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# Short Report

# Burkholderia cepacia complex outbreak originating from contaminated wash gloves

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# SUMMARY

*Burkholderia cepacia* complex isolates were detected from four patients who were admitted to the heart centre of southern Switzerland, between April and June 2019. An outbreak investigation was conducted. The three available patient samples were whole genome sequenced, showing that they all are *Burkholderia cepacia* species, and that two are identical. Isolates grown from sealed packages of disinfectant-free wash gloves used for personal hygiene were also genomically identical. The wash gloves appear to be the origin of the outbreak, contamination of which most likely occurred at the manufacturing site.

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# Introduction

Burkholderia cepacia complex (BCC) is a group of environmental gram-negative bacteria found in soil and water. Isolates are associated with human infections mainly in the setting of hospital-acquired infections linked to use of contaminated medical products [1,2], a contaminated environment or healthcare workers hands [3], and in cases of person-to-person transmission in cystic fibrosis sufferers [4]. This complex raises particular concern because of its multidrug resistance profile and high mortality rate associated with infection [5]. Herein, we report an outbreak of BCC associated with the use of contaminated pre-moistened disinfectant-free wash gloves, detected in the heart centre of southern Switzerland, a 30-bed university-affiliated clinic comprising a cardiology ward, a cardiac surgery ward and an intensive care unit.

# Description of the index cases

#### Patient 1

A 54 year old male patient was admitted to the cardiology unit after a non-ST-elevation myocardial infarction on March 2019. During the coronary angioplasty he developed severe cardio-circulatory compromise and needed support with femoro-femoral extracorporeal membrane oxygenation (ECMO). Subsequently, he developed acute right limb ischemia after ECMO removal, owing to a right femoral artery dissection that required surgical repair with a biosynthetic vascular

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#### Table 1

	Ceftazidime		Meropenem		Levofloxacin		Trimethoprim- sulfamethoxazole	
	MIC (mg/L)	Interpretation	MIC (mg/L)	Interpretation	MIC (mg/L)	Interpretation	MIC (mg/L)	Interpretation
Pat	ient							
1	1.5	S	8.0	I	3.0	I	0.12	I
2	1.5	S	8.0	I	3.0	I	0.12	I
3	2	S	8.0	I	>32	R	0.25	I
Glo	ve							
1	1.5	S	8.0	I	3.0	I	0.12	I
2	1.5	S	8.0	I	3.0	I	0.12	I

Resistance profile of *Burkholderia cepacia* complex isolates (MIC interpreted according to the Clinical and Laboratory Standards Institute (CLSI). Performance standards for antimicrobial susceptibility testing. 29th ed. CLSI; 2019. Supplement M-100)

S: Susceptible, I: Intermediate, R: Resistant.

prosthesis. In the following days, he presented signs of deep surgical site infection on the right groin that required surgical revision. The intraoperative biopsies showed growth of *Escherichia coli* and *Hafnia alvei*. A superficial swab of the left groin performed on May 2019 showed growth of BCC.

#### Patient 2

An 87 year old male patient was admitted to the cardiology unit because of severe cardiac decompensation related to a non-ST elevation myocardial infarction in April 2019. A coronary angioplasty was performed under femoro-femoral ECMO support, which was removed at the end of the procedure. He developed progressive signs of deep surgical site infection on the right groin that required surgical debridement in May 2019. The intraoperative biopsies showed growth of *Escherichia coli* and BCC.

#### Methods

A case was defined as a patient with a BCC isolate from any clinical specimen, detected from January 2019 onwards. The reference microbiology laboratory database was retrospectively reviewed for cases. We established a linelist and performed onsite audits to identify possible environmental sources and breaches in the infection control practices. Clinical samples were cultured on MacConkey Agar, Chocolate Agar + Polyvitex<sup>TM</sup> (Biomerieux) or Columbia Agar + 5% sheep blood (Becton Dickinson); environmental samples were cultured on the selective medium, Burkholderia cepacia Agar (Oxoid Limited). All cultures were incubated for at least 48 hours during the outbreak period. Antimicrobial sensitivity testing was performed using ETests (Biomerieux) and results interpreted according to CLSI guidelines [6]. Whole genome sequencing (WGS) was performed using an ISO/IEC 17025 accredited NextSeq500 Illumina sequencing platform following NexteraXT library preparation (Illumina) to mean coverage over 50x. All read data is available from the ENA (https://www. ebi.ac.uk/ena) under project PRJEB34276.

