Tropical Biomedicine 43(1): 1-4 (2026)
https://doi.org/10.47665/tb.43.1.001

CASE REPORT

Violet-pigmented *Burkholderia contaminans* sequence type 922 bacteremia in an end-stage renal disease patient – a case report and review of the literature

Ahmad, S.[1], **Mohd Sukhaimi, N.A.**[1], **Shahimi, S.S.**[2], **Mahfodz, N.H.**[3], **Soh, Y.H.**[4], **AbuBakar, S.**[3], **Choong, K.Y.**[2*], **Loong, S.K.**[3*]

[1]Pathology Unit, Hospital Jasin, Jalan Utama, 77000 Jasin, Melaka, Malaysia
[2]Department of Pathology, Hospital Melaka, Jalan Mufti Haji Khalil, 75400 Melaka, Malaysia
[3]Tropical Infectious Diseases Research & Education Centre, Higher Institution Centre of Excellence, Universiti Malaya, 50603 Kuala Lumpur, Malaysia
[4]Centers for Disease Control and Prevention Unit, Central Melaka District Health Office, Jalan Bukit Baru, 75150 Melaka, Malaysia
*Corresponding authors: choongky@moh.gov.my; choongkingyen03@yahoo.com; loongsk@um.edu.my; shihkeng@gmail.com

ARTICLE HISTORY

Received: 11 July 2025
Revised: 18 September 2025
Accepted: 19 September 2025
Published: 31 March 2026

ABSTRACT

Burkholderia cepacia complex (Bcc) is an emerging nosocomial pathogen, with violet-pigmented strains representing a rare and possibly neglected but clinically important subset. We report a case of a 62-year-old man with end-stage renal disease on dialysis who presented with fever and cough. Blood cultures from central and peripheral lines grew violet-pigmented, non-lactose fermenting colonies on MacConkey agar, later identified as *Burkholderia contaminans* sequence type 922 (ST922) via a multimodal approach. Initial phenotypic methods (VITEK-2, API20NE and MALDI-ToF) and 16S rDNA sequencing were inconclusive; however, multilocus sequence typing confirmed ST922, a strain previously reported in India and associated with nosocomial outbreaks. The isolate was susceptible to ceftazidime, trimethoprim/sulfamethoxazole, minocycline, and meropenem. The patient responded well to intravenous ceftazidime, with subsequent blood cultures yielding no growth. Notably, antimicrobial susceptibility varied geographically, with some ST922 isolates resistant to third-generation cephalosporins. This case illustrates the diagnostic challenges in Bcc speciation and highlights the value of molecular tools such as MLST. The detection of this strain in Malaysia raises concerns about global dissemination, potentially via contaminated medical devices or water systems. Early recognition of violet-pigmented Bcc in resource-limited settings can facilitate prompt, targeted treatment. This report underscores the need for environmental surveillance and antimicrobial stewardship to prevent spread, while reinforcing Bcc's ecological adaptability and clinical significance, especially in immunocompromised individuals.

Keywords: Infection; Malaysia; neglected; tropical.

INTRODUCTION

Burkholderia spp. are aerobic, Gram-negative, non-fermenting bacilli found extensively in both natural and man-made environments. Initially identified by Walter H. Burkholder in the 1940s as the causative agent of onion rot (*Burkholderia cepacia*), the genus has since expanded to include over 24 phylogenetically related species classified under the *Burkholderia cepacia* complex (Bcc) (Tavares *et al*., 2020). The bacterium's ability to colonize surfaces, including intravenous lines, nebulizers, respiratory devices, and even disinfectants, contributes to its role in hospital infections (Bilgin *et al*., 2021).

The Bcc comprises opportunistic pathogens, particularly hazardous to immunocompromised individuals, cystic fibrosis (CF) patients (Ragupathi & Veeraraghavan, 2019), and even immunocompetent patients (Ranjan *et al*., 2017). Patients may be presented with pneumonia, bloodstream infection and nosocomial infections (De *et al*., 2022). Their clinical significance is compounded by intrinsic resistance to antibiotics and biocides, as well as their ability to contaminate water-based pharmaceutical products, leading to nosocomial outbreaks (Tavares *et al*., 2020). Notably, *Burkholderia cenocepacia* and *Burkholderia multivorans* are the most prevalent species in CF infections (LiPuma, 2010), though other members like *Burkholderia contaminans* and *Burkholderia dolosa* also contribute to severe outcomes (LiPuma, 2010; Tavares *et al*., 2020).

