Late-onset ventilator-associated pneumonia due to *Mycobacterium chelonae* and an unusual transmission pathway

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To the Editor—In healthcare settings, nontuberculous mycobacteria (NTM) are present in tap water and are responsible for healthcare-associated infections (HAIs) through different transmission pathways.[1] A worldwide outbreak of *Mycobacterium chimaera* infections related to contaminated heater–cooler devices was reported in patients after cardiac surgery.[2] The identification of the transmission pathway is essential to prevent the risk of NTM infection. We describe late-onset ventilator-associated pneumonia (VAP), which complicated severe coronavirus disease 2019 (COVID-19), due to *M. chelonae* associated with an unusual route of contamination.

On January 3, 2022, an unvaccinated male patient aged 35 years was admitted to a hospital in the eastern suburbs of Paris for severe COVID-19. The history of the patient was unremarkable. Because of respiratory distress, the patient was artificially ventilated the day after his admission and extracorporeal membrane oxygenation began on January 9. After his transfer to the medical intensive care unit of a tertiary-care teaching hospital, the patient developed several episodes of VAP due to *Enterobacter cloacae* and *Hafnia alvei* without ever being extubated. On April 27, May 5, May 12, and May 24, a strain of *M. chelonae* was identified from respiratory samples. A dedicated antimicrobial treatment was implemented on May 20. The patient died on June 3 of multiorgan failure. The legal representatives of the patient were informed and gave their consent for the exploitation of the clinical data.

We investigated the putative reservoirs and transmission pathways through epidemiological, environmental, and clinical practice investigations. An environmental sampling program included specimens of water from sinks in the patient's room, the adjacent room, and the room 1 floor directly above the patient's room, from 2 drinking fountains connected to the water network of the building, from the 2 heater–cooler units, from the water feeds of the manual disinfection bench and endoscope reprocessor, and from the cold-water supply meter of the building. The samples were tested as previously described.[2] Sequencing of the strains and the identification of single-nucleotide polymorphisms (SNPs) were performed as previously reported (Bioproject PRJEB62124).[3] A control strain (EEQ98) without any epidemiological link was added to the molecular study. In parallel, we performed a large analysis of clinical practices to identify all contacts with nonsterile water sources.

Table 1. Difference in Number of Single-Nucleotide Polymorphisms (SNPs) Between the Whole Genome of the Patient (D, U) and Environmental (A, H, E, G) Strains

		Environmental Strains				Patient Strains	
Strain Type		A	H	E	G	D	LJ
Environmental strains	A	0					
	H	2	0				
	E	0	2	0			
	G	0	2	0	0		
Patient strains	D	1	3	1	1	0	
	LJ	2	3	1	1	2	0

The environmental survey identified 4 *M. chelonae* strains from the sink (cold water) of the patient's (A and H) and neighbor's room and the room above (E and G). We tested 2 strains with different phenotypes obtained from the respiratory specimens of the patient (D and LJ). Compared with the patient and environmental strains, the EEQ98 control strain showed ~73,900 SNPs. Between the patient and water strains instead the enumeration of SNPs showed quasi-identity, with 0–3 SNP differences (Table 1). Regarding the patient's exposure to tap water, we identified several gastric rinses through the gastric tube and 3 gastroscopies on January 24 and February 9 and 14. The last gastroscopy was performed to treat a bezoar; the water from the sink of the room was used to supply the gastroscope during the gastroscopy. We speculate that the pathophysiological process introduced mycobacteria via the gastric tube or via gastroscopy and then pulmonary contamination by reflux and microaspiration.

A French case series reported 85 HAIs due to NTM, mainly after surgical or invasive aesthetic procedures.[1] *M. chelonae* ranked first: this rapid growing species was the second most frequently identified NTM from treated surface water in France.[1,4] A worldwide increase in NTM pulmonary infection and disease was recently highlighted.[5] Baker et al[6,7] suspected tap-water exposure of the aerodigestive tract to be the reservoir and pathway of NTM pulmonary HAI. From a vulnerable population of lung transplant patients, these researchers observed a decrease in hospital-onset respiratory NTM infection after the implementation of a tap-water avoidance policy, especially for oral care and enteral tube irrigation.[6,7] Recently, Klompas et al[8] reported an

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M. abscessus cluster in cardiac surgery patients attributable to contaminated water and ice. We reported for the first time nosocomial *M. chelonae* contamination of a ventilated patient from tap water leading to fatal VAP. The patient was intubated before his admission and was never extubated until his death: this eliminated some putative expositions, such as aerosol contamination. Furthermore, extensive environmental sampling excluded additional reservoirs. The similarity of the clinical and environmental strains was established through whole-genome sequencing. Healthcare workers reported using tap water for dissolving bezoars present in the stomach of patients. Although the French authorities recommended the use of bacteria-free water to rinse the gastroscope after the disinfection process or during gastroscopy, the practitioner used tap water to perform the gastroscopy and managed the bezoar at the bedside.

The reported transmission pathway was probably associated with the extreme severity of the lung injury of the patient. During the COVID-19 pandemic, patients who benefited from extracorporeal membrane oxygenation were particularly susceptible to bacterial superinfection.[9] Furthermore, the patient received 50 mg per day of methylprednisolone during 1 month in the setting of severe renal insufficiency. Our case study has some limitations. The contamination pathway, that is microaspiration, was not formally established; nevertheless, this event is clearly the main etiology of VAP. We did not collect surface samples. The contamination of the environment through splashing from the contaminated water source followed by contamination of the patient by the hands of health care workers is a possible alternative transmission pathway, as reported during a *Burkholderia cepacia* cluster.[10]

NTM are naturally present in tap water; there is no recommendation to routinely monitor them in the hospital water supply. In vulnerable artificially ventilated patients suffering from severe lung damage, potentially contaminated tap water should not be introduced into the stomach.

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