ACCESS MICROBIOLOGY

CASE REPORT

Raible *et al.*, *Access Microbiology* 2022;4:000374

DOI 10.1099/acmi.0.000374

MICROBIOLOGY SOCIETY

OPEN ACCESS

Acetobacter tropicalis bacteraemia in an immunocompromised patient: case report

Kevin M. Raible[1], Jumanah N. Algazaq[2], Genovefa Papanicolaou[2] and N. Esther Babady[1,2,*]

Abstract

Introduction. The published literature characterizing the bacterial genus *Acetobacter* primarily explores the role of these organisms in the fermentation industry. Reports of human infections caused by *Acetobacter* species are rare and are primarily associated with immunocompromised patients.

Case Presentation. A young patient with refractory acute myeloid leukaemia received a peripheral blood stem cell transplant at our institution. Both pre- and post-transplant courses were complicated by polymicrobial bloodstream infections. During this time a bacterium, later identified as *Acetobacter tropicalis*, was isolated from blood cultures. *A. tropicalis* was recovered in consecutive blood cultures for approximately 1 week; during this time the patient's condition deteriorated, ending in fatal cardiorespiratory failure.

Conclusion. This case provides the first report of a human infection with *A. tropicalis*, although the significance of this finding in a complex patient is hard to establish. This illustrates how the routine implementation of molecular identification techniques by clinical microbiology laboratories will result in the reporting of more rare or novel micro-organisms involved in human infections.

INTRODUCTION

The genus *Acetobacter* comprises more than 30 species that occupy a variety of environmental niches, such as plants and insects, and they are are also found in culinary sources such as fermented foods and alcoholic beverages [1]. The ability of *Acetobacter* species to survive in acidic environments and oxidize alcohols into acetic acid has garnered a particular interest in these organisms from the fermentation industry. Despite the prevalence of *Acetobacter* species in nature and in food processing, these organisms have rarely been associated with human disease. We have identified four reports of *Acetobacter*-associated infections in humans, and all involve individuals with severe or chronic underlying health conditions. Two cases of *Acetobacter* bacteraemia have been reported: *A. indonesinensis* in a 9-year-old girl with several invasive devices for the treatment of her late-infantile metachromatic leukodystrophy [2] and *A. cibinongensis* in a 40-year-old man with a history of intravenous drug use being treated for end-stage renal failure [3]. Additionally, two cases of *A. indonesinensis*-associated pneumoniae were reported in post-lung transplantation patients [4, 5].

CASE REPORT

A young patient with refractory acute myeloid leukaemia (AML) was admitted for febrile neutropenia 6 months after receiving an unmodified, matched related donor peripheral blood stem cell transplant. The pre-transplant course was complicated by ecthyma gangrenosum of the right thigh with culture proven *Pseudomonas aeruginosa*, and the patient subsequently developed

Received 28 March 2022; Accepted 20 May 2022; Published 24 November 2022

Author affiliations: [1]Department of Pathology and Laboratory Medicine, Clinical Microbiology Service, Memorial Sloan Kettering Cancer Center, New York, NY, USA; [2]Department of Medicine, Infectious Disease Service, Memorial Sloan Kettering Cancer Center, New York, NY, USA.

***Correspondence:** N. Esther Babady, babadyn@mskcc.org

Keywords: *Acetobacter tropicalis*; bacteraemia; 16S sequencing; clinical microbiology laboratory identification.

Abbreviations: AML, Acute Myeloid Leukeamia; AML, acute myeloid leukaemia; AST, antimicrobial susceptibility testing; AST, Antimicrobial Susceptibility Testing; CLSI, Clinical and Laboratory Standards Institute; CLSI, Clinical and Laboratory Standards Institute; GNR, Gram-negative rod; GNR, Gram-negative rod; MALDI-TOF MS, matrix-assisted laser desorption/ionization time-of- flight spectrometry; MALDI-TOF MS, matrix-assisted laser desorption/ionization time-of-flight spectrometry; PCR, polymerase chain reaction; PCR, Polymerase Chain Reaction; PICC, peripherally inserted central catheter; PICC, peripherally inserted central catheter.