Interestingly, several reports from India have implicated violet-pigmented Bcc strains in the clinical setting. Specifically, four separate reports were published between 2017 and 2024 reporting the culture and identification of violet-pigmented Bcc strains in Meghalaya, Mumbai, New Delhi and Uttar Pradesh in India (Ranjan *et al*., 2017; Rastogi *et al*., 2019; De *et al*., 2022; Shah *et al*., 2024). The peculiar feature of violet pigment production in contrast to other Bcc strains, is hypothesized to be associated with heightened virulence and transmissibility properties (Rastogi *et al*., 2019). Herein, we

Published by Malaysian Society of Parasitology and Tropical Medicine.

describe a case involving violet-pigmented *B. contaminans* isolated from blood cultures of an elderly patient in Malaysia, and a review of other similar cases.

CASE REPORT

A 62-year-old Malay gentleman with underlying end-stage renal failure requiring regular dialysis via an internal jugular venous catheter, as well as diabetes mellitus and hypertension, initially presented to casualty in July 2024 with fever and cough lasting three days. On examination, the patient was found to be febrile (39.4 °C) but was otherwise haemodynamically stable. The patient's vital signs at presentation were stable with normal blood pressure (134/67 mmHg), mild tachycardia (92 bpm), normal respiratory rate (20 breaths/min) and pulse oximetry was 100% under facemask 5 L/min. Blood investigations revealed haemoglobin level of 11.9 g/dL, total white cell count of 9.95 x 10^9/L (neutrophils predominance) and platelet count of 237 10^9/L. Serum investigations revealed elevated creatinine (1137 µmol/L), urea (29.4 mmol/L), and C-reactive protein (93 mg/L) consistent with renal disease and suggestive of infection. Venous blood gas analysis showed: pH 7.38, pCO_2 24 mmHg, pO_2 65 mmHg, SO_2 92%, lactate 4.5 mmol/L, HCO_3 -14.2 mmol/L, and base excess -10.9 mmol/L. Screening for hepatitis B, hepatitis C and human immunodeficiency viruses (HIV) returned negative. Chest radiography revealed no pulmonary infiltrates or consolidations. Given the febrile presentation in a catheter-dependent hemodialysis patient, our primary differential diagnosis centered on catheter-related bloodstream infection (CRBSI). Following standard protocols for CRBSI evaluation, we obtained paired blood cultures (simultaneous peripheral and central catheter draws) which were immediately processed using the BACTEC blood culture system (Becton Dickinson, USA).

Subsequently, aerobic bottles from the central and peripheral sources were flagged positive after 7.89 h followed by inoculation on Columbia agar with 5% horse blood, MacConkey and chocolate agars. The agars were incubated overnight at 37 °C under aerobic conditions. Following overnight incubation, Columbia and chocolate agars managed to show growth of a 1.0-2.0 mm diameter grey colored colonies (Figure 1A) while violet pigmented non-lactose fermenter colonies, measuring 0.5-1.0 mm in diameter were observed on MacConkey agar (Figure 1B). Pure single colonies were obtained from the primary cultures of Columbia, MacConkey and chocolate agars (three bacteria isolates). Rapid biochemical testing of the isolates showed identical catalase and oxidase positive results.

The bacteria isolates were then identified as *B. cepacia* group using two independent semi-automated biochemical tests. All three bacteria isolates recorded similar identification scores on the VITEK-2 and API20NE systems, with the scores of 90 and 99%, excellent identification, respectively. Identification of the isolates was also performed using matrix assisted laser desorption ionization-time of flight mass spectrometry (MALDI-ToF) with the score value of 2.23 and all methods pointed to the identification of the isolates as *B. cepacia*. Antimicrobial susceptibility testing following guidelines by the Clinical and Laboratory Standards Institute (CLSI) (Clinical and Laboratory Standards Institute, 2024) revealed that the isolates were susceptible to ceftazidime, trimethoprim/sulfamethoxazole, minocycline and meropenem.

