

DOI: 10.4274/mjima.galenos.2026.26933
Mediterr J Infect Microb Antimicrob 2026;15:26933
Erişim: <http://dx.doi.org/10.4274/mjima.galenos.2026.26933>

Molecular identification of fatal *Clostridioides manganotii* bloodstream infection in an immunocompromised patient: A case report

Bağıışıklık sistemi baskılanmış bir hastada ölümcül *Clostridioides manganotii* kan dolaşımı enfeksiyonunun genomik olarak tanımlanması: Bir vaka raporu

● Sabeen Zara¹, ● Hamad Abdelhadi¹, ● Ahmad Al Bishawi¹, ● Peter Coyle², ● Faiha Eltayeb³, ● Yunus Panikkaveettii Hamza², ● Sulieman Abu Jarir¹, ● Muna Al Maslamani¹

¹Hamad Medical Corporation, Division of Infectious Diseases, Department of Medicine, Doha, Qatar

²Hamad Medical Corporation, Division of Virology, Department of Laboratory Medicine and Pathology (DLMP), Doha, Qatar

³Hamad Medical Corporation, Division of Microbiology, Department of Laboratory Medicine and Pathology (DLMP), Doha, Qatar

Abstract

Immunocompromised patients are at increased risk of rare opportunistic and emerging infections that can be difficult to diagnose using conventional methods. Molecular approaches can facilitate the identification of unusual pathogens that warrant further investigation. A 36-year-old woman with metastatic invasive ductal carcinoma who had received broad-spectrum antimicrobials for recurrent febrile neutropenia was acutely admitted to the hospital with fever, tachycardia, and hypotension. Septic workup revealed anaerobic Gram-positive bacilli that could not be identified by Matrix-assisted laser desorption/ionization time-of-flight, whereas the VITEK 2 automated system suggested *Clostridioides difficile*. Despite broad-spectrum antibiotics targeting presumed clostridial infection, including piperacillin/tazobactam, meropenem, vancomycin, and metronidazole, her condition rapidly deteriorated to septic shock, and she died within 72 hours of its onset. Because of the unusual presentation and discordant microbiological results, 16S ribosomal RNA (rRNA) gene amplification and sequencing were performed. The isolate was provisionally identified as *Clostridioides manganotii*. This environmental pathogen is closely related to *Clostridioides difficile* but has rarely been implicated in human disease. This case highlights the importance of molecular diagnostics in identifying rare invasive pathogens in immunocompromised hosts.

Keywords: *Clostridioides difficile*, *Clostridioides manganotii*, bloodstream infection, immunocompromised

Öz

Bağıışıklık sistemi baskılanmış hastalar, geleneksel yöntemlerle değerlendirilmesi zor olan nadir fırsatçı enfeksiyonlar ve yeni ortaya çıkan enfeksiyonlar açısından artmış risk altındadır. Moleküler yaklaşımlar, daha fazla araştırma gerektiren alışılmadık patojenlerin tanımlanmasını kolaylaştırabilir. Tekrarlayan ateşli nötropeni nedeniyle geniş spektrumlu antimikrobiyaller alan metastatik invaziv duktal karsinomlu 36 yaşında bir kadın, ateş, taşikardi ve hipotansiyon ile akut olarak hastaneye yatırıldı. Sepsis araştırması, MALDI-TOF ile tanımlanamayan anaerobik Gram-pozitif basiller ortaya koyarken, VITEK 2 otomatik sistemi *Clostridioides difficile*'yi düşündürdü. Geniş spektrumlu antibiyotikler (piperasilin/tazobaktam, meropenem, vankomisin ve metronidazol dahil) ile Clostridium enfeksiyonuna yönelik olası tedavilere rağmen, hasta hızla septik şoka girdi ve başlangıcından itibaren 72 saat içinde hayatını kaybetti. Olağandışı tablo ve uyumsuz mikrobiyolojik sonuçlar nedeniyle, 16S rRNA gen amplifikasyonu ve sekanslama yapıldı. İzolat geçici olarak *Clostridioides manganotii* olarak tanımlandı. Bu çevresel patojen, *Clostridioides difficile* ile yakından ilişkilidir ancak insan hastalığında nadiren rol oynamıştır. Bu vaka, bağışıklık sistemi baskılanmış hastalarda nadir görülen invaziv patojenlerin tanımlanmasında moleküler tanımlamanın önemini vurgulamaktadır.

