A118 Using Microbial Clocks in Human Cadaver Ribs as a Postmortem Tool

Jessica L. Metcalf, PhD, N122 Ramaley Biology, UCB 334, Boulder, CO 80309; Aaron M. Lynne, PhD, 1900 Avenue I, Box 2116, LDB #300, Huntsville, TX 77341; and Jennifer R. Kiely, BS, PO Box 1493, Willis, TX 77378*

After attending this presentation, attendees will have a basic knowledge of the microbiome (study of the genes of microbes) and its application in human decomposition studies. Attendees will be presented with the results of a pilot study, which sought to investigate the bacterial succession in human cadaver ribs during the advanced stages of decomposition.

This presentation will impact the forensic science community by exploring an area with little to no previous research. This pilot study reveals the changes seen in the bacterial communities of cadaver rib marrow, over time, during the later, drier stages of decomposition and its potential usefulness as a Postmortem Interval (PMI) tool.

Determining the PMI is an important aspect of forensic investigations, but accuracy in predicting the interval declines with time. Microbes are important players in the human decomposition process and have been studied on cadaver skin and gravesoil samples during the early, wet decay stages as a potential PMI "clock."[1-5] Bacterial succession on decomposing skin shows promising results, but it becomes less accurate as desiccation occurs and decomposition approaches the skeletonization stage.[1,2] This pilot study investigates the bacterial communities inside the human cadaver rib during the advanced decay stage and into skeletonization.

Twenty-four ribs were excised from three cadavers at the Southeast Texas Applied Forensic Science facility in Huntsville, TX. One rib was sampled from each cadaver every three weeks over a six-month period during the later decay stages (beginning May 2016), representing ~5,000 Accumulated Degree Days (ADD). DNA extracted from the rib samples was sequenced using the MiSeq® Illumina® platform, targeting the 16S recombinant DNA (rRNA) gene region.

Results indicate that bacterial communities shift in community membership with advancing time, with the biggest trend occurring between the first and last sampling periods (advanced decomposition stage and skeletonization stage, respectively). Statistics demonstrate a significant difference in the phylogenetic distance between these samples (first and last). Community composition, more than abundance, may play a role when determining a PMI. Similarly, rarefaction curves trend toward an increase in richness with increasing ADDs, although there were no significant differences found in diversity between samples; however, due to the study's small sample size and unique nature of cadaver research, only generalizations about the microbiome of cadaver bone can be made. A reliable PMI method cannot be formulated from this study at this time, but the results suggest that there is a trend in bacterial succession that could be useful and warrants further investigation.

Reference(s):

1. Hyde E.R., Haarmann D.P., Lynne A.M., Bucheli S.R., Petrosino J.F. The living dead: Bacterial community structure of a cadaver at the onset and end of the bloat stage of decomposition. *PLOS One.* 2013;8(10):e77733.
2. Hyde E.R., Haarmann D.P., Petrosino J.F., Lynne A.M., Bucheli S.R. Initial insights into bacterial succession during human decomposition. *International Journal of Legal Medicine.* 2015;129(3):661-71.
3. Cobaugh K.L., Schaeffer S.M., DeBruyn J.M. Functional and structural succession of soil microbial communities below decomposing human cadavers. *PLOS One.* 2015;10(6):e0130201.
4. Finley S.J., Benbow M.E., Javan G.T. Microbial communities associated with human decomposition and their potential use as postmortem clocks. *International Journal of Legal Medicine*. 2015;129(3):623-32.
5. Metcalf J.L., Xu Z.Z., Weiss S., Lax S., Van Treuren W., Hyde E.R., et al. Microbial community assembly and metabolic function during mammalian corpse decomposition. *Science.* 2016;351(6269):158-62.

Decomposition, Microbiology, Bone

*Presenting Author