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998. Utility of Routine Genomic Sequencing for Infection Control Surveillance

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Session: 134. Where Did That Come From? Transmission Risks in Healthcare
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Background. Recent work indicates that comprehensive genomic sequencing can be a highly effective tool in defining the transmission of microbial pathogens. We have studied the utility of the routine use of genomic sequencing for infection control surveillance in an academic medical center.

Methods. The genomes of inpatient and emergency department isolates of *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Klebsiella pneumoniae*, and *Enterococcus faecium* were sequenced. Within each species, single-nucleotide polymorphisms (SNP) were identified in the core genome for all isolates using alignment-based methods. The number of SNP differences between isolate pairs was determined and used, in combination with the patient's electronic medical records to identify potential transmission events.

Results. Between September 2016 and March 2017, 388 *S. aureus*, 66 *P. aeruginosa*, 48 *K. pneumoniae*, and 29 *E. faecium* isolates were sequenced from 373 patients. There was variation in the distribution of SNP differences between inpatient isolates for the four pathogens; with the least variability for *E. faecium* and greatest for *P. aeruginosa*. The majority of the bacterial isolates from separate patients appeared to be genetically unique exhibiting marked SNP differences from other isolates. There were 19 sets of isolates where the SNP variation between interpatient isolates was either comparable to that of inpatient variation (12) and suggestive of recent transmission events, or with SNP variation somewhat greater than the inpatient SNP variation (7) suggesting relative relatedness. Only one of the highly related sets had been previously identified by standard infection control surveillance. Likely transmissions appeared to have occurred both in the inpatient and outpatient settings, and the transmission routes were not always apparent.

Conclusion. The routine use of genomic sequencing analysis identified previously unrecognized likely transmission events within the institution's patient population that are of relevance to infection control surveillance. This capacity should significantly enhance our understanding of the epidemiology of hospital acquired infections, and assist in developing and implementing new prevention strategies.

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999. Invasive *Mycobacterium abscessus* Infection after Cardiac Surgery: Epidemiology and Clinical Outcomes

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Background. We recently mitigated a clonal outbreak of *Mycobacterium abscessus*, including a large cluster of patients who developed invasive infection after exposure to heater-cooler units (HCU) during cardiac surgery. Recent studies have described a small number of *Mycobacterium chimerica* infections linked to open-heart surgery; however, little is known about the epidemiology and clinical courses of cardiac surgery patients with invasive infection from rapidly-growing mycobacteria, such as *M. abscessus*.

Methods. We retrospectively collected clinical data from all patients who underwent cardiac surgery at our hospital and had positive cultures for *M. abscessus* from 2013 to 2016. We excluded heart transplant recipients and patients who at time of diagnosis had ventricular assist devices. We analyzed patient characteristics, antibiotic treatment courses, surgical interventions, and clinical outcomes.

Results. Nine cardiac surgery patients who met the case definition developed culture-proven invasive infection from *M. abscessus* (Figure 1). Seven (78%) infections occurred after surgeries that included valve replacement. Median time from suspected inoculation in the operating room to first positive culture was 49 days

(interquartile range, 38–115 days). Seven (78%) patients had bloodstream infections, and six (67%) patients had sternal wound infections. Six (67%) patients developed disseminated disease with infection at multiple sites. All patients received combination antimicrobial therapy. The most common majority regimen ($n = 6$) was imipenem, amikacin, and tigecycline. Four (44%) patients experienced therapy-limiting antibiotic toxicities (Figure 2). Seven (78%) patients were well enough to undergo at least one surgical debridement. Five (56%) patients stopped therapy due to presumed cure, but four (44%) patients had deaths attributable to *M. abscessus* infection.

Conclusion. Invasive *M. abscessus* infection after cardiac surgery was associated with high morbidity and mortality. Most patients underwent surgical debridement and received prolonged three-drug antimicrobial therapy, which was complicated by numerous antibiotic toxicities. Treatment cured five patients, but four patients died from mycobacterial disease.

Figure 1. Clinical courses of 9 patients who developed invasive *Mycobacterium abscessus* infection after cardiac surgery. Incubation period is given from time of suspected inoculation in operating room to time that the first positive culture was obtained.

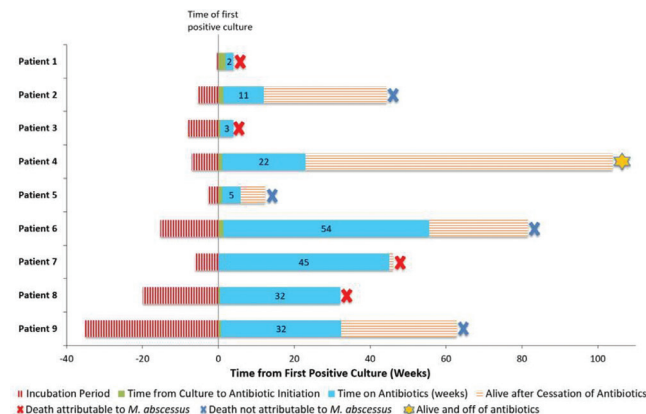
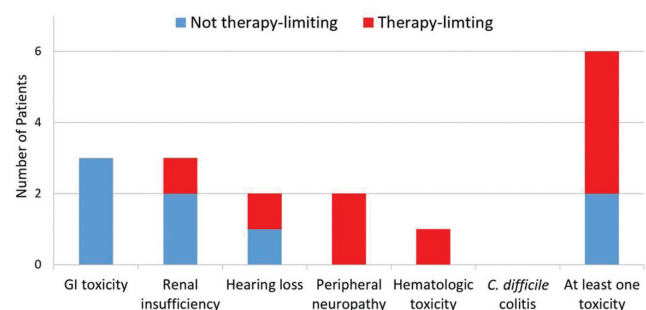


Figure 2. Antibiotic toxicities experienced by 9 cardiac surgery patients treated for invasive *Mycobacterium abscessus* infection. 4 of 6 patients with toxicities required a change in antibiotic regimen.



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1000. Daily Chlorhexidine Bathing in General Hospital Units – Results of the ABATE Infection Trial (Active BATHing to Eliminate Infection)

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Background. Universal decolonization with daily chlorhexidine (CHG) bathing with and without nasal decolonization has significantly reduced positive MRSA clinical cultures and bloodstream infections in adult ICUs in several clinical trials. We