Letter to the Editor



Interhospital outbreak of *Burkholderia cepacia* complex ventilator-associated pneumonia (VAP) caused by contaminated mouthwash in coronavirus disease 2019 (COVID-19) patients

Silvia Maria dos Santos Saalfeld MSc^{1,2}, Danielle Rosani Shinohara MSc¹, Josy Anne Silva MSc²,

Maria Emilia Avelar Machado MD³, Cecilia Saori Mitsugui MSc², Nathalie Kira Tamura MSc²,

Sheila Alexandra Belini Nishiyama PhD¹ and Maria Cristina Bronharo Tognim PhD¹ 💿

¹Department of Basic Health Sciences, State University of Maringá, Maringá, Paraná, Brazil, ²Maringá University Hospital, State University of Maringá, Maringá, Paraná, Brazil and ³Department of Medicine, State University of Maringá, Maringá, Paraná, Brazil

To the Editor—In the global coronavirus disease 2019 (COVID-19) pandemic, up to 80% of the patients in intensive-care units (ICUs) have required invasive mechanical ventilation (IMV).¹ Inpatients receiving endotracheal intubation and IMV have increased risk of ventilator-associated pneumonia (VAP).^{1,2}

Oral hygiene with chlorhexidine-based mouthwash is an important prevention measure for VAP³; however, outbreaks of *Burkholderia cepacia* complex associated with these products have been reported.^{4,5} To our knowledge, this is the first report of a VAP outbreak caused by *B. cepacia* complex in COVID-19 patients admitted in ICUs involving 2 hospitals.

In November and December 2020, in a tertiary-care university hospital (hospital 1) in southern Brazil, 7 patients in a COVID-19 ICU and 3 patients in an adult ICU had positive cultures for *B. cepacia* complex (>10⁶ CFU/mL) from endotracheal aspirate (ETA). During this period, 6 other patients in a mixed ICU in a private hospital (hospital 2) in the same region showed *B. cepacia* complex–positive cultures (Fig. 1).

As part of the intervention, contact-isolation precautions were implemented for all patients with *B. cepacia* complex–positive cultures. Microbiological data were reviewed to track the source of this contamination, and as reported previously, hospital 1 had experienced consecutive outbreaks of *B. cepacia* complex as a result of the use of intrinsically contaminated mouthwash, so this source was investigated first.⁶

Burkholderia cepacia complex isolates recovered from ETA and mouthwashes at hospital 1 were characterized phenotypically using the BD-Phoenix automated system (Becton-Dickinson, Franklin Lakes, NJ). Hospital 2 used the matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) system (Bruker Daltonics GmbH, Leipzig, Germany). All isolates (hospitals 1 and 2) were typed using the enterobacterial repetitive intergenic consensus-PCR (ERIC-PCR) technique.⁷ BioNumerics 6.5 software (Applied Maths, Sint-Martens-Latem, Belgium) was used to analyze band patterns.

Author for correspondence: Maria Cristina Bronharo Tognim, E-mail: mcbtognim@uem.br

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In total, 16 patients had *B. cepacia* complex–positive cultures recovered from ETA; 12 (75%) these patients were hospitalized with COVID-19 (positive RT-PCR for severe acute respiratory coronavirus virus 2 [SARS-CoV-2]) (Fig. 1). The mean age of these patients was 66 years, and 69% were male. All patients received IMV from the first day of ICU admission. The median time between the beginning of IMV and the first isolation of *B. cepacia* complex was 14 days (interquartile range [IQR], 9–16).

Burkholderia cepacia complex was recovered (> 2.7×10^5 CFU/mL) in unopened mouthwash bottles containing 0.12% chlorhexidine used in both hospital 1 (batch C9252, 250 mL) and hospital 2 (batch C9275, 1000 mL), all from the same company. This company's mouthwashes had been used at hospital 1 since January 2020 without isolation of *B. cepacia* complex in infections.

All isolates evaluated showed 100% genetic similarity, characterizing a monoclonal outbreak involving 3 ICUs and 2 hospitals caused by *B. cepacia* (confirmed by MALDI-TOF MS).

The manufacturer of these contaminated batches was implicated in a previous *B. cepacia* complex outbreak at hospital 1, 4 years prior (data reported by our research group).⁶ In the current outbreak, the hospitals notified again the National Health Surveillance Agency (ANVISA) and the manufacturer. More effectively, a voluntary national recall on December 16, 2020, by the manufacturer resulted in removal of all affected batches. According to the FDA, a likely source of *B. cepacia* complex contamination in aqueous products appears to be contaminated water used in manufacturing.⁴ The presence of *B. cepacia* complex in unopened bottles from different batches of mouthwash strongly suggests contamination during the manufacturing process, and as with *B. lata* in a study conducted by Leong et al⁸, our findings also suggest contamination during manufacturing.

Nosocomial cross transmission between patients with *B. cepacia* complex appears unlikely in this case. In hospital 1, the facilities and staff are not shared between the ICUs, and the adult ICU has single-bed rooms and the COVID-19 ICU 2-bed rooms. In hospital 2, inpatients with COVID-19 are single-bed rooms.

