G75 A Preliminary Survey of a Postmortem Skin Microbiome on Oahu

David O. Carter, PhD, Chaminade University of Honolulu, Div of Natural Sciences & Math, 3140 Waialae Avenue, Honolulu, HI 96816; Rob Knight, PhD, University of Colorado, Dept of Chemistry & Biochemistry, Boulder, CO 80309; and Jessica L. Metcalf, PhD, Chemistry and Biochemistry, Jennie Smoly Caruthers Biotech Bldg, Boulder, CO 80309*

After attending this presentation, attendees will understand how postmortem skin microbial communities change as a carcass decomposes.

This presentation will impact the forensic science community by demonstrating that the postmortem skin microbial community can change rapidly after death. This change is characterized by a shift from a microbial community that includes aerobic bacteria that respire along with representatives from perimortem environment to a microbial community that is dominated by anaerobic fermentative bacteria typically associated with putrefaction, endospore formation, and acidic habitats.

The experimental unit was a swine carcass (*Sus scrofa domesticus*) placed on the soil surface at the Chaminade University of Honolulu Facility for Forensic Taphonomy within one hour of death. This facility is a 900m^2 outdoor facility located in a Tropical Savanna climate on the western slope of the Palolo Valley near Honolulu, Hawaii. The site is approximately 285 feet above sea level. Mean annual precipitation equals approximately 700mm, 70% of which arrives in the autumn and winter (October-March). The vegetation at the site is representative of a Tropical Savanna ecosystem on Oahu; it is rocky and dominated by pili grass (*Heteropogon contortus*) with night-blooming cereus (*Hylocereus undatus*), shrub aloe (*Aloe arborescens*), and carrion plants (*Stapelia* spp.). Few scavengers are present at the site; only the small Asian mongoose (*Herpestes javanicus*) has been observed. Decomposition was monitored at intervals of approximately 8 hours for 58 hours postmortem. The head was swabbed at 4, 34, and 58 hours postmortem with sterile cotton swabs. At each of the three time points, the head was swabbed five times to help quantify variability within versus across time points. A total of 30 swabs were immediately placed in sterile tubes and transported to the laboratory. Swabs were then stored at -20°C for three days until they were shipped to the Second Genome in San Bruno, California, for sequencing. Interpretations of microbial community structure were limited to phyla and families that represented at least 2% of the whole microbiome.

By 58 hours postmortem, the carcass was in an advanced stage of decay with maggots migrating to pupariate. Throughout decomposition, the postmortem microbiome was dominated by bacteria from phylum *Firmicutes*. The overall community changed significantly ($P<0.01$) at each sampling time. The microbiome at four hours postmortem was one that was relatively diverse (4 phyla, 14 families) and included taxa commonly associated with skin, fecal matter, or soil. Microbial diversity was less (3 phyla, 9 families) at 58 hours postmortem and comprised taxa that are typically associated with the skin or putrefaction. In fact, most of the families that represented ->2% of the microbiome at four hours postmortem decreased to an abundance of <2% by 58 hours postmortem.

Over the course of decomposition, the abundance of bacterial families followed one of three patterns. Three families maintained a consistent abundance. These included taxa from *Actinobacteria* (*Bifidobacteriaceae* and *Corynebacteriaceae*) and *Firmicutes* (*Carnobacteriaceae*). Ten families decreased in abundance. These included taxa from *Bacteroidetes* (*Flexibacteriaceae*, *Planococcaceae*, and *Prevotellaceae*), *Firmicutes* (*Lachnospiraceae*, *Streptococcaceae*, *Ruminococcaceae*, and *Veillonellaceae*), and *Proteobacteria* (*Bradyrhizobiaceae*, *Moraxellaceae*, and *Sphingomonadaceae*). Five families increased in abundance and included taxa from *Firmicutes* (*Clostridiaceae*, *Enterococcaceae*, *Lactobacillaceae*, and *Staphylococcaceae*) and *Proteobacteria* (*Enterobacteriaceae* and *Xanthomonadaceae*). From a physiological perspective, these results indicate a shift from a microbial community that includes aerobic bacteria that generate energy through respiration to a microbial community that was dominated by anaerobic bacteria that generate energy through fermentation. These bacteria have the ability to form endospores (e.g., C*lostridium*) or ferment lactic acid (e.g., S*taphylococcus* and *Lactobacillus*). Interestingly, most of the taxa that dominated the microbiome throughout decomposition were always at an abundance of at least 2%. This might indicate that endospores from the putrefactive bacteria are present on the skin during the early stages of decomposition, but do not proliferate until the condition of the corpse supports their germination. It also indicates that the lactic acid bacteria on the skin have the ability to proliferate soon after death.

Microbiology, Taphonomy, Decomposition

 ** Presenting Author*