Anahtar Kelimeler: *Clostridioides difficile*, *Clostridioides manganotii*, kan dolaşımı enfeksiyonu, bağışıklık sistemi baskılanmış



Address for Correspondence/Yazışma Adresi: Sabeen Zara, MD, Hamad Medical Corporation, Division of Infectious Diseases, Department of Medicine, Doha, Qatar

E-mail: SZara1@hamad.qa **ORCID ID:** orcid.org/0000-0002-4868-6748

Received/Geliş Tarihi: 25.06.2026 **Accepted/Kabul Tarihi:** 03.09.2026 **Published/Yayınlanma tarihi:** 16.10.2026

Cite this article as/Atıf: Zara S, Abdelhadi H, Al Bishawi A, Coyle P, Eltayeb F, Hamza YP, Abu Jarir S, Al Maslamani M. Genomic identification of fatal *Clostridioides manganotii* bloodstream infection in an immunocompromised patient: A case report. Mediterr J Infect Microb Antimicrob. 2026;15:317-322



©Copyright 2026 The Author(s). Published by Galenos Publishing House on behalf of Infectious Diseases and Clinical Microbiology Specialty Society of Turkey. Licensed under a Creative Commons Attribution-NonCommercial-NoDerivatives 4.0 International License (CC BY-NC-ND 4.0)

Introduction

Clostridioides manganotii is a Gram-positive, spore-forming anaerobic bacillus that grows under mesophilic, strictly anaerobic conditions. Although closely related to *Clostridioides difficile*, genomic reclassification has identified it as a distinct species^[1]. While *Clostridioides difficile* is a recognized human pathogen, *Clostridioides manganotii* is primarily an environmental organism and has been isolated from soil, water, and animal stool^[2]. Its endospore-forming ability enables it to survive under extreme environmental conditions, including temperature variation, pH shifts, chemical exposure, and radiation^[3-5]. Although rare, members of the genus *Clostridioides* have been reported to cause invasive infections, such as bacteremia and septicemia^[6]. The broader use of molecular diagnostics and the increasing number of immunocompromised patients may explain the increased recognition of these uncommon pathogens.

To our knowledge, *Clostridioides manganotii* has not previously been reported as a cause of human bloodstream infection, and this may represent the first reported fatal case in an immunocompromised patient. After repeated failure of matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) to identify the organism, it was provisionally identified by 16S ribosomal RNA (rRNA) sequencing and bioinformatic comparison with reference 16S databases.

Case Report

A 36-year-old woman with stage IV invasive ductal carcinoma metastatic to the lungs, lymph nodes, bones, and brain was receiving palliative gemcitabine/carboplatin and whole-brain radiotherapy. Four days after her second chemotherapy cycle,

she was admitted with fever, myalgia, and malaise. Diagnosed with febrile neutropenia, she received piperacillin/tazobactam (4.5 g every 6 hours) and was discharged after neutrophil recovery and negative cultures.

Before her third cycle, she was readmitted with diffuse pain and general deterioration. She appeared unwell and distressed but was afebrile, with stable hemodynamics and oxygenation. Multiple enlarged lymph nodes were palpable in the cervical and inguinal regions. She had no diarrhea, abdominal pain, vomiting, or other gastrointestinal symptoms, and there was no clinical evidence of mucositis or colitis. Because she had no gastrointestinal symptoms, *Clostridioides difficile* toxin testing was not performed. She did not have a central venous catheter. On day 3 of admission, she developed fever (38.9°C), tachycardia (133 bpm), tachypnea (24/min), oxygen saturation of 92%-93% on room air, and hypotension (96/66 mm Hg). Blood cultures were obtained, and piperacillin/tazobactam (4.5 g every 6 hours) was started with intravenous fluids. Laboratory findings are summarized in Table 1.

