Infection Control & Hospital Epidemiology (2023), **44**, 1342–1344
doi:10.1017/ice.2022.263

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Concise Communication

Investigation of a *Mycobacterium fortuitum* catheter-related bloodstream infection in an oncology unit

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Abstract

We describe a case of healthcare-associated bloodstream infection due to *Mycobacterium fortuitum*. Whole-genome sequencing showed that the same strain was isolated from the shared shower water of the unit. Nontuberculous mycobacteria frequently contaminate hospital water networks. Preventative actions are needed to reduce the exposure risk for immunocompromised patients.

(Received 1 August 2022; accepted 27 September 2022; electronically published 20 February 2023)

The growing use of medical devices and immunosuppressive medications has contributed to the increasing incidence of rapidly growing mycobacteria related infections.[1] These are nontuberculous mycobacteria (NTM) commonly found in environmental reservoirs, such as water sources.[2] *Mycobacterium fortuitum* is one of the most frequently isolated rapidly growing mycobacteria in clinical samples.[3] This bacterium is responsible for a variety of clinical diseases, sometimes severe, and is recognized to be involved in nosocomial infections.[4,5] Identifying the environmental source in this context is essential to implement appropriate actions and prevent further cases. However, the contaminating source is rarely identified. Here, we present the investigation of a healthcare-associated bloodstream infection (BSI) caused by *M. fortuitum*.

Methods

Case description

A 68-year-old woman was diagnosed with colon adenocarcinoma in November 2019. She was initially treated by right hemicolectomy and adjuvant chemotherapy, then by 4 lines of chemotherapies for peritoneal relapse. Chemotherapies were administered through a totally implantable venous access port (port-a-cath or PAC) inserted in December 2019. She received the last chemotherapy cycle in April 2021, and 7 days later she was admitted to our oncology department for an upper-digestive occlusion (Supplementary Fig. 1 online). A month after admission, she was transferred 2 days to the medical intensive care unit for the decompensation of newly discovered steroid-induced diabetes. Upon admission to this department, she had an isolated fever of up to 38.5°C. Results of a physical examination were unremarkable. However, 6 aerobic bottles of blood cultures (n = 3 from peripheral and n = 3 from the PAC) collected at different times, showed growth of *M. fortuitum* (time-to-positivity range [peripheral], 79–86 hours; PAC, 65–73 hours). The patient was given imipenem for 2 weeks in association with amikacin for a week (minimum inhibitory concentrations, 4 mg/L and <1 mg/L, respectively). The PAC was removed despite the absence of local inflammation. More than 10^4 colony-forming units per mL of *M. fortuitum* were isolated from the inner side of the PAC. Negative blood cultures were obtained 24 hours after the PAC removal, on day 2 following the antibiotic treatment. However, the patient died 4 weeks later because of probable digestive bacterial translocation.

Microbial investigation

The infection control team conducted the investigation. A retrospective review of the microbiology database did not find any additional cases of *M. fortuitum* BSI since 2014. Water samples were performed to identify the contaminating source. Two potential sources of exposure of the patient were sampled: the bathroom tap in her hospital room and the shared shower of the oncology

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Cite this article: Faury HB, *et al.* (2023). Investigation of a *Mycobacterium fortuitum* catheter-related bloodstream infection in an oncology unit. *Infection Control & Hospital Epidemiology*, 44: 1342–1344, https://doi.org/10.1017/ice.2022.263

Table 1. Nontuberculous Mycobacteria Species Identified in the Hospital Water Samples

Buildings	Total Samples, No. (No. With Filter)	Cultures With NTM, No.	Sources of NTM[a] (No.)	NTM Species (No., RGM or SGM)
A[b]	11 (0)	6	Tap water (1) Shared shower (1) Shower (4)	*M. septicum* (1, RGM) *M. fortuitum* (1, RGM) *M. septicum* (1, RGM) *M. porcinum* (1, RGM) *M. gordonae* (2, SGM)
B	5 (2)	1	Shower (1)	*M. gordonae* (1, SGM)
C	5 (0)	3	Tap water (1) Shower (2)	*M. paragordonae* (1, SGM) *M. paragordonae* (2, SGM)
D	2 (1)	0		
E	9 (1)	0		
F	4 (0)	1	Tap water (1)	*M. tusciae* (1, SGM)
G	5 (4)	0		

Note. NTM, nontuberculous mycobacteria; RGM, rapidly growing mycobacteria; SGM, slowly growing mycobacteria.
[a]The terms 'tap water' and 'shower' are relative to samples in patient rooms. The term 'shared shower' corresponds to sample from the shared shower of the unit.
[b]Building A corresponds to the oncology department.

