H8 A Preliminary Study of Shifting Bacterial Communities of the Face During Human Cadaver Decomposition in Southeast Texas

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After attending this presentation, attendees will better understand fine-scale variations of population structures of the microbiome related to human decomposition.

This presentation will impact the forensic science community by providing standardization of sampling methods using in forensic research studies for the future application of estimating the postmortem interval. The presented data can help validate similar studies as well as fine-tune protocols currently used in related research.

Human decomposition is a process marked by events categorized into five stages. These stages occur as a fluid procession rather than through precise demarcation of events and may lead to cadavers experiencing multiple stages of decomposition at once. Previous studies have investigated biodiversity of necrophagous bacteria and insects at predefined stages of decomposition with a focus on taphonomy. One area yet to be explored is fine-scale temporal and spatial influence on these findings. The pilot studies and early data have shown that there are shifts in the microbiome present on the skin of human cadavers, which also follow the shifts in stages of decomposition.

As part of a separate ongoing study, two human cadavers were placed outdoors at the Southeast Texas Applied Forensic Science (STAFS) facility in Huntsville, TX, on July 31, 2013. The face of each cadaver was divided into a grid to be sampled to ascertain the spatial and temporal influence that fine-scale sampling can have on bacterial community structures. These cadavers were sampled at 18 locations on the face every six hours over the course of four days. The samples were subject to 16S rRNA gene sequencing using the Illumina® platform, then analyzed using the Quantitative Insights Into Microbial Ecology (QIIME) software. Results from the fine-scale study follow different initial trends but mirror trends that have been observed during the larger scale analyses. Cadaver STAFS 2012.035 follows the trend of human-associated bacteria (*Staphylococcus* and *Pseudomonas*) shifting to insect-associated bacteria (*Ignatzschineria* and *Wohlfhartiimonas*) that then shifts to soil-associated bacteria (*Sporosarcinia*). Cadaver STAFS 2013.026 follows a similar trend with a surprising interval of *Clostridium* dominating the sample set between the initial samples and the time when insect-associated bacteria is dominant in the samples.

While these two cadavers do not follow the same trend of shifting bacterial communities, the data helps to bring insight into the overall goal of understanding bacterial succession during human decomposition. Over the course of a single day, these data show that time of day likely plays a factor in the bacterial community composition in a sample. Between sample locations, there is also indication of differences in bacterial communities. The significance of these differences will determine future sampling techniques as well as help standardize the way in which the microbiome of human decomposition is studied and used as a predictive model for estimating the time since death. The overall goal of studying the microbiome of human decomposition is to provide another tool for estimating the postmortem interval for forensic applications and investigations.

Human Decomposition, Microbiome, Postmortem Interval

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