Microbiological Investigations

Two sets of blood cultures were collected from two separate peripheral venipuncture sites (right and left upper limbs), with both anaerobic bottles flagging positive after 15 hours of incubation. Gram staining of the positive bottles demonstrated Gram-positive bacilli (Figure 1a). Subculture under anaerobic conditions yielded metronidazole-sensitive gray colonies after 48 hours on anaerobic blood agar (Figure 1b). MALDI-TOF mass spectrometry (MALDI-TOF MS; Bruker Daltonics, Billerica, MA, USA) repeatedly failed to identify the organism, both directly from the positive blood culture bottles and from pure colony growth. The isolate was then tested using the VITEK 2 automated system (bioMérieux, Marcy-l'Étoile,

Table 1. Laboratory findings on admission and day 3.

Laboratory parameter	On admission	Day 3 of admission	Reference range
Hemoglobin	7.1 g/dL	7.4 g/dL	13–17 g/dL
WBC	$5.3 \times 10^3/\mu\text{L}$	$4.0 \times 10^3/\mu\text{L}$	$4.0\text{--}10 \times 10^3/\mu\text{L}$
ANC	$4.1 \times 10^3/\mu\text{L}$	$3.1 \times 10^3/\mu\text{L}$	$2.0\text{--}4.7 \times 10^3/\mu\text{L}$
Platelets	$24 \times 10^3/\mu\text{L}$	$16 \times 10^3/\mu\text{L}$	$150\text{--}410 \times 10^3/\mu\text{L}$
Urea	4.8 mmol/L	1.8 mmol/L	2.5–7.8 mmol/L
Creatinine	37 $\mu\text{mol/L}$	26 $\mu\text{mol/L}$	62–106 $\mu\text{mol/L}$
ALT	57 U/L	50 U/L	0–41 U/L
AST	38 U/L	62 U/L	0–40 U/L
CRP	70 mg/L	242 mg/L	0–5 mg/L
Procalcitonin	0.09 ng/mL	0.57 ng/mL	—
Lactate	—	5.10 mmol/L	0.36–1.60 mmol/L
Fibrinogen	—	2.70 g/L	2–4 g/L

WBC, white blood cell; ANC, absolute neutrophil count; ALT, alanine aminotransferase; AST, aspartate aminotransferase; CRP, C-reactive protein.

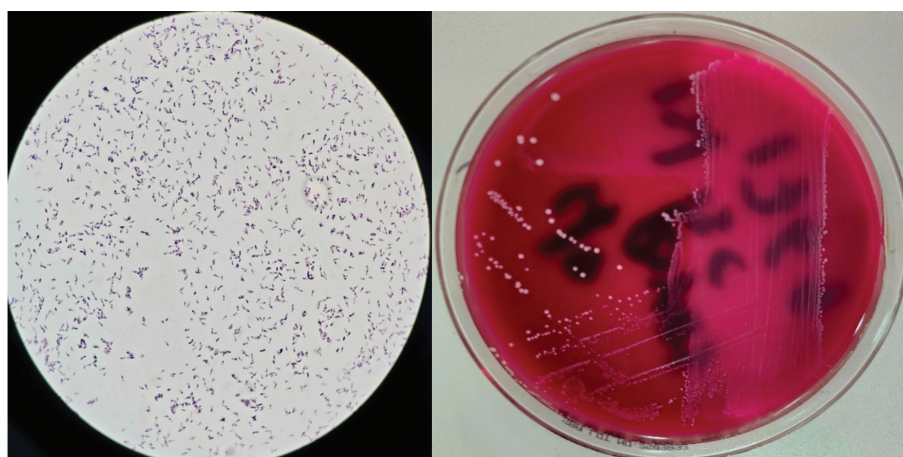


Figure 1. (a) Gram stain showing Gram-positive bacilli. (b) Colony morphology of *Clostridioides manganotii* on anaerobic blood agar after 48 hours of incubation.

