G72 Just How Filthy Are Maggots? Bacteria Associated With the Blow Fly Sister Species *Lucilia Sericata* and *Lucilia Cuprina* (Diptera: *Calliphoridae*)

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After attending this presentation, attendees will have a better understanding of the bacteria associated with forensically important flies feeding on decomposing vertebrate tissue, how their communities may change over time in association with the insects, and whether such microbes are trans-generationally or environmentally transmitted.

This presentation will impact the forensic science community by clarifying the mechanisms that influence microbial shifts on decomposing remains associated with forensically important flies, as well as the bacterial groups affected by these flies. This is critical information as current information suggests microbial succession on remains is predictive of the postmortem interval and affected by insects.

Improved biological knowledge of flies from the blow fly (Diptera: *Calliphoridae*) genus *Lucilia* (Linnaeus), especially *L. Sericata* (Meigen) and *L. Cuprina* (Wiedmann) benefits forensic science endeavors.[1-3] Since they can be primary colonizers of carrion, developmental data from these species can be useful for estimating the postmortem interval.[4-6] Both species engage in myiasis, transmit pathogens, and are also at the center of numerous lawsuits related to the abuse of dependents, pets, and livestock.[7-10] Accordingly, knowledge of microbial population associated with these flies can help ameliorate the negative and promote the beneficial properties of *Lucilia* biology.

In all of the examples listed above, there is a likely microbial role that could be investigated. Insect-microbe interactions are well documented.[11,12] Given the interest in studies of the properties of blow fly-microbe interactions, especially new research targeted toward predicting a postmortem interval with microbial data, a study was conducted to address the following questions: (1) What microbes are associated with these species?; (2) How similar are the microbe communities associated with each species?; (3) What species are trans-generationally transmitted?; and, (4) What species are horizontally transmitted? To address these questions, this study conducted a survey of bacterial communities associated with these sister species using 16S rDNA 454-pyrosequencing.

The results of this study indicated considerable environmental effects on fly-associated communities. Typically, within-generation communities appear to be similar, with trans-generational bacterial communities appearing to turn over quickly. A comparison of female, new liver, old liver, and larval bacterial communities show that there is a small number of potentially important transmitted and facilitated bacteria. Some of these microbes are known pathogens and others are known to affect fly biology.

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