## Results

An outbreak investigation was launched in May 2019, because of an unusual detection of BCC in clinical samples from

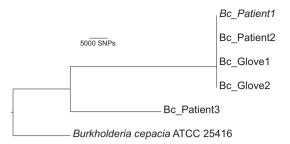
two index patients. The retrospective case finding through the microbiology laboratory database identified a further suspected case in April 2019, involving a patient with urinary colonisation with BCC (patient 3). A fourth case (patient 4) was prospectively detected on June 2019, also involving a patient with urinary colonisation with BCC. All patients were hospitalized in the heart centre of southern Switzerland before the detection of the first positive sample for BCC; no other common location was identified. A summary of the patients is shown in Supplementary TableS1.

Isolates from patient 1 and 2 exhibited the same antimicrobial resistance phenotypic profile with sensitivity to ceftazidime, trimethoprim-sulfamethoxazole and intermediate level of resistance to meropenem and levofloxacin (Table 1). The isolate from patient 3 was resistant to levofloxacin and exhibited a higher MIC for ceftazidime and trimethoprim-sulfamethoxazole. Isolate from patient 4 was no longer available for further testing.

Through a line list, the intensive care unit and the cardiology unit were identified as possible common locations. Because of the initial detection of BCC in clinical samples from the groin, ultrasound gel used for vascular ultrasound, disinfectant used for groin wound care and personal hygiene products were first tested. A total of six single products (each in two different Lot number) were sent to the microbiology laboratory. On June 21, 2019, growth of BCC was detected in two sealed packages from the two different Lot numbers of disinfectant-free wash gloves (COCUNE, Stöpler Medical B.V, and the Netherland). The remaining ten sampled medical products showed no bacterial growth. All clinical and environmental isolates grew within 24 hours incubation.

The sequenced bacterial isolates from patients and wash gloves were assembled by Unicycler v 0.3.0b [7]. PubMLST (https://pubmlst.org/bcc/; [8]) was used on the assemblies to identify the species as *Burkholderia cepacia*, and all isolates showed novel sequence types. The WGS typing results showed that two clinical isolates (Patient 1, Patient 2) are genomically identical to each other and to the two isolates from the two sealed glove packages (Figure 1). Patient 3 was not related to the outbreak (>66,000 SNPs divergence between isolates); Patient 4 isolates were not available for testing.

The incident was announced on June 21, 2019 to the Swiss agency for therapeutic products (Swissmedic) and to the local distributor of the wash gloves. No other hospital in the region of southern Switzerland was found to use the same medical



**Figure 1. Whole genome SNP phylogeny of the isolates.** The isolates from Patients 1 and 2, and Gloves 1 and 2 are identical across the whole genome. The genome of the isolate from Patient 1 (in italics) was used as the reference, and *Burkholderia cepacia* reference strain ATCC 25416 added for context. The scale shows the number of SNP differences, and the phylogeny is not rooted. The group of isolates including Patient 1, Patient 2, Glove 1 and Glove 2 are identical at the SNP level. This analysis was performed in CLC genomics workbench (v10.1.1).

product. No further cases were reported up to September 30, 2019.

# Discussion

Here we describe a small local outbreak of *Burkholderia cepacia* linked to contaminated wash gloves, promptly elucidated through the use of WGS. Since sealed packages from two different Lot numbers were tested, we conclude that the primary contamination most likely occurred at the manufacturing site. Contamination with *Burkholderia* species has been observed in a vast variety of medical products including: mouthwash solutions, liquid laxatives, eye drops, nasal spray and inhalation drugs, saline solutions, intravenous drugs, disinfectant solutions, disinfection wipes, ultrasound probe gel, body lotions, and new outbreaks are constantly reported in the literature [1,2,9].

Wash gloves are Class I (i.e. non-invasive) medical devices and are commonly used to optimize and facilitate patient personal hygiene. According to the European Union Regulation (EU) 2017/745 on medical devices, the quality assessment of this class of product remain under the sole responsibility of the manufacturer [10].

Only two other outbreaks linked to similar products have been reported in the literature so far. The first, linked to contaminated washcloths, described an outbreak in two tertiary care hospitals in Germany that involved 51 patients, eight of whom (15.7%) presented invasive infections [9]. The second, linked to contaminated wash gloves, described a national outbreak in Switzerland that involved a total of 46 patients, 22 of whom (47.8%) presented invasive infections [2]. This latter was unrelated to the present outbreak and involved a different manufacturer and *Burkholderia* species (*Bulkholderia stabilis*).

Our report includes only two confirmed, non-invasive cases, thanks to the rapid identification of the contaminated source. Nonetheless, it is likely that the more patients were affected but were not detected in the absence of surveillance screening. We can yet speculate a low rate of associated infections, which would have been otherwise detected by clinically-driven sampling. Despite being non-invasive devices, wash gloves can still be associated with outbreaks with potentially serious consequences in acute care settings. In our opinion, additional steps are necessary to standardise quality assessment requirements for this class of products when they are used for acute patient care.

#### Funding source

None.

# **Conflicts of interest**

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

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# Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.infpip.2020.100039.

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