France), which identified it as *Clostridioides difficile* and reported susceptibility to amoxicillin-clavulanate, piperacillin/tazobactam, meropenem, and metronidazole, with resistance to clindamycin. Antimicrobial susceptibility results were interpreted according to Clinical and Laboratory Standards Institute criteria.

The patient continued to deteriorate, with hypotension, respiratory distress, altered mentation, and escalating oxygen requirements, progressing from supplemental oxygen via nasal cannula and a non-rebreather mask to non-invasive ventilatory support with continuous positive airway pressure. Her quick Sequential Organ Failure Assessment score was 3. Antibiotic therapy was escalated to meropenem (1 g every 8 hours) and intravenous metronidazole (500 mg every 8 hours), with the addition of oral vancomycin for presumed severe *Clostridioides difficile* infection. Vasopressor support was not initiated. Disseminated intravascular coagulation was not clinically suspected. Given her advanced metastatic malignancy and continued clinical deterioration, the family subsequently opted for comfort-focused management, and no further radiological investigations, laboratory testing, or invasive procedures were pursued. A do-not-attempt-resuscitation order was instituted. Despite broad-spectrum antimicrobial therapy and supportive care, she continued to deteriorate and died 72 hours after the onset of septic shock. An autopsy was not performed.

Molecular Identification of the Isolate

Because of the atypical clinical presentation, repeated failure of MALDI-TOF identification, and concern regarding possible misidentification by VITEK 2, molecular characterization of the isolate was undertaken. Genomic DNA was extracted from a colony of the bacterial isolate using the Qiagen Virus Mini Purification Kit 2.0 (Qiagen, Hilden, Germany) and quantified using a Qubit 2.0 Fluorometer (Thermo Fisher Scientific, Waltham, MA, USA). A DNA concentration of 10 ng was achieved

by buffer modification.

DNA was barcoded using the SQK-16S024 kit (Oxford Nanopore Technologies, Oxford, UK), which contains 16S-specific primers 27F (5'-AGAGTTTGATCCTGGCTCAG-3') and 1492R (5'-TACGGYTACCTTGTACGACTT-3') for amplification of the complete 16S rRNA gene. Sequencing was performed on a MinION platform (Mk1C MC110319; Oxford Nanopore Technologies, Oxford, UK) using a FLO-MIN106D Spot-On Flow Cell (R9 version; Oxford Nanopore Technologies, Oxford, UK). A 50-μL reaction volume was used, and the purified library was loaded onto the flow cell according to the manufacturer's protocol.

Live base calling was performed using Guppy. Taxonomic assignment was generated using the wf-metagenomics workflow on the EPI2ME platform (Oxford Nanopore Technologies, Oxford, UK), with comparison against the National Center for Biotechnology Information 16S rRNA bacterial database. The isolate showed 95% 16S rRNA sequence homology with published *Clostridioides manganotii* reference sequences and clustered with *Clostridioides manganotii* in phylogenetic analysis (Figure 2). The 95% sequence homology is below the commonly accepted threshold for definitive species-level identification and was therefore interpreted in conjunction with the phylogenetic clustering. Additionally, a recent study reported 96.36% diagnostic accuracy for Nanopore 16S rRNA sequencing compared with Sanger sequencing, supporting its utility in identifying previously unrecognized bacterial isolates^[7]. The sequencing data generated in this study were deposited in the Sequence Read Archive under accession number SRR34968737.

