G76 Swine as a Model for Decomposition: A Comparison of Postmortem Microbiomes

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After attending this presentation, attendees will have a better understanding of the similarities and differences in microbiomes associated with swine and human remains. Swine (*Sus scrofa L.*) are often used as a model for humans in forensic research.

This presentation will impact the forensic science community by determining if vertebrates of different species represent feasible models for human microbial decomposition research.

It is known that microbes are important to the decomposition process and that significant temporal changes in the bacterial community structure occur on carcasses in both terrestrial and aquatic environments.[1-3] In this study, human and pig cadavers were sampled daily for five days under identical conditions after placement in the savannah terrain of the Edwards Plateau of Texas (TX-humans and TX-swine). In addition, a comparison to swine decomposition (OH-swine) in the temperate forest of Ohio was considered, where bacteria communities were sampled at 0, 1, 3, and 5 days of decomposition. Sterile cotton swabs were used for sample collection from buccal and skin regions. DNA was obtained from these samples using an organic extraction method. Bacterial variable regions (V1-V3) of the 16S rRNA gene were targeted for amplification using primer pairs 28F and 519R.[4] The bacterial community structure was determined by modified bacterial tag-encoded FLX amplicon pyrosequencing.[5] Resulting sequences were processed using Mothur v. 1.29.[6]

There were bacterial genera common to both species, but there were also substantial differences in community structure. In the first study, only 13% of the bacteria were shared between both species and both ecoregions. These primarily included the genera *Corynebacterium*, *Ignatzschineria*, *Staphylococcus*, and *Acinetobacter*. Additionally, 21%, 10%, and 3% of bacteria were shared by TX-swine/TX-human, OH-swine/TX-human, and TX-swine/OH-swine, respectively. Finally, substantial proportions (totaling 54%) of the bacterial species were unique to the species and ecoregion combined; 27%, 17%, and 10% of bacteria were unique to TX-swine, TX-humans, or OH-swine, respectively. The data shows that microbial communities, at the genus level, vary with the ecoregion where decomposition occurs and reveals disparity between bacterial genera from vertebrates of different species. The study demonstrates that each of the two vertebrate species contains its own unique genera and that those populations are influenced by their surrounding environment. More research is needed in this area to determine the potential for swine to be used as prediction models for human and wildlife forensics.

References:

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***Sus scrofa*, Microbiomes, Decomposition**