unit where she showered daily, whereas she had a Huber needle in place protected solely by a transparent dressing. Additionally, 39 supplementary water samples (including 8 with 0.45-µm pore-size filters) were taken from 7 different hospital buildings (including 9 samples in the oncology building) to determine the extent of the contamination of the hospital water network. Briefly, 250 mL mixed water (temperature range, 24.6–38.3°C) was collected in sterile vials containing sodium thiosulphate after running the water for 30 seconds. Then, 20 mL of each sample was decontaminated with L-acetylcysteine/NaOH and centrifuged for 20 minutes at 3,000×*g*. Coletsos medium (Bio-Rad, Marnes-la-Coquette, France) was inoculated with the pellet and incubated at 30°C for 2 months. Suspect colonies were identified by matrix-assisted laser desorption/ionization–time-of-flight mass spectrometry using the MycoEx protocol.[6] Further analyses were performed by the French National Reference Center for Mycobacteria and Antimycobacterial Resistance. The species identification of the *M. fortuitum* complex was confirmed by *hsp65* gene sequencing and strains of *M. fortuitum* were then compared using whole-genome sequencing using Nextera XT technology (Illumina, San Diego, CA) according to methods recently reported.[7] Reads were deposited to the Sequence Read Archive (accession no. PRJNA843029).

Ethical approval

Ethical approval was not required for this study because anonymous data were used and no medical interventions were made on human subjects.

Results

Overall, NTM grew from 11 (26.8%) of the 41 samples (Table 1). We identified rapidly growing mycobacteria in 4 of the positive cultures. *M. fortuitum* was only found in the shared shower of the oncology unit (after 8 days of culture). No NTM was isolated from the patient's bathroom tap water and none grew when a 0.45-µm pore-size filter was present at the sampled points of use.

In addition, 2 strains of *M. fortuitum* from the patient (peripheral and PAC blood cultures) and the strain from the shower were referred to the National Reference Center. Identification at the subspecies level was confirmed as *M. fortuitum* subsp *fortuitum*. Additionally, whole-genome sequencing showed that the 2 clinical strains were closely related to the environmental strain isolated 3 weeks later with a maximum of 7 single-nucleotide polymorphisms between them (Table 2). In this context, the strains were considered clonally related, suggesting probable transmission.

Table 2. Matrix of Single-Nucleotide Polymorphism Differences Between the Clinical and Environmental Isolates of *M. fortuitum*

Origin of the *M. fortuitum* Isolate	Blood Culture (Peripheral)	Blood Culture (PAC)	Water of the Shared Shower	Reference Strain (ATCC 6841)
Blood culture (peripheral)	0			
Blood culture (PAC)	1	0		
Water of the shared shower	6	7	0	
Reference strain (ATCC 6841)	> 200	> 200	> 200	0

Note. PAC, port-a-cath; ATCC, American Type Culture Collection.

Following this investigation, a 0.45-µm pore-size filter was placed at the showerhead of the oncology shower. No additional cases of infection by *M. fortuitum* have been detected to date. Samples of the contaminated shower (with and without filter) from the oncology unit were found to be negative for NTM in October 2021.

Discussion

We describe a case of a *M. fortuitum* catheter-related BSI originating from the shared shower of the oncology unit. To date, 30 cases of *M. fortuitum* BSI have been reported in the PubMed database. Most BSIs caused by *M. fortuitum* are catheter-related BSIs.[8] In this report, the patient had a favorable outcome after PAC removal associated with a combination of amikacin and imipenem, in agreement with the literature.[9] However, the source of

https://doi.org/10.1017/ice.2022.263 Published online by Cambridge University Press

M. fortuitum BSI has been rarely identified and was reported to be hospital water in a single paper.[5]

We found the contamination of hospital water by NTM to be frequent (26.8%). This result is consistent with those of a previous report, which showed an even higher contamination rate of 52.2%.[2] The presence of NTM in the water supply can be explained by their ability to produce biofilms and resist commonly used disinfectants.[9] Hospital water poses a potential threat that can lead to the transmission of NTM to severely immunocompromised patients at risk of developing invasive diseases. Therefore, the environmental investigation of any cases of NTM-associated infection is crucial to identify the source and implement control measures. Here, we applied a 0.45-µm membrane filter on the showerhead to prevent exposure. The implementation of filters on showerheads in high-risk units (eg, oncology and hematology) should be encouraged. Moreover, these filters could prevent other serious diseases due to environmental organisms, such as Legionnaire's disease. However, filters are expensive and must be changed regularly according to the providers' recommendations (generally every 1 or 2 months), which can be an obstacle to their use.

Patients with PAC should be advised that it is not recommended to shower when a Huber needle is in place.[10] If patients shower, it is essential to protect the needle using an impermeable dressing and to verify its integrity before and after showering.[10]

In conclusion, *M. fortuitum* is a rare healthcare-related cause of BSI. Environmental samples are essential to identify the source and implement appropriate actions to reduce the risk of exposure.

Supplementary material. For supplementary material accompanying this paper visit https://doi.org/10.1017/ice.2022.263

Acknowledgments. We thank the infection control team of the Saint-Antoine Hospital and the technicians of the CNR-MYRMA for their contribution to this study.

Financial support. No financial support was provided relevant to this article.

Conflicts of interest. All authors report no conflicts of interest relevant to this article.

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