Review of Literature

Members of the genera *Clostridioides* and *Clostridium* are ubiquitous, Gram-positive, anaerobic, spore-forming rods

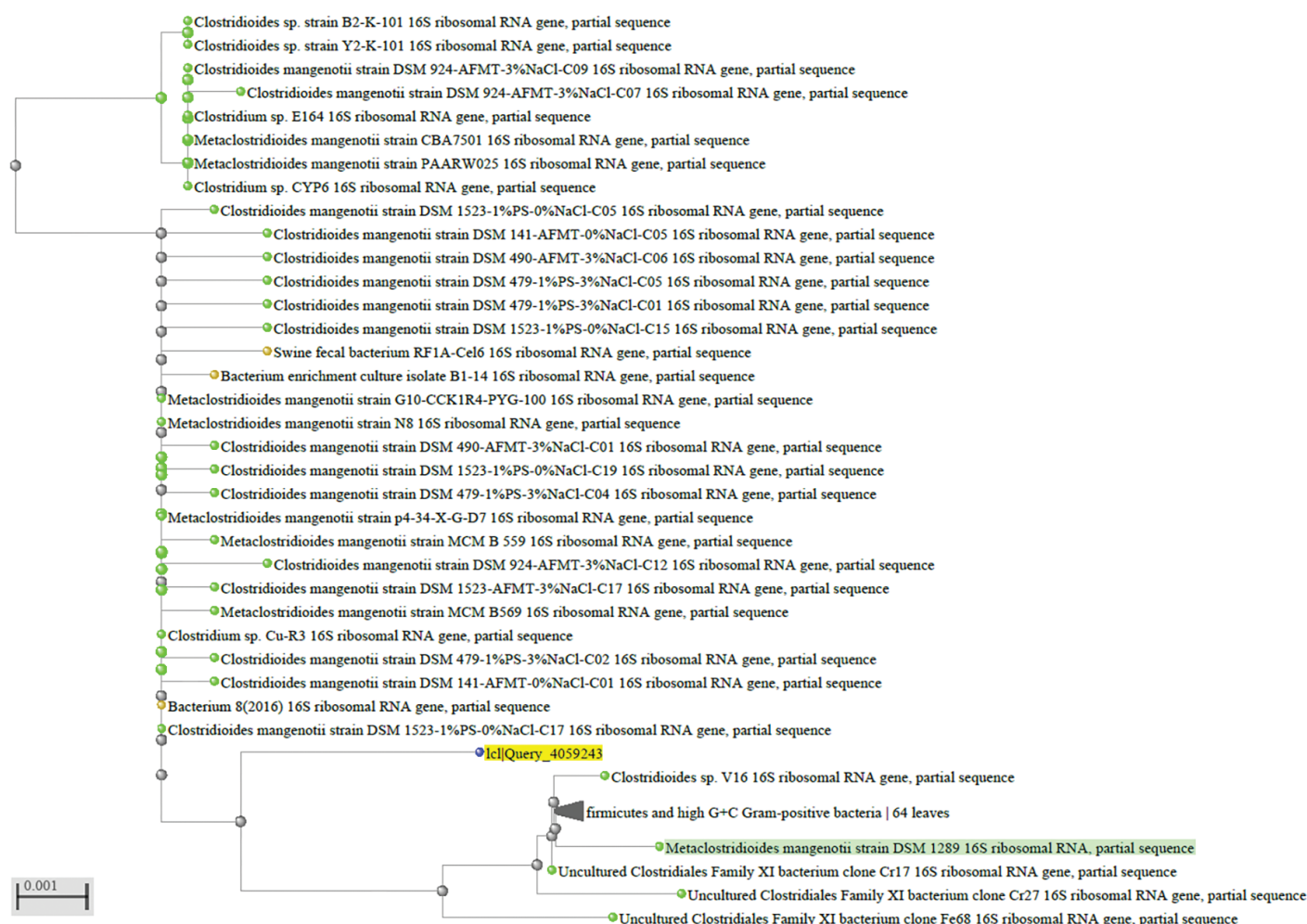


Figure 2. Phylogenetic identification of *Clostridioides manganotii* using 16S rRNA sequencing.

found in soil, water, and the gastrointestinal tracts of animals and humans. These genera collectively contain more than 200 species, among which *Clostridioides difficile*, *Clostridium perfringens*, *Clostridium botulinum*, and *Clostridium tetani* are most commonly associated with human disease. Their key virulence traits include spore formation, which enhances environmental survival, and the production of potent exotoxins that contribute to the rapid and sometimes fatal course of infection^[8].

