## H59 Fluorescent Bacteria in the Gut of Mice Carcasses Provides Insight on Postmortem Microbial Translocation

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After attending this presentation, attendees will better understand how host commensal microorganisms transmigrate and thrive immediately following the death and decomposition of the host. In addition, these microbial communities possess investigative potential during the discovery of remains in determining the postmortem interval.

This presentation will impact the forensic science community by providing original data that investigates how commensal bacterial populations transmigrate, colonize, and proliferate following death and the successional decomposition of the associated host. Data obtained will significantly further knowledge of how genetically marked commensal bacteria in the gut transmigrate through their host as decomposition progresses.

Microorganisms play a vital role in the decomposition of remains. Bacteria, archaea, and eukaryotes begin competing against each other to break down and utilize highly nutritious tissues. Organisms able to withstand the changing environment and equipped with proteins that allow more efficient tissue destruction and cell motility have a competitive advantage. Recent work has shown that these bacterial communities are dynamic during decomposition, leading to questions of their utility for either taxonomic or metabolic markers to the postmortem interval. This presentation describes how two genetically labelled communities of *Staphylococcus aureus*-RFP and *Clostridium perfringens*-pZMB2 were orally introduced to a mouse model for colonization of the gut in a living host and subsequently tracked as they migrated through the carcass during decomposition. Aerobic and anaerobic bacteria were monitored in each organ by plate counts, and genetically labelled organisms were tracked using Real-Time quantitative Polymerase Chain Reaction (RT-qPCR). *S. aureus*-RFP was able to be detected by fluorescent imaging *in vivo* to determine colonization routes associated with different physiological events of host decomposition. Mice were dissected and organs harvested at timepoints starting at 1 hour and up 30 days after death. The organs were swabbed for plating, then preserved for total RNA extraction. The total RNA was used for RT-qPCR to identify the inoculated *C. perfringens* and *S. aureus* loads in each organ at each timepoint. These methods provide original data to uncover how commensal bacterial populations transmigrate, colonize, and proliferate across multiple organs following death and the successional decomposition of the associated host. Data obtained significantly furthers investigations identifying microbial behavior during decomposition that may be unique to the postmortem interval to allow for measurements of the time of death used in forensic investigations.

**Microbial Transmigration, Decomposition, Postmortem Interval**



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