G78 Postmortem Microbial Community Change of Corpse Decomposition on Three Contrasting Soil Types in a Mouse Model System

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After attending this presentation, attendees will understand recent advances in the microbial ecology of corpse decomposition and why it may be important for medicolegal death investigation. Attendees will be presented with results from recent experiments in which microbial community change associated with mouse decomposition on three contrasting soil types was characterized over time.

This presentation will impact the forensic science community by revealing the potential for next-generation sequencing of microbial communities associated with decomposition for estimating the Postmortem Interval (PMI) and locating clandestine grave sites.

Advances in sequencing technologies have allowed for in-depth characterization of microbial communities across space and time in a wide range of environments. Given that microbes have a nearly ubiquitous distribution and succession-like responses to disturbances, they are excellent targets for tracking the temporal changes in corpse decomposition. However, the feasibility of using microbes for forensic purposes is only just beginning to be rigorously tested. In an initial experiment characterizing microbial community change associated with mouse corpse decomposition on a single soil type, this study concluded that estimating the postmortem interval may be possible by assessing the microbes present at various stages of decomposition. Although these preliminary observations show promise, additional vigorous testing under different conditions is necessary to determine their applicability to forensic science.

This research recently established that bacterial and microbial eukaryotic community data associated with decomposing mouse corpses was sufficiently measurable and directional enough to allow for accurate predictions of PMI as well as the identification of gravesoil. In a follow-up experiment, this study tested how contrasting grave soil-types (e.g., from desert, forest, and grassland environments) affected microbial community change associated with decomposition. It was hypothesized that mouse-associated microbial communities would become progressively different from the starting communities regardless of grave soil type, although late stage corpse-associated microbial communities may be more influenced by underlying soil type. It was also hypothesized that at least some proportion of the soil microbial community associated with late-stage decomposition would be shared despite soil type differences, an important factor for assessing microbes as a forensic tool in grave identification.

A laboratory experiment was performed to characterize microbial communities associated with mouse corpses as they decomposed on three contrasting soil types under controlled conditions for 71 days. Microbial communities (bacterial, archeaeal, fungal, and other microbial eukaryotes) were characterized from the skin, abdominal cavity, and gravesoil of five replicate mice at eight time points by sequencing 16S, 18S, and ITS amplicons using the Illumina® HiSeq platform.

This research discovered that microbial communities changed progressively over time at each sample site (skin of head and body, abdominal cavity, and corpse-associated soil). For both abdominal and skin sites, bacterial community change was significantly associated with time, regardless of soil type. Additionally, bacterial communities were initially highly different among soil types, but these communities became progressively more similar as decomposition progressed. For example, *Gammaproteobacteria* in the family *Pseudomonadaceae*, *Betaproteobacteria* of the family *Alcaligenaceae*, and *Firmicutes* of the family *Bacillaceae* increased in abundance in each sample site during decomposition. These trends suggest that a proportion of the soil bacterial decomposer communities are common across contrasting soil types, which makes bacterial communities associated with decomposition very attractive as a forensic tool.

Microbial eukaryotic communities also showed consistent shifts during decomposition with late stage communities dominated by nematodes, amoebae, cercozoa, and fungi. Sequencing of the 18S amplicons revealed that the highest abundance organism in each sample type was nematodes of the Class *Chromadorea*. Samples associated with each soil type were dominated by a different family of *Chromadorea* (desert soil: *Aphelenchidae*; forest soil: *Cephalobidae*; and grassland: *Pangrolaimidae* and *Aphelenchidae*). The amoebae *Heterolobosea tetramitia* was also prevalent in late-stage decomposer communities regardless of soil type, but at highly variable levels. Sequencing of the fungal specific Internal Transcribed Spacer (ITS) amplicons revealed a shift from fungi in the Phylum *Basidiomycota* and Class *Agaricomycetes* to fungi in the Phylum *Ascomycota* and Class *Sordariomycetes* in late stages of decomposition regardless of soil type. Most of the *Soriomycetes* belonged to the Family *Nectriaceae* and Genus *Haematonectria.*

These results show that postmortem soil microbial communities have great potential as physical evidence because they follow predictable trends.

Postmortem Microbial Ecology, Decomposition, Postmortem Interval