Of the total of 12 patients with VAP by *B. cepacia* complex and with COVID-19, 9 (75%) died. Of the 4 patients with VAP by *B. cepacia* complex and without COVID-19, only 1 (25%) died

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| | | | Patient | Age - years | Gender | Reason for ICU admission | Bcc collection date | Sample | IMV-Bcc detection ^a | ICU Outcome | ERIC profile |
|-------------|------------------------|------------------------|----------------------|----------------|----------|--------------------------|------------------------|-------------------|--------------------------------|----------------|--------------|
| HOSPITAL I | Mouthwash - batch 9252 | COVID-19 ICU | 1 | 74 | Male | COVID-19 | 20-Nov-20 | ETA | 8 | Death | Α |
| | | | 2 | 35 | Male | COVID-19 | 9-Dec-20 | ETA | 9 | Discharge | Α |
| | | | 3 | 62 | Male | COVID-19 | 11-Dec-20 | ETA | 16 | Death | Α |
| | | | 4 | 76 | Male | COVID-19 | 11-Dec-20 27-Dec-20 | ETA ETA, Blood | 10 | Death | A A |
| | | | 5 | 89 | Female | COVID-19 | 15-Dec-20 | ETA | 16 | Death | Α |
| | | | 6 | 69 | Female | COVID-19 | 21-Dec-20 | ETA | 14 | Discharge | Α |
| | | | 7 | 70 | Female | COVID-19 | 28-Dec-20 | ETA | 22 | Discharge | А |
| | | Adult ICU | 1 | 56 | Male | IGS | 4-Dec-20 | ETA, Blood | 24 | Discharge | Α |
| | | | 2 | 30 | Male | Drugs, after CA | 7-Dec-20 | ETA | 9 | Discharge | Α |
| | | | 3 | 44 | Male | Seizure, ARpI | 15-Dec-20 | ETA | 12 | Discharge | Α |
| | | | Commercial mouthwash | | | | 11-Dec-20 | Unopened bottle | | | А |
| HOSPITAL II | Mouthwash - batch 9275 | Mixed ICU ^b | 1 | 68 | Male | COVID-19 | 23-Nov-20 | ETA | 13 | Death | Α |
| | | | 2 | 72 | Female | COVID-19 | 3-Dec-20 | ETA, Blood | 8 | Death | А |
| | | | 3 | 77 | Male | IGS | 6-Dec-20 | ETA, Blood | 15 | Death | Α |
| | | | 4 | 58 | Male | COVID-19 | 16-Dec-20 | ETA | 16 | Death | А |
| | | | 5 | 79 | Male | COVID-19 | 10-Dec-20 | ETA | 11 | Death | А |
| | | | 6 | 63 | Female | COVID-19 | 8-Dec-20 | ETA, Blood | 16 | Death | Α |
| | | | Comm | ercial m | outhwash | | 9-Dec-20 | Unopened bottle | | | Á |
| | | | | | | | | | | | |

Fig. 1. Schematic description of *B. cepacia* complex isolates recovered from mechanically ventilated patients and unopened mouthwash bottles in an intra- and interhospital outbreak. (a) Time (in days) between the beginning of invasive mechanical ventilation (IMV) and *B. cepacia* complex detection (collection of clinical sample). (b) Patients with and without COVID-19 are admitted to the mixed ICU. Note. ICU, intensive care unit; IGS, Instability after gastrointestinal surgery; CA, cardiac arrest; ARpI, acute respiratory insufficiency; ETA, endotracheal aspirate; ERIC, Enterobacterial repetitive intergenic consensus polymerase chain reaction.

(Fig. 1). The time of IVM of these patients (without COVID-19) was 54.8% shorter than the patients with *B. cepacia* complex and SARS-CoV-2 coinfection. The median times of IVM were 31 for patients with COVID-19 and 17 days for patients without COVID-19. These results suggest that coinfection with SARS-CoV-2 and *B. cepacia* complex may increase the time of IMV, similarly to the case reported by Osman and Nguyen.⁹

Another observation here was the high number of deaths, although attributable mortality was not calculated. Although data on coinfection between SARS-CoV-2, fungi or bacteria, including *B. cepacia* complex, were reported,¹⁰ data on the time of IMV and mortality attributed to these patients are still little explored and require further investigation.

Outbreaks of *B. cepacia* complex PAV caused by intrinsically contaminated chlorhexidine-based mouthwashes have been well reported.⁴⁻⁶ The ability of *B. cepacia* complex to remain viable in chlorhexidine appears to result from a combination of efflux pump activity, biofilm formation, and cell-wall impermeability.⁸ These factors in themselves are extremely important because these products are used for critically ill patients. However, in the context of the COVID-19 pandemic, an outbreak appears to have even more serious consequences. The few cases reported in hospital 2 showed that VAP occurred in a short period, with a high incidence (50%) of bacteremia secondary to VAP and 100% mortality of affected patients.

In conclusion, effective surveillance with practical monitoring by a multidisciplinary team and rapid implementation of outbreak control are even more necessary in mixed ICUs and COVID-19 ICUs. We strongly suggest that national regulatory authorities establish protocols for the detection of *B. cepacia* complex in chlorhexidine-based products, ensuring microbiological quality of the finished product in addition to patient safety, so that similar outbreaks can be prevented.

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