Evaluating Bacterial Succession and its Influence on Decomposition

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Forensic Science

Physical Poster

Investigative

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Abstract

In recent years, forensic biology has revolutionized the field of criminal justice, from the application of entomology to DNA analysis. However, while these specializations have been standardized, relatively little research has been conducted to understand the application of microbiology to crime scene investigations. To this end, this project investigated the succession of bacterial communities on pig cadavers over 24-hour increments for the course of 7 days. Initially, two pig cadavers were placed in separate cages to decompose under natural conditions. Samples were collected by swabbing the pigs' mouths, ears, cheeks, noses, and genitalia, and the swabs were placed in separate paper wrappings for subsequent laboratory analysis. The bacteria which was collected from the various anatomical sites were isolated on R2A medium and qualitatively and quantitatively analyzed prior to identification via 16S ribosomal RNA (16S rRNA) sequencing. During preliminary research, several different phyla were identified initially (Time 0) which consisted of many genera commonly associated with the human microbiome. During the 7-day timeframe, data shows that several microbial families and genera increased in numbers while many other microbial species' presence diminished, suggesting a pattern which

may exist during the decomposition process between those 24-hour intervals. Such information may have great implications for crime scene investigations especially concerning the determination of a post-mortem interval (PMI).