## H126 Life After Human Death: The Thanatomicrobiome

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After attending this presentation, attendees will understand the meaning of the word "thantomicrobiome" and the new field of study of which little is known.

This presentation will impact the forensic science community by increasing understanding of the microbiology of decaying human bodies and provide additional information to those who are interested in a new possible way to determine Postmortem Interval (PMI) based on the human microbiome.

A paradigm shift in our understanding of cells in the human body has occurred as a result of human microbiome studies. Consider this: before birth, all cells in a baby's body are human. This is the only stage of development that humans are essentially "microbial-cell free." When a baby passes through the uterus, consumes food, and interacts with other humans and the environment, it becomes inoculated with microbes that live and thrive in its body. One of the truly amazing findings of the human microbiome studies is that, in adulthood, most cells in a human body are not human at all—rather, 90% are microbes. This means that microbes are very much a part of "us" and implies that they play important roles in both our health and disease. Given these facts, the study postulated the role of the microbiome after a human dies. To date, all human microbiome studies have focused on the microbes of living beings. Amazingly, almost nothing is known about the composition and abundance of the human microbiome after death. Here are the sparse details we do know: (1) microbial cells proliferate in the body after death because the immune system ceases to function and there is a massive release of nutrients from human cells that lose membrane integrity; (2) the microbial proliferation is time/temperature-dependent, and begins at the ileocecal area, spreads to the spleen and liver, and eventually the heart and brain; and, (3) microbes colonize the ileocecal area by invading capillaries of the lymphatic and vascular systems and, in the case of the respiratory system, by invading the mucus membranes.

Based on this information, the following working hypothesis was formulated: the composition and abundance of microbes in the human thanatomicrobiome (i.e., *death*-microbiome) varies by organ and changes as a function of time and temperature. This hypothesis is relevant to the determination of PMI because the abundance of certain microbes in different organs could be indicative of the elapse time since death. This hypothesis is also relevant to human evolution studies because, just as microbes have evolved in human development, it is likely that they have evolved with us in human death. To test the hypothesis, the thanatomicrobiome in blood, liver, spleen, heart and brain samples of human cadavers having a range of known PMIs was surveyed. Surveying the thanatomicrobiome was accomplished by extracting DNA from the organs, amplifying the 16S ribosomal RNA genes, and sequencing the genes on a 454 pyrosequencer. The obtained sequences were uploaded to MG-RAST for annotation and determination of the microbial abundances at different levels of taxonomic resolution. Because the PMI and temperature conditions for each cadaver are known, the thanatomicrobiome in different organs will be determined and related to the time of death. It is thought that this is the first study of the human thanatomicrobiome to use DNA sequencing technology.

**Thantomicrobiome, Postmortem Interval, DNA Sequencing**

 ** Presenting Author*