H106 Does Carcass Mass Influence the Structure of Grave Soil Microbial Communities?

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After attending this presentation, attendees will understand that decomposing carcasses of contrasting mass can have similar effects on the changes in the structure of postmortem microbial communities.

This presentation will impact the forensic science community by illustrating that changes in grave soil microbial communities associated with swine carcasses in a field setting are similar to those observed with other mammals, including humans, as well as those conducted in controlled laboratory settings.

Postmortem microbial communities are crucial and dynamic contributors to the decomposition of a corpse. The activity of these decomposer microorganisms drives many postmortem changes, such as bloating and ethanol production. The development of soil microorganisms as physical evidence requires answers to several fundamental questions about the relationships between corpses, decomposition, and microbial communities. Yet one variable has received little experimental attention: how does the corpse mass influence the structure of postmortem microbial communities?

To investigate the effect of corpse mass on the structure of postmortem microbial communities, gravesoils associated with decomposing swine (*Sus scrofa domesticus*) carcasses in a pasture near Mead, NE, were collected in the summer from one to 15 days postmortem. 16S rRNA amplicons and 18S rRNA amplicons were sequenced to characterize the bacterial and archaeal communities (100 basepair reads) and eukaryote communities (~120 basepair reads), respectively.

The decomposition of all carcasses resulted in a significant change in gravesoil bacterial and archaeal communities. These differences were characterized by a decrease in acidotrophic bacteria (Acidobacteria) and basal soil-dwelling bacteria (Planctomycetes, Verrucomicrobia), which coincided with increases in the abundance of Proteobacteria, particularly Gammaproteobacteria. Significant differences were also observed between control soil eukaryote communities and those associated with post-rupture carcasses (days 9 and 15), with the exception of the 1kg neonate carcasses, which may be due to day 15 samples failing to sequence for these samples. As seen in decomposition studies both in laboratory and field settings, Rhabitidae nematodes bloomed after rupture in the other gravesoil and completely dominated microbial eukaryotic communities at day 15.

It is concluded that regardless of carcass mass, decomposition has a significant effect on soil microbial communities, although this needs to be confirmed for microbial eukaryotic communities associated with 1kg neonates. It is recommended that the decomposition of corpses greater than 50kg should be investigated in detail to determine if trends discovered in this study's data set extend to larger decomposing subjects (i.e., are corpses greater than 50kg associated with different gravesoil microbial communities?).

The current findings are similar to those of other recent investigations into the postmortem microbiome. It is becoming clear that a predictable succession-like change in microbial communities occurs to decomposition. Importantly, this study demonstrates that carcass mass has little overall effect on the decomposer microbial community, which is similar to previous studies into the release of bioavailable chemicals into gravesoils. This research has important implications for forensic science because it suggests that a microbial clock for estimating the postmortem interval may be robust to mass of a decomposing carcass.

Postmortem Microbiology, Forensic Taphonomy, Decomposition