H128 Do Postmortem Skin Microbial Communities Change During Morgue Transit and Cooler Storage?

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After attending this presentation, attendees will understand the impact of morgue storage and handling of a decedent on postmortem skin microbial communities.

This presentation will impact the forensic science community by identifying an optimal timeframe during which to collect microbial evidence from skin.

Microbial communities change throughout the decomposition process. Because these changes are predictable, microbial communities have the potential to be used to estimate Postmortem Interval (PMI); however, there are many factors affecting microorganisms that must still be researched, including cause of death, antibiotic/drug use, environment, and others. One unexplored variable that is relevant to most death investigations is the storage and handling of the decedent prior to autopsy. This process includes transport to the morgue, general intake procedures, and cooler storage leading up to autopsy.

It is important to learn how morgue storage and handling of the decedent prior to autopsy affects skin microbial communities because it could affect the estimation of PMI and also the potential use of microbes as trace evidence. Individual skin microbial communities are personalized and relatively stable over time. The forensic value of these communities is that they are transferred to locations and objects with which a person interacts/contacts. Therefore, individuals can be associated with objects and locations. Establishing a timeline of skin microbial community change, if there is any, during morgue transit and cooler storage can provide valuable information to a death investigation because it has the potential to provide an optimal timeframe during which to collect microbial evidence from the skin of the deceased. Furthermore, skin microbial communities can corroborate other forms of trace evidence and fingerprint analysis and also have the potential to provide a positive identification when traditional forms of evidence are either unavailable or provide insufficient information.

To investigate the effect of storage and handling on the skin microbial community after death, ten death scenes under the jurisdiction of the City and County of Honolulu Department of the Medical Examiner were attended. Both hands of the deceased were swabbed upon arrival. Objects (e.g., door knobs, light switches, phones) that the deceased commonly touched were also swabbed. Once at the morgue, both hands were swabbed at six-hour intervals until an autopsy was conducted or the body was released following external examination. To establish the microbiome of the morgue environment, samples were also collected from transport surfaces, the inside of new and used body bags, morgue cooler surfaces, and the autopsy room surfaces.

All swabs were stored at -20°C until analysis. DNA was extracted from the swabs using the PowerSoil® DNA isolation kit and stored at -20°C. 16S small subunit ribosomal RNA (rRNA) genes were used to characterize bacterial communities. Polymerase Chain Reaction (PCR) amplicons were combined from each sample and sequenced on the Illumina® HiSeq™ 2500 platform. Sequence data were processed and analyzed using the bioinformatics pipeline available in the Quantitative Insights into Microbial Ecology (QIIME) open-source software. Resulting sequences were filtered to remove low-quality sequences, classified into Operational Taxonomic Units (OUT) and identified to known taxonomy through the Greengenes reference database. QIIME and the phylogenetic metric UniFrac were used to estimate alpha diversity and beta diversity. Supervised learning and Bayesian source-tracking methods were used to estimate the ability to accurately link microbial samples with a deceased person.

These data were used to test this study's null hypothesis that skin microbial communities will not change during storage and handling of the deceased. Results will be presented.

Taphonomy, Bacteria, Microbiome

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