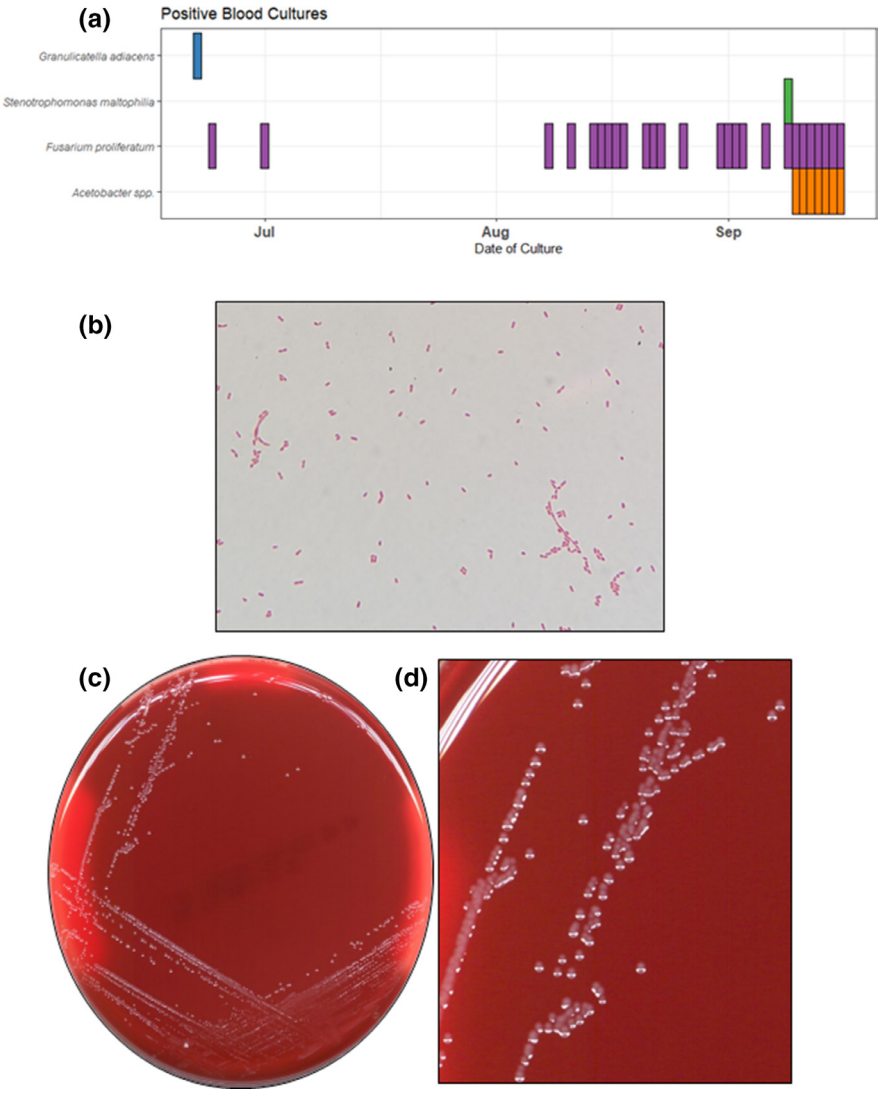

Fig. 1. (a) A clinical timeline of fevers, bacterial and fungal organisms isolated from the patient presented in this case. Each individual bar represents a unique blood culture order where the corresponding organism was isolated. (b) Image of a Gram stain of Acetobacter tropicalis showing short pleomorphic GNRs. (c) Colony morphology on Columbia agar with 5% sheep blood growing A. tropicalis at 48 h incubation. (d) Colonies enhanced 2.25×.