Molecular identification of the isolates via amplification and sequencing of the partial 16S rDNA gene (Chua *et al*., 2024) revealed that isolates that were cultured on the respective agars had identical nucleotide sequences (Accession no. PV875208). However, subsequent BLAST analyses showed that the partial 16S rDNA gene nucleotide sequences have 100% homology with *B. cepacia*, *B. cenocepacia*, *B. contaminans* and *Burkholderia lata*, complicating the identification of the microorganism. This prompted the application of multilocus sequence typing (MLST) according to the Bcc scheme (Baldwin *et al*., 2005) for the subsequent characterization of the Bcc isolates. MLST determined that all the isolates in the present study had allelic profiles (*atpD*: allele 361, *gltB*: allele 325, *gyrB*: allele 640, *recA*: allele 382, *lepA*: allele 431, *phaC*: allele 329, and *trpB*: allele 330) corresponding to sequence type 922 (ST922). Examination into the PubMLST database housing the Bcc molecular typing data (https://pubmlst.org/organisms/burkholderia-cepacia-complex) (Jolley *et al*., 2018) classified ST922 as *B. contaminans*.

As soon as the attending clinician was informed about the microorganism's antimicrobial susceptibility, the patient that was previously given intravenous cloxacillin (2 g every 6 h) was switched to intravenous ceftazidime (2 g every 48 h). Subsequent blood cultures showed no bacteria, indicating that the *B. contaminans* bacteremia had been resolved after the seven-day antibiotic course. The patient demonstrated significant clinical improvement - remaining afebrile, tolerating oral intake, and maintaining adequate oxygen saturation on room air - and was subsequently discharged with a plan for outpatient intravenous ceftazidime (2 g every 48 h) for seven additional days.

Review of the literature (as of July 2025) found four previously published clinical reports describing the clinical identification and isolation of violet-pigmented Bcc strains (Table 1). All the previously

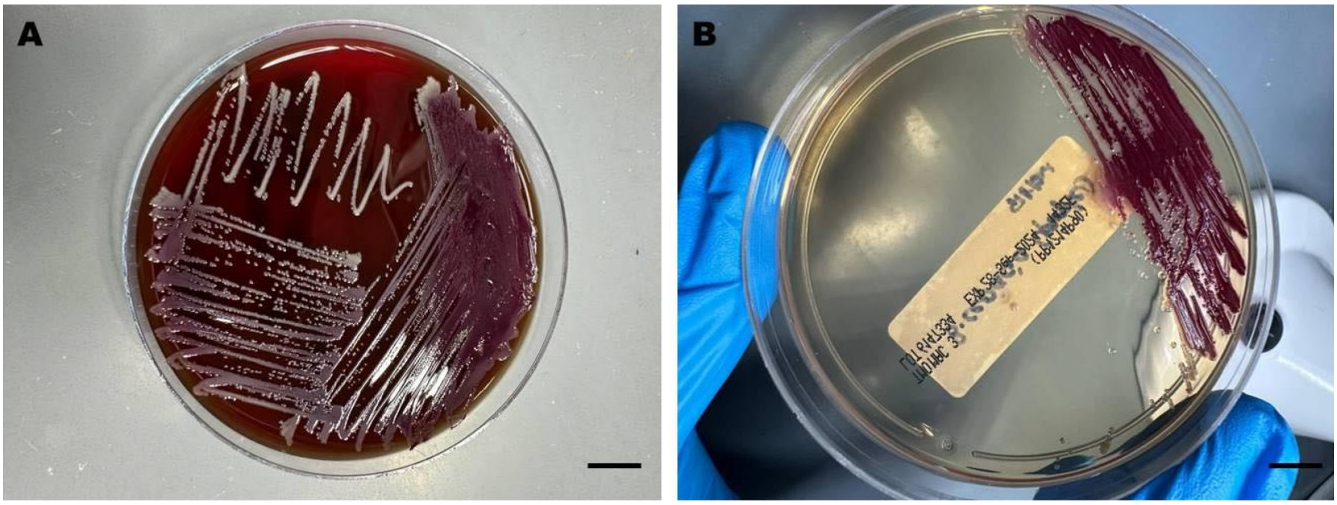

Figure 1. Cultures of the Bcc isolates on (A) Columbia agar with 5% horse blood and (B) MacConkey agar (violet-pigmented colonies). Scale is equivalent to approximately 1.5 cm.