Clostridioides manganotii was initially grouped with *Clostridioides difficile* because of their close genotypic and phenotypic similarities. However, advances in molecular analysis, including whole-genome sequencing (WGS), have supported its classification as a distinct species. In 2016, Lawson et al.^[1] analyzed 16S rRNA sequences and reported 95% identity between *Clostridioides difficile* and *Clostridioides manganotii*, indicating a close phylogenetic relationship. In contrast, Knight et al.^[9] demonstrated through whole-genome analysis that the

two species share only 77% average nucleotide identity, well below the 95% threshold for species delineation, supporting their taxonomic separation. Subsequent phylogenomic studies further proposed reclassifying *Clostridioides manganotii* into a new genus, *Metaclostridioides*, based on low amino acid identity and the presence of unique conserved signature indels^[10].

The pathogen has primarily been isolated from environmental sources such as soil and animal feces but has not previously been associated with human infections^[2]. Genomic analysis of the timber rattlesnake isolate revealed 68 genes related to virulence, defense mechanisms, and antimicrobial resistance, including resistance to vancomycin, fluoroquinolones, zinc, and arsenic^[2]. Despite these findings, its virulence mechanisms remain poorly understood because of the rarity of reported cases. Among other uncommon clostridial pathogens, *Clostridium tertium* has been particularly associated with immunocompromised and neutropenic patients; in a recent

cohort, it accounted for 62 of 601 (10%) *Clostridium* species bacteremias, with 50% of patients having neutropenia or hematologic malignancy^[11].

Discussion

Our patient initially presented with diffuse myalgia followed by fever and signs of sepsis. Despite early microbiological evidence of Gram-positive anaerobic bacteremia, conventional identification methods failed to provide a reliable diagnosis. MALDI-TOF repeatedly failed to identify the isolate, whereas VITEK 2 suggested *Clostridioides difficile*, leading to treatment directed at presumed severe clostridial infection. As her condition rapidly deteriorated with profound hypotension, respiratory distress, and altered consciousness, treatment was escalated to meropenem with additional agents directed against presumed severe *Clostridioides difficile* infection^[12].

A major strength of this case is the use of molecular testing to resolve discordant conventional microbiological results. MALDI-TOF is a widely accepted rapid diagnostic tool for common bacterial pathogens, including Gram-positive anaerobes such as *Clostridioides difficile*, with accuracy approaching 100%^[13]. The repeated failure to identify the isolate, despite its presence in the instrument library, suggests the possibility of a distinct or atypical species. Although the VITEK 2 system identified the organism as *Clostridioides difficile*, misidentification remains possible because of the close genetic homology between the two pathogens, and comparative studies have consistently demonstrated higher accuracy with MALDI-TOF^[14]. Because of this discrepancy, the isolate underwent full-length 16S rRNA gene sequencing and phylogenetic analysis, which supported its provisional identification as *Clostridioides manganotii*. However, WGS was not performed and would have enabled more robust species-level confirmation, representing a limitation of this case. Furthermore, the 95% 16S rRNA sequence homology is below the commonly accepted threshold for definitive species-level identification and should therefore be interpreted with caution.

The antimicrobial susceptibility results should also be interpreted carefully because the isolate was initially identified by VITEK 2 as *Clostridioides difficile*, and validated species-specific susceptibility criteria for *Clostridioides manganotii* have not been established. The isolate was reported as susceptible to piperacillin/tazobactam, meropenem, and metronidazole, all of which were administered during the clinical course. Therefore, the poor clinical outcome was likely multifactorial, reflecting the patient's advanced metastatic malignancy, profound immunocompromised status, and severity of sepsis.