P. aeruginosa and *Staphylococcus epidermidis* bloodstream infections (BSIs), in addition to numerous pulmonary nodules of unclear aetiology. The post-transplant course was complicated by *Gemella haemolysans* BSI, *Clostridium difficile* infection and ongoing parvovirus positivity on respiratory panel polymerase chain reaction (PCR). On later admission for febrile neutropenia, blood cultures grew *Granulicatella adiacens* (Fig. 1a). The patient completed a course of linezolid, but fevers persisted despite antibiotic therapy and the patient was found to have disseminated *Fusarium proliferatum* with biopsy-confirmed skin involvement, presenting as diffuse purpuric lesions and positive blood cultures, despite antifungal therapy. In addition to the ongoing *F. proliferatum* BSI, *Stenotrophomonas maltophilia* was isolated from peripherally inserted central catheter (PICC) line blood cultures and treated with ceftazidime and levofloxacin.

Shortly thereafter, another set of blood cultures became positive after 28 h of incubation and direct Gram stain demonstrated the presence of both fungal septate hyphae and small pleomorphic Gram-negative rods (GNRs) (Fig. 1b). The blood culture bottles were sub-cultured at 37 °C and 5% CO_2, yielding the growth of two organisms; a white mould – later identified as *F. proliferatum* – and grey bacterial colonies on the Columbia sheep blood agar (Fig. 1c) and chocolate agar, with no growth on MacConkey agar. Bacterial identification could not be achieved using matrix-assisted laser desorption/ionization time-of-flight spectrometry (MALDI-TOF MS) on the GNR isolates from the blood cultures. Partial 16S rRNA gene sequencing was performed in our laboratory and interpreted using the Clinical and Laboratory Standards Institute (CLSI) criteria [6]. Using these criteria, the GNR could only be identified to the genus level as *Acetobacter* [6, 7]. Subsequent phylogenetic analysis of the 16S sequence

