay, and dry decomposition. Few studies have focused on the dynamics of existing microbial communities located internally and externally of a living individual prior to death, such as in or on the gastrointestinal tract or skin. These microbial communities thrive by utilizing nutrients and surface areas provided by the host, but are usually kept to a specific niche (e.g., stomach, liver) by the host's immune system. Host death renders the immune response relatively inactive, and within 24 hours, bacteria proliferate and translocate to previously sterile spaces inside the body. Determining postmortem microbial community responses to decomposition may prove useful in determining colonization routes correlating to the PMI estimate.

Using a mouse model, this study investigated the postmortem microbial community structure, translocation, and gene expression of the bacterial species present in a controlled setting, minimizing outside microbial influence, focusing only on host-associated bacteria. Immunocompetent mice (n=60) were inoculated intranasally with commensals, *Staphylococcus aureus*-RFP and *Clostridium perfringens*, to introduce controlled aerobic and anaerobic communities, respectively, with the ability to degrade host tissue through protease production. Thirty inoculated mice were immediately surface sterilized with a 10% bleach solution following sacrifice to disrupt the influence of external microbiota. DNA and RNA were isolated and purified from heart, lung, intestine, and bone marrow samples one hour to seven days postmortem, for use in quantitative Polymerase Chain Reaction (qPCR), real-time qPCR, and meta-transcriptomic sequencing. Results of qPCR targeting *S. aureus*-RFP revealed transmigration into many of the tissues in as early as one hour, including previously sterile spaces, such as bone marrow. Additionally, ongoing gene expression analyses show differential expression relative to organ and PMI. Altogether, these early results suggest the bacterial translocation and expression demonstrate promise to be sufficiently predictable for utility in forensic science and the criminal justice system.

Necrobiome, Microbial Community, Gene Expression