



H56 A Comparison of the Geographical Variability of the Thanatomicrobiome of Finnish and American Corpses

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After attending this presentation, attendees will better understand the comparison of the 30S small subunit of the prokaryotic ribosome-based sequencing to characterize the thanatomicrobiome of postmortem liver from corpses derived from different geographical locations, namely the United States and Finland.

This presentation will impact the forensic science community by providing results to support the Human Postmortem Microbiome Project (HPMP) catalog. This presentation will also add to research in regard to distinct geographical locations in which corpses originate.

Human thanatomicrobiome studies have shown that microorganisms inhabit and proliferate externally and internally throughout the body and are the primary mediators of putrefaction after death. Yet little is known about the source and diversity of the thanatomicrobiome in regard to geographical factors in which corpses are found. Prokaryotic 16S ribosomal RNA (rRNA) gene sequences are extensively used in forensic microbiology as reliable biomarkers for the taxonomic classification and phylogenetic analysis of the thanatomicrobiome. Upon death, all immune mechanisms in the human body that were operational during life cease, and commensal bacteria start to degrade the body as a part of the natural calendar of death. Presumably, the postmortem microbial composition dynamics of internal organs (e.g., liver) are distinct due to geographical variabilities. The richness of postmortem bacterial abundances in the liver is due, in part, to several factors: its location juxtaposed to the microbe-rich intestinal tract; its location near pancreatic enzymes, stomach acids, and gallbladder fluids that initiate putrefaction through autolysis that spreads quickly to the liver; and its reservation of nutrient-rich blood from the portal vein and hepatic artery that are excellent growth media for bacteria.

This study investigated the microorganisms obtained from the liver of corpses from Finland and the United States. The thanatos model assessed liver samples from 65 human remains from the two countries ($n=130$) with postmortem intervals ranging from 3 hours to 264 hours. To distinguish the composition and diversity of thanatomicrobiomic signatures, Polymerase Chain Reaction (PCR) and high-throughput sequencing targeting the V4 region (Class I) of the 16S rRNA gene using bacterial primers 515F-806R was performed. The bioinformatic results revealed that there were significant differences ($p<0.001$) among location (Finland versus the United States) and postmortem interval in unweighted and weighted UniFrac Adonis tests. Also, recent thanatomicrobiome findings for United States cadavers discovered that a majority of the microorganisms in the human body after death were the obligate anaerobes, *Clostridium* spp. On the contrary, in the current study, there was a paucity of *Clostridium* spp. in the Finland corpses.

In conclusion, the influence of different geographic locations in determining the distinct microbial community profiles to provide empirical data that will potentially build predictive thanatos models that can further designate the recovery of bodies from discrete locations was demonstrated.

Thanatomicrobiome, Corpse, 16S rRNA