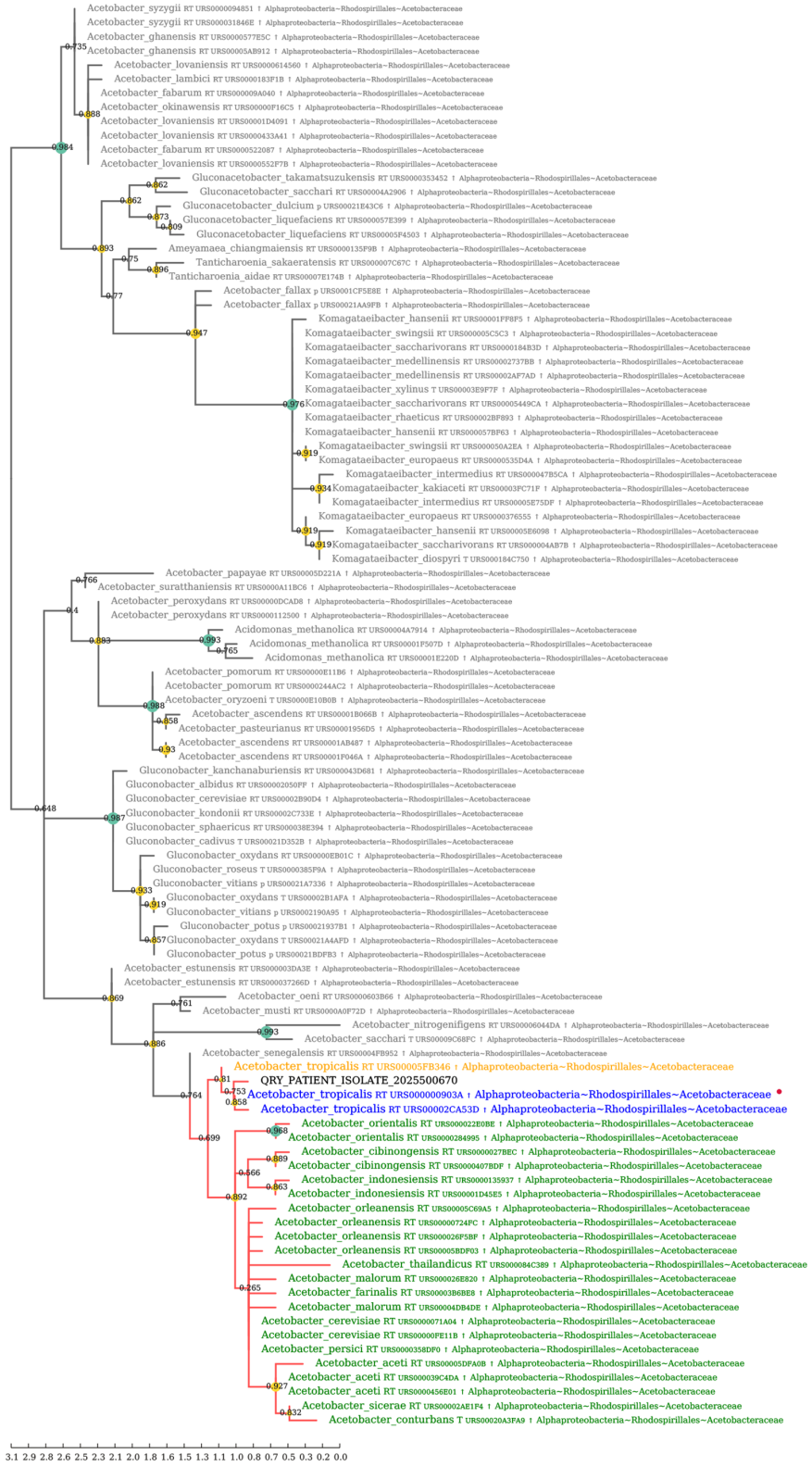

Fig. 2. The phylogenetic tree of the sequence data for the isolate presented in this case indicating the sequence is part of the genus Acetobacter (QRY_PATIENT_ISOLATE_2025500670) and falls within Acetobacter tropicalis cluster. These data are generated using the leBIBI IV SSU-rDNA (16S) Automated ProKaryotes Phylogeny software (https://umr5558-proka.univ-lyon1.fr/PKPhy/PKPhy.html) which BLAST, aligns and assigns phylogeny to sequence data using an approximately maximum-likelihood approach. The query sequence (black) is surrounded by closely related nodes (orange and blue), as well as nodes that share common ancestors (green), while distantly related nodes are grey. Scale bar indicates nucleotide substitutions per site.

Table 1. Antimicrobial susceptibility testing (AST) results for the *Acetobacter tropicalis* isolate presented in this case. AST testing was performed by microbroth dilution using the MicroScan Gram-Negative MIC Panel Type 53 and read on the MicroScan WalkAway instrument

Antimicrobial drugs	MIC (μg ml^{-1})
Amikacin	≤16
Amoxicillin/clavulanate	≤8/4
Ampicillin/sulbactam	8/4
Ampicillin	>16
Aztreonam	≤4
Cefazolin	8
Cefepime	≤2
Cefotaxime	32
Cefotaxime/clavulanate	≤0.5
Cefotaxime/ESBL	>1
Cefoxitin	≤8
Ceftazidime	≤1
Ceftazidime/clavulanate	≤0.25
Ceftriaxone	≤1
Cefuroxime	16
Ciprofloxacin	≤1
Ertapenem	>1
Gentamicin	≤2
Levofloxacin	≤2
Meropenem	2
Moxifloxacin	>4
Nitrofurantoin	≤32
Piperacillin/tazobactam	≤8
Tetracycline	≤4
Tobramycin	≤2
Trimethoprim/sulfamethoxazole	≤2/38

data using a maximum-likelihood approach and a *k*-nearest neighbour classifier rRNA sequence database query identified the isolate to species-level as *A. tropicalis* (Fig. 2) [8]. Unfortunately, due to poor prognosis in the setting of refractory AML without treatment options or anticipated count recovery, ongoing fungaemia and bacteraemia despite multiple antimicrobial therapy, the patient was found to be unresponsive in cardiorespiratory failure and succumbed to the illness.

DISCUSSION

A. tropicalis– which was first isolated from a coconut– shares 96.5–98.9% sequence homology in its rDNA gene with other *Acetobacter* species [1]. This species has largely been characterized as part of the gut biome of fruit flies and has been shown to modulate carbohydrate metabolism in these insects [9]. To our knowledge, this is the first time *A. tropicalis* has been associated with a human infection. Given the patient's vulnerability to opportunistic infections it is most likely the patient became infected through an environmental exposure, although the aetiological source of this infection remains unknown.