published studies from India relied on commercially available phenotypic identification systems (VITEK-2 and MicroScan) for the identification of the Bcc isolates. Rastogi *et al*. (2019) performed additional MLST as part of their epidemiological investigation and to track the source of infection. In the present study, we complemented phenotypic identification with molecular identification methods for the accurate identification of the *B. contaminans* ST922 isolates. Bcc isolates were cultured from the blood of all the cases (Table 1), indicating that all patients had bacteremia, with most of them also carrying indwelling catheters. Collectively, the Bcc isolates were susceptible to ceftazidime, trimethoprim/sulfamethoxazole, minocycline, tigecycline, ciprofloxacin, levofloxacin, imipenem and meropenem.

DISCUSSION

Burkholderia cepacia complex consists of gram-negative bacteria that belong to the β-proteobacteria subdivision, known for its opportunistic nature and are frequently associated with nosocomial infections (Bilgin *et al*., 2021; de Sá Paraskevopoulos *et al*., 2025). Bcc infection increases morbidity and mortality by up to 75% (Branstetter *et al*., 2020), especially in hospitalized patients, because of its capacity for tolerance for a broad spectrum of environmental conditions (Bilgin *et al*., 2021).

The identification of the violet-pigmented *B. contaminans* ST922 in this case employed a multimodal approach, surpassing the limitations of phenotypic methods used in prior studies (Table 1). While earlier reports from India relied solely on automated systems (VITEK-2, MicroScan) (Ranjan *et al*., 2017; De *et al*., 2022; Shah *et al*., 2024), the present study integrated: conventional biochemical assays (catalase and oxidase tests), commercially available phenotypic identification systems (VITEK-2 and API20NE), mass spectrometry, and molecular typing methods. Even though 16S rDNA sequencing has been recommended to be a practical bacteria identification method (Chua *et al*., 2024), it could not distinguish Bcc species in this case, highlighting its limitations for species level resolution. MLST on the other hand definitively identified the *B. contaminans* ST922 isolates, and this approach aligns with recommendations by Tavares *et al*. (2020), who emphasize genotypic methods to overcome phenotypic ambiguities in Bcc.

Antimicrobial susceptibility testing revealed that the *B. contaminans* ST922 isolate was susceptible to ceftazidime, trimethoprim/sulfamethoxazole, minocycline and meropenem, aligning with susceptibility patterns observed in most Indian Bcc isolates (Table 1). Notably, this finding contrasts with ST922 strains from New Delhi (Rastogi *et al*., 2019), which demonstrated resistance to third-generation cephalosporins. This discrepancy highlights strain-specific resistance profiles within the same sequence type (ST922), emphasizing that susceptibility patterns can vary even among clonally related isolates. Such variability reinforces the importance of local antimicrobial susceptibility testing to guide therapy, as Bcc resistance is influenced by both genetic factors and regional antimicrobial pressure (LiPuma, 2010).

The detection of *B. contaminans* ST922 in Malaysia, India (Rastogi *et al*., 2019), and personal care products in China (Wen *et al*., 2020) underscores its broad geographic spread and environmental resilience. Notably, the PubMLST Bcc database records further document ST922 in the USA, Spain, and Belgium, suggesting a wider and possibly underreported distribution. This strain's persistence in industrial products even amid harsh preservatives, demonstrates a striking capacity to thrive in hostile environments (de Sá Paraskevopoulos *et al*., 2025), reinforcing its role as a tenacious nosocomial and community-acquired pathogen.

