H60 Autopsy Sampling to Uncover Human Resistome Diversity

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After attending this presentation, attendees will be informed regarding a novel method for uncovering the human resistome within a given population and will be familiar with an Antibiotic Resistance (AbxR) gene dataset from samples collected during routine death investigation in Detroit, MI.

This presentation will impact the forensic science community by providing novel data characterizing antibiotic-resistance genes identified through samples collected at autopsy of bodies within 24 hours of death. This presentation offers unique methodology demonstrating the utility of autopsy sampling in order to surveil antibiotic resistance within a population to predict potential outbreaks of antibiotic-resistant threatening bacteria. Per research, this is a first-of-its-kind study.

Bacteria have expressed AbxR genes long before the antibiotic era, but the use of antibiotics in agriculture and human medicine has dramatically increased their prevalence and intra- and interspecies transfer (e.g., human-to-livestock and microbe-to-microbe). Most studies have focused on the gut, using fecal samples or other minimally invasive sampling methods in healthy individuals to characterize the human resistome; however, the body contains many unique microbial communities not easily accessible in a living individual that likely also contribute to AbxR. Also, surveillance efforts focus on the clinical cases themselves and seldom focus on the potential cases that can arise in the general population.

This study investigated the ability to use postmortem microbiome sampling during autopsy as a method to detect the AbxR genes present in a human population located in Wayne County, MI. Cases were sampled (as previously described) within 24h after death to assess AbxR gene prevalence, identity, and transfer potential in a human population. Thirty-nine bodies were systematically swabbed during autopsy at eight anatomic sites to collect microbial DNA. The DNA from multiple body locations was combined from 20 individual cases to represent the "overall" body postmortem resistome. The samples were analyzed for the presence of 84 known AbxR genes using quantitative Polymerase Chain Reaction (qPCR) arrays. Samples from the calvarial trabecular space/interhemispheric fissure from the remaining 19 bodies were sequenced using Whole Genome Shotgun (WGS) sequencing and assembled into metagenomes that were aligned to known and putative AbxR genes.

Results from qPCR assays revealed that each of the 20 cases had an average of 7.1 AbxR genes. The most commonly positive AbxR genes detected were *ermB* and *mefA*, which were present in 90% of bodies. Genes resistant to the macrolide antibiotic class predominated, with 46% of all the positive AbxR genes. WGS revealed an average of 13.25 AbxR genes per body with *tetQ* as the most commonly found AbxR gene (42% of all the positive) out of the unique 42 AbxR genes detected. Results of this work expand human resistome research to include samples from locations not easily accessible by using samples taken during autopsy.

These novel surveillance methods will allow investigators to sample multiple anatomic sites in a wide range of individuals in the population to obtain information on the incidence and prevalence of antibiotic resistance genes and their presence in the community. Since death is, to some extent, a process with fewer selection biases and wide geographic distribution, sampling at autopsy can help reduce sampling bias and provide a more robust approach to detect the presence of AbxR genes associated with clinically important drugs, such as vancomycin, methicillin, and polymyxins, in the general population. Continuous sampling will also allow for uninterrupted surveillance of these genes once a baseline for their presence is established and serve as a sentinel when new ones are introduced, potentially even before they become clinically significant.

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