



Contamination of Hospital Plumbing

A Source or a Sink for Antibiotic-Resistant Organisms?

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In recent years there have been an increasing number of reports of contamination of hospital plumbing with multidrug-resistant gram-negative organisms, with speculation that this contamination poses a significant risk to patients.¹ Hopman and colleagues² add to this body of literature with the report of a patient with a carbapenemase-producing *Pseudomonas aeruginosa* (CP-PA) infection that was shown to be genetically related to a strain of *P aeruginosa* from the shower in the patient's room. The patient was a man in his early 60s who had undergone a left-sided pneumonectomy and adjuvant radiotherapy. Subsequent to the procedure, this patient developed a wound infection with a Verona integron-mediated metallo- β -lactamase (VIM)-carrying strain of *P aeruginosa*. A series of surveillance cultures with negative results for *P aeruginosa* prior to the patient's infection indicated that his infection was acquired in the hospital. Surveillance culturing of all other patients on the same unit as the case patient failed to uncover any additional patients with positive results for *P aeruginosa* who might have been the source of his infection. The lack of colonized patients ultimately motivated environmental surveillance to identify potential reservoirs of *P aeruginosa* in the hospital. Environmental screening revealed CP-PA contamination in the shower drain in the case patient's room, as well as in showers and sinks in adjacent rooms that were connected to a common sewage collection point. The application of whole-genome sequencing (WGS) to patient and environmental isolates supported a single introduction into the hospital seeding both the patient's infection and the contamination of the plumbing. To evaluate the plausibility of airborne transmission from the contaminated shower drain to the patient, the authors evaluated air samples for CP-PA after running the shower for 10 minutes and 15 minutes after the shower had been turned off and found 1 positive result out of several dozen cultures. The hospital ultimately implemented enhanced disinfection of drains, which appeared to eliminate CP-PA from the plumbing. However, on returning to standard disinfection protocols, CP-PA regrowth was observed, which is consistent with findings from other studies that have reported challenges in achieving sustained decontamination of plumbing.³

A major strength of this work was its use of WGS to demonstrate that environmental contamination across the ward was likely mediated by introduction of *P aeruginosa* into a single drain. This result highlights how contamination of sink and shower drains can propagate to proximate rooms via plumbing, and illuminates an epidemiologic signature that may be associated with plumbing-mediated outbreaks. However, this study also highlights the challenges in ascertaining the risk that contaminated plumbing poses to patients. In particular, even with a convincing link between the patient and environment provided by WGS, the directionality of the transmission is not evident from the data and analyses provided. Although Hopman et al² favor an interpretation wherein the contaminated shower seeded the case patient's infection, other plausible scenarios exist that could have yielded the same epidemiologic and genomic observations. Among the alternative hypotheses consistent with the data are the existence of an unidentified source patient who seeded both the case patient's infection and the plumbing contamination or the case patient himself seeding the plumbing contamination after acquiring his infection from an unknown source patient. Given that the patient who imported the observed CP-PA strain into the hospital was never identified, and that comprehensive patient and environmental surveillance began only after the identification of the case patient, the potential role of an unidentified source patient cannot be refuted. Similarly, while the

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authors favor an aerosol-mediated transmission event based on their experimental analysis, the observation that aerolization from the shower is possible in no way proves that this is what happened in this case and it does not quantify the risk with which this type of exposure is associated. Although there is value in experimentally evaluating plausible transmission scenarios, care should be taken when attempting to generalize these results to what is actually happening in the context of patient care.

This study is by no means the first to implicate contaminated plumbing in the transmission of gram-negative organisms. It has long been known that water-hearty organisms such as *P aeruginosa* and *Serratia marcescens* can contaminate water in the health care environment, leading to patient infections.⁴ More recently, numerous reports have hypothesized that transmission via persistent contamination of hospital plumbing has driven long-term outbreaks.⁵ Signatures of long periods between observed cases and the resolution of outbreaks after replacement of plumbing infrastructure are consistent with contaminated plumbing being a source of transmission.³ However, in many of these studies, interventions included more standard infection prevention bundles focusing on health care worker-mediated transmission, making the contribution of plumbing interventions difficult to discern.⁶

Given the increasing number of reports of hospital plumbing contaminated with antibiotic-resistant organisms, it is important that studies be undertaken to better understand the risk that contaminated plumbing poses to patients, so that necessary interventions can be undertaken.⁷ I believe that the definitive studies will include the application of WGS to comprehensive patient and environmental isolate collections, thereby allowing for testing of alternative epidemiologic hypotheses for the origin of patient infections.⁸ For example, WGS can be used to evaluate the existence of epidemiologic signatures that are expected to be associated with plumbing-to-patient transmission, such as transmission links between subsequent occupants of the same room. Similarly, WGS can be used to gain a more nuanced understanding of the basis for reductions in infection or colonization rates that follow interventions (eg, reduced importation into the hospital vs reduced patient-to-patient transmission or plumbing-to-patient transmission). It will be interesting to consider whether sustained outbreaks mediated by contaminated plumbing may leave other genomic signatures that could inform infection prevention practitioners. For instance, the observation of patient infection isolates with elevated resistance to cleaning products used in hospital drains provides support for the patient's strain having been exposed to this environment prior to coming into contact with the patient.⁹ Furthermore, while little is known about the evolutionary rate of organisms in the context of long-term colonization of plumbing infrastructure, it will be interesting to evaluate whether the level of genetic diversity in contaminating populations can be used to draw inferences regarding how long ago the organism was introduced into the hospital.¹⁰ It is clear that WGS can fundamentally alter our level of understanding of antibiotic resistance propagation in health care facilities, and the challenge now resides in collecting isolates and designing studies that can leverage the resolution provided by WGS to discern the role of alternative pathways leading to patient infections with antibiotic-resistant organisms.

ARTICLE INFORMATION

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