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Letter to the Editor

A cluster of Burkholderia contaminans bloodstream infections in a rural hospital in Sierra Leone

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Dear Editor,

Burkholderia cepacia complex (BCC) are Gram-negative, non-fermenting organisms commonly found in soil and water, which are able to survive for months in humid environments.[1] BCC comprises more than 20 closely related species including *B. cepacia*, *B. cenocepacia*, and *B. contaminans*.[2] BCC are recognized opportunistic pathogens in patients with cystic fibrosis,[3] but due to their low virulence, they are rare causes of infection among the general population. In healthcare settings, outbreaks of BCC were associated with contaminated surfaces, equipment, or liquid medicinal products and disinfectants.[1] *B. cepacia* is the most common species involved, with *B. contaminans* reported in only 4% (n = 5/121) of cases.[1] In this study we aimed to describe a cluster of *B. contaminans* bloodstream infections from a referral hospital in Sierra Leone.

Masanga Teaching Hospital, located in Tonkolili District in Sierra Leone, is a rural hospital with 120 beds providing health care for about 12,000 patients annually. Between April and October 2023, BCC was isolated from blood cultures of six patients. Four patients, three from the pediatric ward and one adult from the maternity ward had BCC bacteremia between April and August 2023.

The hospital infection prevention and control team presumed that contaminated intravenous solutions could be the source.[4] Contamination probably occurred extrinsically, from environmental sources, because of repeated use. These solutions were used to flush peripheral intravenous catheters over several days after being opened for multiple patients. The solutions may have been contaminated either through leaving syringe needles attached to an opened bag and/or through lacking disinfection of the rubber top when accessing a previously opened bag.

On August 27, 2023, nurses on the ward were requested not to use intravenous solutions packages for longer than two days after opening. Additionally, hand hygiene practices and adherence to sterile procedures were reinforced. Two additional patients, both from the pediatric ward, had positive blood cultures with BCC in October 2023 likely due to continuing practices. Following this, infection prevention and control practices were reinforced, and no other cases occurred.

Available BCC isolates from blood cultures from this time period (n = 5, as one isolate could not be recovered for sequencing) and an additional isolate from a wound swab from a patient who presented to the Masanga Teaching Hospital in 2019 (outlier isolate) underwent whole genome sequencing (WGS). WGS was conducted at the University Hospital Münster in 2024; sequences were submitted to BioProject (PRJNA1196134).

Four isolates, all from the pediatric ward were confirmed by WGS as *B. contaminans* belonging to sequence type ST2327 (Supplement). They differed by only ≤2 alleles of the 1,857 target genes in the BCC cgMLST typing scheme and were considered identical. Of the four patients, two had overlapping stays on the same ward in April and the other two in October 2023. The other isolates, which were from an adult from the maternity unit, and another one from a patient presenting with osteomyelitis in 2019 were *B. cepacia* (ST2325 and ST2328, Figure 1). Without any known related cases identified, the infection of the adult patient could also have been due to contaminated solutions.

Microbiological testing of the intravenous solutions and environmental sampling, which might have enabled us to establish the origin of the cluster, were not conducted because of resource constraints.

A systematic review of outbreaks due to contaminated substances found that multiuse solutions were linked to outbreaks in almost half of cases, with BCC as a leading causative organism.[5] However, few studies from low- and middle-income countries[5] were included likely due to considerable underreporting. The lack of identification of outbreaks in low-resource settings is largely due to limited access to microbiology testing, the need for patients to pay out of pocket for health care including diagnostics, and the difficulties in conducting environmental sampling within hospital facilities. Recognition of outbreaks due to BCC may be further challenged by difficulties in identification of these organisms using manual methods and the cost and availability of laboratory consumables needed for identification.