The absence of documented human infections and limited understanding of the pathogenesis of *Clostridioides manganotii*

likely contributed to the diagnostic delay. This underscores the critical role of molecular diagnostics in detecting rare or unusual pathogens, particularly when conventional methods have limited capacity to identify uncommon or previously unrecognized pathogens^[15]. This diagnostic challenge extends beyond rare anaerobic bacteria in hemato-oncological patients, with recent literature also highlighting unusual and emerging invasive fungal pathogens, including the *Fusarium proliferatum* species complex, which may pose significant diagnostic and therapeutic challenges in immunocompromised hosts^[16].

Clinically, the patient presented with systemic signs of sepsis, including fever, altered consciousness, profound hypotension, and respiratory distress, progressing to multiorgan failure and death. This contrasts with primary *Clostridioides difficile* infection, which typically presents with gastrointestinal symptoms, mainly abdominal pain and diarrhea resulting from colitis. The absence of gastrointestinal symptoms in this case complicated the diagnosis. The patient's rapid deterioration despite aggressive therapy suggests that *Clostridioides manganotii* may possess significant virulence and may be capable of causing severe sepsis and septic shock, particularly in immunocompromised individuals.

To our knowledge, this may represent the first reported human case of fatal *Clostridioides manganotii* bloodstream infection in an immunocompromised patient. Its misidentification by conventional methods highlights the potential for diagnostic confusion with closely related organisms, underscoring the limitations of standard diagnostic methods and the need for broader adoption of molecular and genomic testing in atypical infections.

Given the pathogen's rarity, further research is warranted. Future studies should explore the pathogenic mechanisms of *Clostridioides manganotii*, particularly the role of its 68 identified virulence-related genes. Investigating its antimicrobial resistance profile is crucial, particularly because validated species-specific susceptibility criteria are lacking. Furthermore, given the limited clinical data, additional case reports facilitated by advances in identification techniques and genomic studies will help improve understanding, evaluation, and management of this emerging pathogen.

Conclusion

Immunocompromised patients are particularly vulnerable to rare, opportunistic, and emerging infections that may evade detection by conventional methods. Incorporating molecular approaches can facilitate the identification of unusual pathogens that warrant further investigation. To our knowledge, this may represent the first reported human case of fatal *Clostridioides manganotii* bloodstream infection in an immunocompromised patient.

Ethics

Informed Consent: Written informed consent was obtained from the patient's family for publication of this report in accordance with the journal's patient consent policy.

Footnotes

Authorship Contributions

Concept: S.Z., A.A.B., S.A.J., M.A.M., Design: S.Z., A.A.B., S.A.J., M.A.M., Data Collection or Processing: S.Z., P.C., Y.P.H., Analysis or Interpretation: S.Z., A.A.B., P.C., F.E., Y.P.H., Literature Search: S.Z., H.A., Writing: S.Z., H.A., P.C., F.E.

Conflict of Interest: No conflict of interest was declared by the authors.

Financial Disclosure: The authors declared that this study received no financial support.

