H126 Drugs and Bugs (Bacteria): Does What You Use Relate to What You Grow?

Jennifer L. Pechal, PhD, Michigan State University, 243 Natural Science Bldg, East Lansing, MI 48824; Carl J. Schmidt, MD, Wayne County MEO, 1300 Warren, Detroit, MI 48207; Heather R. Jordan, PhD, Mississippi State University, PO Box GY, Mississippi State, MS 39762; and M. Eric Benbow, PhD, Michigan State University, Depts of Entomology & Osteopathic Med Specialties, 288 Farm Lane, East Lansing, MI 48824*

After attending this presentation, attendees will understand how drug use impacts the human postmortem microbiome. While several studies have documented shifts in microbial community composition and abundance from various locations on a body during the decomposition process, much less is understood about how the postmortem microbiome varies among groups of individuals that have a history of substance use/abuse or whose death results from it. This presentation will include data from the largest set of postmortem microbiome human remains, which have been swabbed from six locations on each body, providing insight into how drug use, such as hydrocodone, cocaine, opiates, or heroin, may potentially be associated with the postmortem microbiome and perhaps be an indicator of antemortem interactions of the microbiome and lifestyle.

This presentation will impact the forensic science community by providing the only database to date of the human postmortem microbial communities found on human cadavers resulting from drug-related deaths. Researchers have typically focused on the potential effects of drugs on the microbiome of living individuals in pharmaceutical development for personalized health care or the impacts of illicit drug use on perinatal health and mortality; however, there has yet to be a study characterizing the postmortem microbial communities of individuals with substance abuse. This presentation will add to the research targeted on identifying microbial communities after death and provide real-world data for advancing the field of forensic microbiology with the ultimate goal of increasing the potential to routinely use microbial communities in death investigations.

Microorganisms are ubiquitous in the environment and associated with humans both antemortem and postmortem, but are often overlooked and underutilized biological indicators of circumstances and length of time since death. Due to the ability to culture only a small subset of currently known microbes (e.g., pathogenic bacteria), they have received little research attention for their potential use in forensic sciences. There is a paucity of data available describing the postmortem microbiology and microorganism biodiversity occurring on human cadavers, particularly on the naturally occurring variation of indigenous microflora residing on or in the human body during decomposition; however, recent work studying decomposition of model organisms (e.g., swine and mouse carcasses) suggests that microbial communities are quite dynamic during the postmortem interval. The goal of this study was to describe the human postmortem human microbiome associated with individuals in a major metropolitan city (Detroit, MI) whose deaths resulted from a variety of drug usages.

Microbial samples were collected from human remains received into the Wayne County Medical Examiner's Office in Detroit, MI. Samples were collected from 40 human cadavers (male and female) representing different causes of death (e.g., drug type). DNA-free (sterile) cotton-tipped swabs were used to aseptically collect individual microbial communities from six anatomic locations: the external auditory canal, nose, mouth, umbilicus, rectum, and the trabecular space between the inner and outer tables of the occipital bone. DNA was extracted using a modified protocol of a commercially available kit; all DNA was quantified to ensure quality samples for metagenomic sequencing. The 16S ribosomal RNA (rRNA) V4 gene region was sequenced for each sample using a 2x250bp paired-end approach using a high-throughput metagenomic sequencing platform. The microbial community composition of cadavers resulting from drug use was statistically significantly different ($P < 0.05$) from those microbial communities detected on individuals that died from natural disease (cardiovascular in origin). Additionally, there were distinct microbial communities among the sets of remains that varied based on sex and anatomic region from which the sample was obtained; however, the differences of microbe communities were not as distinct among comparisons of the various types of drugs present in the individual. Overall, these data demonstrate that the postmortem human microbiome is different in deaths due to drug use, although how drug use affects the living microbiome is also unknown at this time and may affect the resulting postmortem microbiome.

*Presenting Author

In conclusion, this study contributes a unique data set to previous research of the postmortem microbiome; specifically, partnering with a medical examiner's office allowed the opportunity to characterize microbial communities associated with deaths due to drug use. These data provide striking evidence that drug use influences the postmortem microbial community of an individual, and future work with additional partnerships with medical examiners' offices should be considered to expand upon the current data set. It also suggests that the microbiome in the living may be different in drug users compared to the rest of the population: such a relationship could prove valuable in future forensic contexts.

Postmortem Microbiome, Drug Use, Medical Examiners