



Pathology/Biology Section - 2014

G73 An Initial Assessment of the Structure and Function of the Postmortem Human Microbiome: Forensic Applications

M. Eric Benbow, PhD*, Department of Biology, 300 College Park, Dayton, OH 45469-2320; Jennifer Pechal, PhD, Michigan State University, 293 Farm Lane Road, Room 324, East Lansing, MI 48824; Baneshwar Singh, PhD, Virginia Commonwealth University, Dept of Forensic Science, 1015 Floyd Avenue, Rm 2015, Richmond, VA 23284; Jeffery K. Tomberlin, PhD, TAMU 2475, Dept of Entomology, College Station, TX 77843-2475; Aaron M. Tarone, PhD, Department of Entomology, College Station, TX 77843; Maureen Burke, MS, Texas State University, College of Health Professions, San Marcos, TX; Rodney Rohde, PhD, TSU, College of Health Prof, Clinical Lab Science, HPB 363, 601 University Drive, San Marcos, TX 78666; and Tawni L. Crippen, PhD, Agricultural Research Service, U.S. Dept of Agriculture, College Station, TX 77845

After attending this presentation, attendees will have a greater appreciation and understanding of the bacterial communities associated with human remains and how this information has the potential to be used to make estimates of a minimum Postmortem Interval (PMI_{min}).

This presentation will impact the forensic science community by providing results of some of the first data on bacterial communities associated with human remains, their postmortem community changes, and variation in such changes among epinecrotic communities taken from different areas of a decomposing body.

There are several methods for using biological information in PMI_{min} estimates; however, bacterial assemblages have only recently been investigated for such purposes.¹ With the development and refinement of high-throughput metagenomic sequencing and cost-effective metabolic assay methods, the potential of using data on bacterial succession on human remains for PMI_{min} estimates is quickly becoming a reality.

Epinecrotic communities have been defined as the microbial (i.e., bacteria and fungi) consortia that develop biofilms on the surfaces (external and internal) of decaying organic matter, including animal carrion and human remains.¹ These communities provide the foundation of the necrobiome foodweb and have been reported to affect blow fly attraction to decomposing remains.²

In order to effectively use such information, a better understanding of the postmortem human epinecrotic microbial community, or the microbiome, will be important for developing models to estimate or predict the PMI_{min}. These communities are known to go through a series of taxon replacement over time, much like plant ecological succession or the succession of insect taxon on decomposing remains, a foundation of forensic entomology. Much like insect succession information that is used in forensic entomology to make estimates of the PMI_{min}, recent studies using swine carcasses have demonstrated that postmortem epinecrotic communities show strong promise for use in forensics. This presentation provides some of the first data on the human postmortem epinecrotic communities, demonstrating the potential for using either the taxonomic structure or metabolic functional descriptions of these communities in estimating the PMI_{min}.

This study evaluates the structure (taxonomic) and function (metabolic profiles) of the postmortem human epinecrotic communities in a series of on-going studies in Texas and briefly discusses how this information can potentially be used in PMI_{min} estimates. A structure/function approach is taken to describe these communities from the skin, buccal, and anal epinecrotic communities. The taxonomic structure of these communities was described using pyrosequencing methods given in an earlier study by a collaborative research group.¹ Metabolic profiles were described using Biolog EcoPlates™ based on methods described by Garland.³

It was found that there were significant taxonomic changes in the postmortem human epinecrotic communities throughout decomposition among sampling days and between sampling areas, but there was no interaction effect. The communities were dominated by the following phyla: *Proteobacteria*, *Actinobacter*, *Firmicutes*, and *Bacteroidetes*. There was an inverse relationship between the relative abundance of *Proteobacteria* and *Firmicutes*, with the latter representing on average 44% of the total community early in decomposition and changing to 13% later in decomposition. There were similar trends in phylum changes over decomposition for each sampling area. However, the epinecrotic community metabolic profiles were not significantly different among sampling days, among sampling areas of the body, and there was not an interaction effect.

These data are an important contribution to the growing understanding of the human microbiome and how these communities can be used postmortem in a forensic context, and demonstrate the potential of using both the taxonomic and functional profiles of epinecrotic communities in estimating the PMI_{min}.



Pathology/Biology Section - 2014

Additional research in this area could lead to a greater understanding of the time interval from death to human remains discovery.

References:

1. Pechal, JL, Crippen, TL, Benbow, ME, Tarone, AM, Tomberlin, JK. The potential use of bacterial community succession in forensics as described by high throughput metagenomic sequencing. *Int J Legal Med*, DOI 10.1007/s00414-00013-00872-00411 (2013).
 2. Ma, Q, Fonseca, A, Liu, W, Fields, AT, Pimsler, ML, Spindola, AF, Tarone, AM, Crippen, TL, Tomberlin, JK, Wood, TK. *Proteus mirabilis* interkingdom swarming signals attract blow flies. *ISME J*, doi:<http://www.nature.com/ismej/journal/vaop/ncurrent/supinfo/ismej2011210s1.html> (2012).
 3. Garland, JL. Analysis and interpretation of community-level physiological profiles in microbial ecology. *FEMS Microbiology Ecology* 24, 289-300 (1997).
-

Microbiome, Microbial Succession, Bacteria