Antimicrobial susceptibility testing (AST) was performed using the microbroth dilution method. To date, there are no CLSI-recommended antimicrobial interpretative guidelines for *Acetobacter* species, probably due to the rarity of reported human infections caused by this genus. AST demonstrated *in vitro* activity against the isolate with amikacin, aztreonam, cefepime,

cefoxitin, ceftazidime, ceftriaxone, ciprofloxacin, gentamicin, levofloxacin, nitrofurantoin, piperacillin/tazobactam, tetracycline, tobramycin and trimethoprim/sulfamethoxazole (Table 1). However, reduced antibiotic activity was observed for ampicillin, cefotaxime, cefuroxime, ertapenem and moxifloxacin. Decreased susceptibility to multiple classes of antibiotics has been reported in previous *Acetobacter* species case reports [2, 4].

This case highlights the importance of 16S rRNA sequencing to identify environmental micro-organisms that cannot be identified using traditional clinical laboratory techniques. However, the true clinical impact of rarely reported micro-organisms such as *A. tropicalis* remains difficult to identify, particularly in polymicrobial infections. Routine 16S sequencing performed by clinical microbiology laboratories may help elucidate the role these organisms play in infections as more clinical data are accumulated and reported. These types of analyses are of particular importance in vulnerable patient populations such as those seen at our institution.

Funding information
This work was supported in part through the National Institute of Heath/National Cancer Institute Cancer Center Support [Grant P30 CA008748].

Author contributions
K.M.R. and J.N.A. contributed equally to this case report. K.M.R. and N.E.B. supervised the identification of the causative pathogen. J.N.A. and G.P. participated in the clinical care for the case. K.M.R., J.N.A. and N.E.B. drafted the manuscript. All authors read and approved the submitted version of the manuscript.

Conflicts of interest
All authors declare that they have no competing interests.

Ethical statement
This case report was reviewed by the Institutional Review Board at MSKCC and consent for publication was not deemed necessary.

References

1. Lisdiyanti P, Kawasaki H, Seki T, Yamada Y, Uchimura T, *et al*. Systematic study of the genus *Acetobacter* with descriptions of *Acetobacter indonesiensis* sp. nov., *Acetobacter tropicalis* sp. nov., *Acetobacter orleanensis* (Henneberg 1906) comb. nov., *Acetobacter lovaniensis* (Frateur 1950) comb. nov., and *Acetobacter estunensis* (Carr 1958) comb. nov. *J Gen Appl Microbiol* 2000;46:147–165.
2. Kohlmann R, Barenberg K, Anders A, Gatermann SG. *Acetobacter indonesiensis* bacteremia in child with metachromatic leukodystrophy. *Emerg Infect Dis* 2016;22:1681–1683.
3. Gouby A, Teyssier C, Vecina F, Marchandin H, Granolleras C, *et al*. *Acetobacter cibinongensis* bacteremia in human. *Emerg Infect Dis* 2007;13:784–785.
4. Basu SS, Delaney ML, Li N, Onderdonk AB, Bry L. *Acetobacter indonesiensis* pneumonia after lung transplantation. *Emerg Infect Dis* 2018;24:598–599.
5. Bittar F, Reynaud-Gaubert M, Thomas P, Boniface S, Raoult D, *et al*. *Acetobacter indonesiensis* pneumonia after lung transplant. *Emerg Infect Dis* 2008;14:997–998.
6. CLSI. *Interpretive Criteria for Identification of Bacteria and Fungi by Targeted DNA Sequencing*. 2nd ed. Wayne, PA: Clinical and Laboratory Standards Institute; 2018.
7. NCBI Resource Coordinators. Database resources of the National Center for Biotechnology Information. *Nucleic Acids Res* 2016;44:D7-19.
8. Flandrois J-P, Perrière G, Gouy M. leBIBIQBPP: a set of databases and a webtool for automatic phylogenetic analysis of prokaryotic sequences. *BMC Bioinformatics* 2015;16:251.
9. Huang J-H, Douglas AE. Consumption of dietary sugar by gut bacteria determines Drosophila lipid content. *Biol Lett* 2015;11:20150469.