

Polyclonal *Burkholderia cepacia* outbreak originating from contaminated wash gloves

INTRODUCTION

Burkholderia cepacia complex (Bcc) bacteria are opportunistic pathogens that cause infections in cystic fibrosis and immunocompromised patients. Bcc bacteria can spread among hospitalised patients through person-to-person transmission, contaminated liquids and surfaces and are notorious for their persistence in aqueous solutions. We describe two episodes of a polyclonal *B. cepacia* outbreak at a Belgian intensive care unit due to contaminated wash gloves.

MATERIALS & METHODS

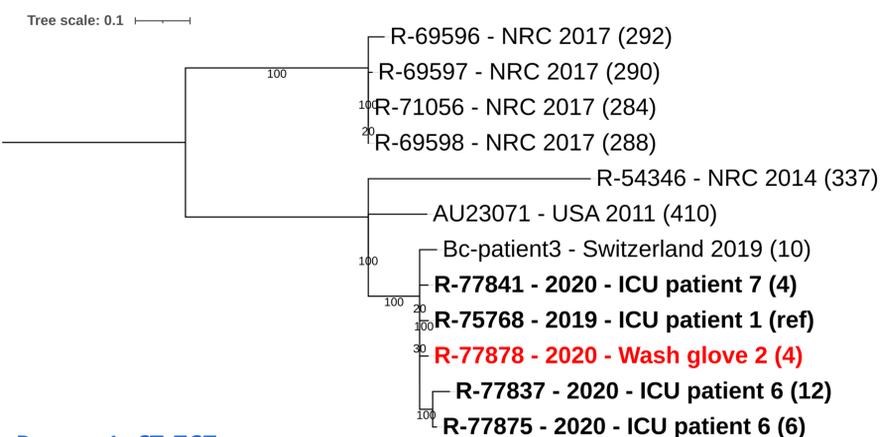
Bcc was isolated from routine clinical samples from nine Belgian ICU patients in April-May 2019 and January 2020. Cultures for Bcc were taken from several hygienic products and the suspected wash gloves. In the framework of the NRC Bcc, all resulting Bcc isolates were investigated by MALDI-TOF MS for identification and RAPD for typing. Identification and typing were confirmed by *recA* gene sequence analysis and whole-genome sequence based MLST, respectively. More detailed genomic analyses were performed using SNP analyses.

RESULTS

Five out of seven patient isolates from April-May 2019 were identified as *B. cepacia* (n=5). One of two tested wash glove packages was culture positive and the investigated wash glove isolate was identified as *B. cepacia*. RAPD typing showed an identical pattern for four *B. cepacia* patient isolates and the wash glove isolate, and a different pattern for the remaining *B. cepacia* patient isolate. MLST analysis confirmed the RAPD typing results and identified the two *B. cepacia* RAPD patterns as ST-1649 (n=5) and ST-767 (n=1). The manufacturer confirmed the contamination of one lot by *Burkholderia* (but provided no cultures) and reported to have taken measures to avoid further contamination.

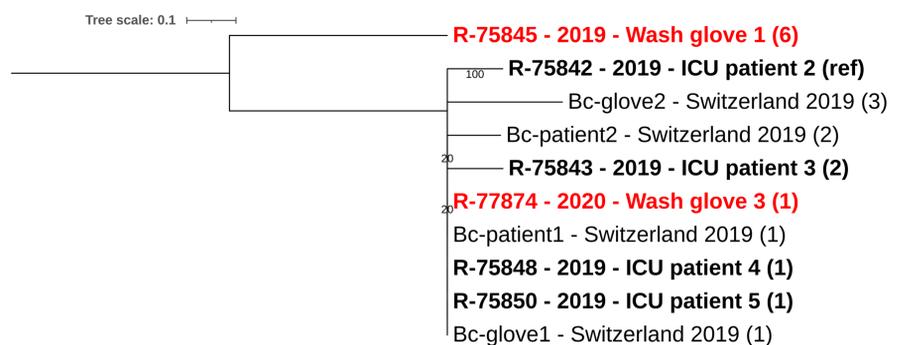
The three patient isolates from January 2020 were all *B. cepacia* ST-767 (n=3, two isolates from same patient). One out of four tested wash glove lots was culture positive and yielded both *B. cepacia* ST-767 and ST-1649. After abandoning the use of wash gloves from this manufacturer no new cases were recorded.

SNP analysis (snippy) was performed on ST-767 and ST-1649 genomes from the present study and GenBank. RAxML was used for phylogenetic analysis (100 bootstraps) on the core SNP alignments (136 and 10 nucleotides for ST-767 and ST-1649, respectively).



B. cepacia ST-767

- 4-12 SNPs in genomes from ICU patients and wash gloves
- 10 SNPs in genome from wash glove outbreak Switzerland
- 288-410 SNPs with other ST-767 genomes from GenBank



B. cepacia ST-1649

- 1-6 SNPs in genomes from ICU patients and wash gloves
- 1-3 SNPs in genomes from wash glove outbreak Switzerland
- No other genomes with ST-1649 in GenBank

CONCLUSION

Recovery of *B. cepacia* from several ICU patients led to a small-scale outbreak investigation and identified contaminated wash gloves as the outbreak common source. Remarkably, in the course of the present study, *B. cepacia* ST-767 and ST-1649 contaminated wash gloves from the same manufacturer were reported as the cause of an outbreak in a heart clinic in Switzerland^[1].

[1]: Priore *et al.* Infection Prevention in Practice, 2020.