Table 1. Clinical and microbiology descriptions of violet-pigmented Bcc cases obtained from the literature, in chronological order

Location	Identification method	Clinical and microbiology information	Reference
Melaka, Malaysia	VITEK-2, API20NE, MALDI-ToF, 16s rDNA sequencing and MLST	– The patient had an internal jugular venous catheter. – *B. contaminans* ST922 was susceptible to ceftazidime, trimethoprim/sulfamethoxazole, minocycline and meropenem. – Treated with ceftazidime and discharged.	The present study
Meghalaya, India	VITEK-2	– Four patients with indwelling catheters. – All Bcc isolates were susceptible to minocycline, levofloxacin, trimethoprim/sulfamethoxazole, and meropenem. – All patients were treated with levofloxacin and discharged.	Shah *et al*., 2024
Mumbai, India	VITEK-2	– Five patients with sepsis (one acute myeloid leukemia patient was on mechanical ventilator and the other four did not have indwelling catheter). – All Bcc isolates were susceptible to meropenem, trimethoprim/sulfamethoxazole and ceftazidime but were resistant to gentamicin and polymyxin B. – Treated with ceftazidime, trimethoprim/sulfamethoxazole, imipenem/meropenem and ceftriaxone.	De *et al*., 2022
New Delhi, India	VITEK-2, *recA* sequencing and MLST	– Bcc outbreak at a neurotrauma intensive care unit (48 patients had Bcc bacteraemia). – All clinical isolates were classified as ST922. – Bcc was also isolated from the water source. – All Bcc isolates were sensitive to carbapenems and resistant to third generation cephalosporins (however, ceftazidime was not tested) and piperacillin–tazobactam.	Rastogi *et al*., 2019
Uttar Pradesh, India	MicroScan	– Immunocompetent outpatient presenting with Multiple Organ Dysfunction Syndrome (MODS). – Bcc isolate was susceptible to ciprofloxacin, levofloxacin, imipenem and meropenem. – Patient was treated with ciprofloxacin and discharged.	Ranjan *et al*., 2017

While the source of infection in this case remains unconfirmed, the jugular venous catheter is a plausible portal, consistent with prior ST922 bacteremia linked to indwelling devices (Rastogi *et al*., 2019; Shah *et al*., 2024). However, alternative routes cannot be dismissed. Bcc's affinity for aqueous environments (Tavares *et al*., 2020) raises the possibility of transmission via contaminated water or solutions, as demonstrated by outbreaks tied to hospital water sources (Rastogi *et al*., 2019) and bath products (de Sá Paraskevopoulos *et al*., 2025). A clinically significant Bcc case from Uttar Pradesh, India (Ranjan *et al*., 2017; Table 1) involved an immunocompetent patient who developed bacteremia with gastrointestinal symptoms (vomiting, abdominal pain) progressing to MODS. This presentation, occurring without indwelling catheters or other typical risk factors, strongly suggests possible oral transmission through contaminated water. Such cases underscore the importance of investigating alternative infection routes beyond medical devices, particularly for immunocompetent individuals.

CONCLUSION

This case report advances the characterization of violet-pigmented *B. contaminans* ST922 through a multimodal diagnostic approach, revealing its genetic link to strains from India, China, USA, Spain, and Belgium, underscoring its potential global spread. The isolate's antimicrobial susceptibility profile supports current treatment strategies while highlighting the need for robust surveillance. These findings emphasize the importance of environmental monitoring in healthcare settings and antimicrobial stewardship to mitigate the threat of this adaptable pathogen.

Conflict of Interest Statement

The authors declare that they have no conflicts of interest.

ACKNOWLEDGEMENTS

This study was supported in parts by the Ministry of Higher Education, Malaysia under the Higher Institution Centre of Excellence (HICoE) program for niche area research (MO002-2019 and TIDREC-2023).

REFERENCES

Baldwin, A., Mahenthiralingam, E., Thickett, K.M., Honeybourne, D., Maiden, M.C.J., Govan, J.R., Speert, D.P., Lipuma, J.J., Vandamme, P. & Dowson, C.G. (2005). Multilocus sequence typing scheme that provides both species and strain differentiation for the *Burkholderia cepacia* complex. *Journal of Clinical Microbiology* **43**: 4665-4673. https://doi.org/10.1128/JCM.43.9.4665-4673.2005

Bilgin, H., Gelmez, G.A., Bayrakdar, F., Sayın, E., Gül, F., Pazar, N., Çulha, G., Yıldız, S., Cinel, I. & Korten, V. (2021). An outbreak investigation of *Burkholderia cepacia* infections related with contaminated chlorhexidine mouthwash solution in a tertiary care center in Turkey. *Antimicrobial Resistance and Infection Control* **10**: 143. https://doi.org/10.1186/s13756-021-01004-8