References

1. Lawson PA, Citron DM, Tyrrell KL, Finegold SM. Reclassification of *Clostridium difficile* as *Clostridioides difficile* (Hall and O'Toole 1935) Prévot 1938. *Anaerobe*. 2016;40:95-99.
2. McLaughlin RW, Cochran PA, Dowd SE, Andersen K, Anderson N, Brennan R, Brook N, Callaway T, Diamante K, Duberstone A, Fitch K, Freiheit H, Godlewski C, Gorman K, Haubrich M, Hernandez M, Hirtreiter A, Ivanoski B, Jaminet X, Kirkpatrick T, Kratowicz J, Latus C, Leable T, Lingafelt N, Lowe D, Lowrance H, Malsack L, Mazurkiewicz J, Merlos P, Messley J, Montemurro D, Nakitare S, Nelson C, Nye A, Pazera V, Pierangeli G, Rellora A, Reyes A, Roberts J, Robins S, Robinson J, Schultz A, Seifert S, Sigler E, Spangler J, Swift E, Tencate R, Thurber J, Vallee K, Wamboldt J, Whitten S, Woods D, Wright A, Yankunas D. Draft genome sequence of *Clostridium manganotii* TR, isolated from the fecal material of a timber rattlesnake. *Genome Announc*. 2014;2:e01107-e01113.
3. Nerber HN, Sorg JA. The small acid-soluble proteins of *Clostridioides difficile* are important for UV resistance and serve as a check point for sporulation. *PLoS Pathog*. 2021;17:e1009516.
4. Wetzel D, McBride SM. The impact of pH on *Clostridioides difficile* sporulation and physiology. *Appl Environ Microbiol*. 2020;86:e02706-e02719.
5. Malyshev D, Jones IA, McCracken M, Öberg R, Harper GM, Joshi LT, Andersson M. Hypervirulent R20291 *Clostridioides difficile* spores show disinfection resilience to sodium hypochlorite despite structural changes. *BMC Microbiol*. 2023;23:59.
6. Yang CC, Hsu PC, Chang HJ, Cheng CW, Lee MH. Clinical significance and outcomes of *Clostridium perfringens* bacteremia—a 10-year experience at a tertiary care hospital. *Int J Infect Dis*. 2013;17:e955-e960.
7. Lao HY, Ng TT, Wong RY, Wong CS, Lee LK, Wong DS, Chan CT, Jim SH, Leung JS, Lo HW, Wong IT, Yau MC, Lam JY, Wu AK, Siu GK. The clinical utility of two high-throughput 16S rRNA gene sequencing workflows for taxonomic assignment of unidentifiable bacterial pathogens in matrix-assisted laser desorption/ionization-time of flight mass spectrometry. *J Clin Microbiol*. 2022;60:e0176921.
8. Garvey M. Foodborne *Clostridioides* species: Pathogenicity, virulence and biocontrol options. *Microorganisms*. 2023;11:2483.
9. Knight DR, Imwattana K, Kullin B, Guerrero-Araya E, Paredes-Sabja D, Didelot X, Dingle KE, Eyre DW, Rodríguez C, Riley TV. Major genetic discontinuity and novel toxigenic species in *Clostridioides difficile* taxonomy. *Elife*. 2021;10:e64325.
10. Bello S, McQuay S, Rudra B, Gupta RS. Robust demarcation of the family *Peptostreptococcaceae* and its main genera based on phylogenomic studies and taxon-specific molecular markers. *Int J Syst Evol Microbiol*. 2024;74.
11. Kim H, Seo H, Park S, Chung H, Sung H, Kim MN, Bae S, Jung J, Kim MJ, Kim SH, Lee SO, Choi SH, Kim YS, Chong YP. Clinical significance and outcomes of *Clostridium tertium* bacteremia: analysis of 62 cases in neutropenic and non-neutropenic patients. *Eur J Clin Microbiol Infect Dis*. 2023;42:183-191.
12. Gergely Szabo B, Kadar B, Szidonia Lenart K, Dezsényi B, Kunovszki P, Fried K, Kamotsay K, Nikolova R, Prinz G. Use of intravenous tigecycline in patients with severe *Clostridium difficile* infection: a retrospective observational cohort study. *Clin Microbiol Infect*. 2016;22:990-995.
13. Hsu YM, Burnham CAD. MALDI-TOF MS identification of anaerobic bacteria: assessment of pre-analytical variables and specimen preparation techniques. *Diagn Microbiol Infect Dis*. 2014;79:144-148.
14. Guo L, Ye L, Zhao Q, Ma Y, Yang J, Luo Y. Comparative study of MALDI-TOF MS and VITEK 2 in bacteria identification. *J Thorac Dis*. 2014;6:534-538.
15. Zhao Y, Zhang W, Zhang X. Application of metagenomic next-generation sequencing in the diagnosis of infectious diseases. *Front Cell Infect Microbiol*. 2024;14:1458316.
16. Ezer B, Ceylan A, Arazi-Kan SN, Uğraklı S, Bulut R, Demircioğlu S. Fungemia caused by *Fusarium proliferatum* species complex in a patient with acute myeloid leukemia: a rare case report. *Klimik Derg*. 2025;38:198-200.