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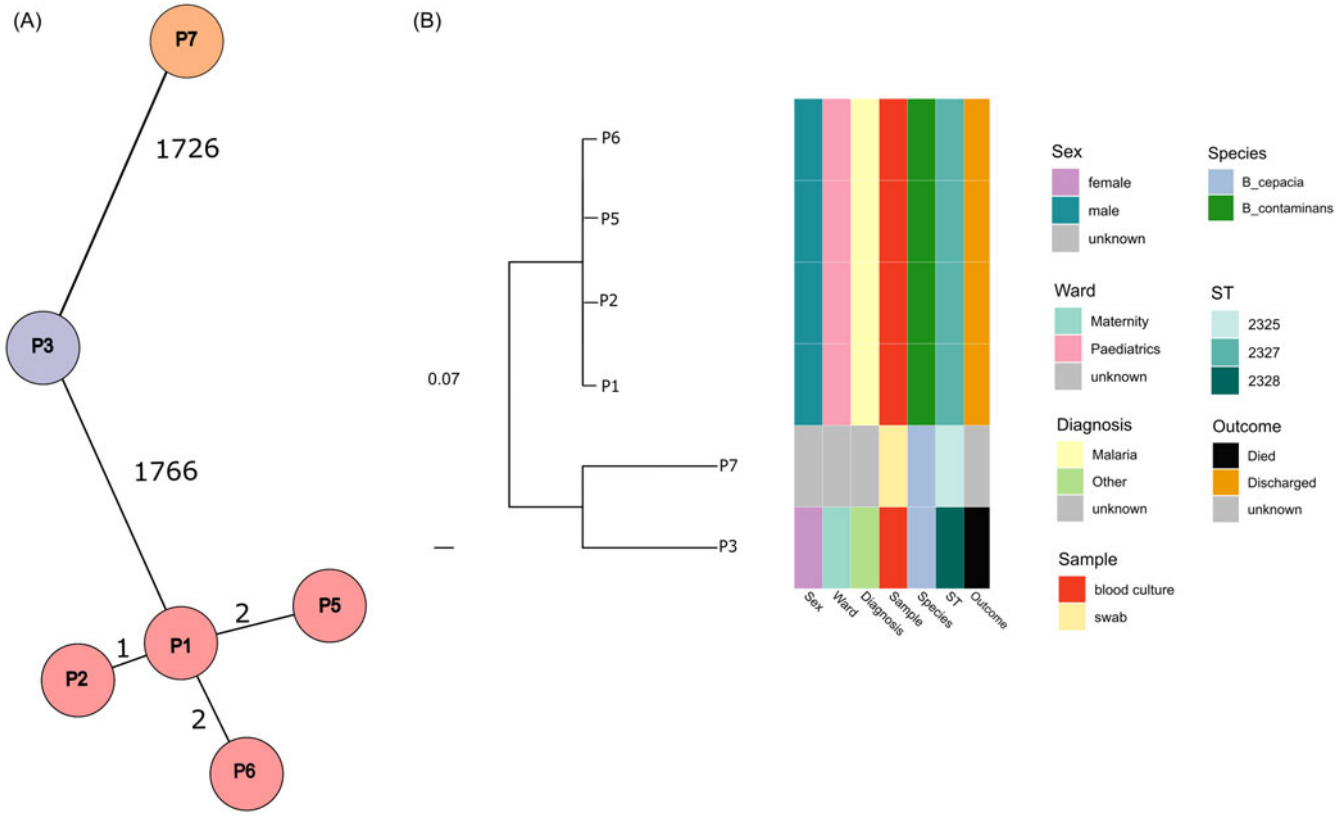

Figure 1. Genomic relatedness of the *Burkholderia cepacia* complex isolates from Masanga Hospital and clinical characteristics of patients. The minimum spanning tree (A) was constructed using the 1,857 genes of the BCC core genome multilocus sequence typing (cgMLST) scheme. Nodes are labeled with the patient numbers (P1 to P7). Numbers between the nodes indicate the numbers of differing alleles between isolates. The neighbor-joining tree (B) was constructed using the concatenated sequence of the cgMLST typing scheme. Sex, wards, diagnosis sample, species, sequence type (ST), and outcome were color-coded. The phylogenetic analysis was visualized using R version 4.4.1 (packages ggtree, pheatmap and treeio.

Overall, few studies from Africa report outbreaks due to contamination of solutions for parenteral use.[6–8] A study in Gambian neonates identified contamination of intravenous fluids and the multiple use of single-dose antibiotics as sources for outbreaks with *Klebsiella pneumoniae* and *B. cepacia*. The study included 49 neonates with *B. cepacia* bacteremia and was associated with a considerable mortality.[7] Generally, the mortality reported for BCC outbreaks is low (1%).[1] In our study, none of the four children with related BCC isolates died. It is unclear whether the adult patient died because of the BCC infection or due to complications following delivery. Despite the low mortality, outbreaks can be associated with substantial costs due to prolonged hospital stays and the need for conducting outbreak investigations.[1] Furthermore, BCC is intrinsically resistant to many antimicrobials which importantly limits treatment options, particularly in low-resource settings.

It is possible that bacteremia episodes due to BCC also occurred in other hospitalized patients without being identified as blood cultures are not usually collected after the initial presentation.

These findings from a rural hospital in Sierra Leone highlight the importance of the availability of microbiology diagnosis for outbreak identification and for the implementation of control measures. Although multiuse intravenous solutions have repeatedly been linked to outbreaks, these practices remain common in limited resource settings.

Supplementary material. The supplementary material for this article can be found at https://doi.org/10.1017/ice.2025.63

Data availability statement. The data for this work has been made available in the manuscript. The whole genome sequences of the bacterial isolates were submitted to BioProject (PRJNA1196134).

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Competing interests. The authors declare none.

Ethical standard. Hospital policies relating to data privacy were followed.

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