Branstetter, J.W., Yarbrough, A. & Poole, C. (2020). Management of cepacia syndrome with a combination of intravenous and inhaled antimicrobials in a non-cystic fibrosis pediatric patient. *The Journal of Pediatric Pharmacology and Therapeutics* **25**: 730-734. https://doi.org/10.5863/1551-6776-25.8.730

Chua, H.S., Soh, Y.H., Ibrahim, S., Abdullah, N.H., Che Mat Seri, N.A.A., AbuBakar, S. & Loong, S.K. (2024). Novel *Vibrio vulnificus* sequence type 540 infection in a hepatitis patient. *Tropical Biomedicine* **41**: 220-223. https://doi.org/10.47665/tb.41.2.014

Clinical and Laboratory Standards Institute. (2024). Performance Standards for Antimicrobial Susceptibility Testing. 34th edition CLSI M100. Wayne, PA.

De, A., Shastri, J.S., Malak, N.I., Kedia, M. & Sisodia, H. (2022). Unusual violet coloured pigment produced by *Burkholderia cepacia* complex: a report of five cases from a tertiary care hospital in Mumbai. *Journal of Medical Sciences and Health* **8**: 173-176. https://doi.org/10.46347/jmsh.v8i2.21.188

de Sá Paraskevopoulos, D.K., Camargo, C.H., Kodato, P.K., Yamada, A.Y., Almodovar, A.A.B., Hilinski, E.G., de Paula, A.I., Irineu, E.F., Barrio, S.R., Fonseca, C.L. *et al*. (2025). A *Burkholderia contaminans* outbreak in an intensive care unit associated with contaminated bath solution: control and microbiological findings. *American Journal of Infection Control* **53**: 308-313. https://doi.org/10.1016/j.ajic.2024.10.006

Jolley, K.A., Bray, J.E. & Maiden, M.C.J. (2018). Open-access bacterial population genomics: BIGSdb software, the PubMLST.org website and their applications. *Wellcome Open Research* **3**: 124. https://doi.org/10.12688/wellcomeopenres.14826.1

LiPuma, J.J. (2010). The changing microbial epidemiology in cystic fibrosis. *Clinical Microbiology Reviews* **23**: 299-323. https://doi.org/10.1128/CMR.00068-09

Ranjan, R., Chowdhary, P. & Kamra, A. (2017). Community acquired *Burkholderia cepacia* bacteraemia presenting as MODS in an immunocompetent individual: an unusual case. *Journal of Clinical and Diagnostic Research* **11**: DD01-DD02. https://doi.org/10.7860/JCDR/2017/16285.9435

Rastogi, N., Khurana, S., Veeraraghavan, B., Inbanathan, F.Y., Sekar, S.K.R., Gupta, D., Goyal, K., Bindra, A., Sokhal, N., Panda, A. *et al*. (2019). Epidemiological investigation and successful management of a *Burkholderia cepacia* outbreak in a neurotrauma intensive care unit. *International Journal of Infectious Diseases* **79**: 4-11. https://doi.org/10.1016/j.ijid.2018.10.008

Ragupathi, N.K.D. & Veeraraghavan, B. (2019). Accurate identification and epidemiological characterization of *Burkholderia cepacia* complex: an update. *Annals of Clinical Microbiology and Antimicrobials* **18**: 7. https://doi.org/10.1186/s12941-019-0306-0

Shah, K., Ngairangbam, M., Gogoi, N., Chakraborty, P. & Lyngdoh, W.V. (2024). *Burkholderia cepacia* complex producing a peculiar violet pigment: a case series from a tertiary care hospital in Meghalaya. *Cureus* **16**: e64126. https://doi.org/10.7759/cureus.64126

Tavares, M., Kozak, M., Balola, A. & Sá-Correia, I. (2020). *Burkholderia cepacia* complex bacteria: a feared contamination risk in water-based pharmaceutical products. *Clinical Microbiology Reviews* **33**: e00139-19. https://doi.org/10.1128/CMR.00139-19

Wen, X., Xie, X., Zhang, S., Sun, T., Liu, J. & Li, W. (2020). *Burkholderia cepacia* complex in personal care products: molecular epidemiology and susceptibility to preservatives. *Journal of Cosmetic Science* **71**: 133-148.