

Testing and near real-time surveillance of *B. parapertussis* are needed to enhance prompt response to clinical outbreaks and contamination events, both of which have been reported (1,10). Determining the clinical implications of the observed *B. parapertussis* surge may help inform patient management and public health action.

The data obtained by bioMérieux are subject to the terms and conditions of a data-use agreement by and between bioMérieux and each facility participating in the BIOFIRE Syndromic Trends program. If a dataset is requested, bioMérieux will review such request internally to ensure that any disclosure does not conflict with bioMérieux obligations and restrictions set forth in the data-use agreement. Code available upon reasonable request.

All authors are employees of bioMérieux.

About the Author

Dr. Noble is a data scientist at bioMérieux, Salt Lake City, Utah. Her research interests include syndromic testing and spatiotemporal trends of infectious diseases.

References:

1. Watanabe M, Nagai M. Whooping cough due to *Bordetella parapertussis*: an unresolved problem. *Expert Rev Anti Infect Ther*. 2004;2:447–54. <https://doi.org/10.1586/14787210.2.3.447>
2. Faulkner A, Skoff TH, Martin SW, Cassiday PK, Tondella ML, Liang JL. Chapter 10: Pertussis. In: Manual for the surveillance of vaccine-preventable diseases [cited 2024 Apr 10]. A <https://www.cdc.gov/vaccines/pubs/surv-manual/chpt10-pertussis.html>
3. Cherry JD, Seaton BL. Patterns of *Bordetella parapertussis* respiratory illnesses: 2008–2010. *Clin Infect Dis*. 2012;54:534–7. <https://doi.org/10.1093/cid/cir860>
4. Leber AL, Everhart K, Daly JA, Hopper A, Harrington A, Schreckenberger P, et al. Multicenter evaluation of BioFire FilmArray respiratory panel 2 for detection of viruses and bacteria in nasopharyngeal swab samples. *J Clin Microbiol*. 2018;56:e01945–17. <https://doi.org/10.1128/JCM.01945-17>
5. BioFire Diagnostics LLC BioFire® Respiratory Panel 2.1 (RP2.1) de novo instructions for use. 2021 [cited 2024 Jan 12]. <https://www.biofire.qarad.eifu.online/III/US/all?keycode=ITII0105>
6. Meyers L, Ginocchio CC, Faucett AN, Nolte FS, Gesteland PH, Leber A, et al. Automated real-time collection of pathogen-specific diagnostic data: syndromic infectious disease epidemiology. *JMIR Public Health Surveill*. 2018;4:e59. <https://doi.org/10.2196/publichealth.9876>
7. Lautrop H. Epidemics of parapertussis. 20 years' observations in Denmark. *Lancet*. 1971;297:1195–8. [https://doi.org/10.1016/S0140-6736\(71\)91713-2](https://doi.org/10.1016/S0140-6736(71)91713-2)
8. Bhattacharyya S, Ferrari MJ, Bjørnstad ON. Species interactions may help explain the erratic periodicity of whooping cough dynamics. *Epidemics*. 2018;23:64–70. <https://doi.org/10.1016/j.epidem.2017.12.005>
9. Shaw D, Abad R, Amin-Chowdhury Z, Bautista A, Bennett D, Broughton K, et al. Trends in invasive bacterial diseases during the first 2 years of the COVID-19 pandemic: analyses of prospective surveillance data from 30 countries and territories in the IRIS Consortium. *Lancet Digit Health*. 2023;5:e582–93. [https://doi.org/10.1016/S2589-7500\(23\)00108-5](https://doi.org/10.1016/S2589-7500(23)00108-5)
10. Flipse J, Tromp AT, Bosman J, Ten Hove C, Beks H, Kortbeek T, et al. Pseudo-outbreak of *Bordetella parapertussis* caused by contaminated swabs in the Netherlands. *Emerg Infect Dis*. 2022;28:890–2. <https://doi.org/10.3201/eid2804.212097>

Address for correspondence: Brooklyn A. Noble, bioMérieux, 1201 S 4800 W, Salt Lake City, UT 84104, USA; email: brooklyn.noble@biomerieux.com

Sphingobium yanoikuyae Bacteremia, Japan

Yayoi Miyamatsu,¹ Ryutarō Tanizaki,¹ Satoko Yamada

Author affiliation: Ise Municipal General Hospital, Ise, Japan

DOI: <https://doi.org/10.3201/eid3005.231514>

We report a case of *Sphingobium yanoikuyae* bacteremia in an 89-year-old patient in Japan. No standard antimicrobial regimen has been established for *S. yanoikuyae* infections. However, ceftriaxone and ceftazidime treatments were effective in this case. Increased antimicrobial susceptibility data are needed to establish appropriate treatments for *S. yanoikuyae*.

The genus *Sphingomonas* was divided into 4 clusters, and *Sphingomonas yanoikuyae* was renamed *Sphingobium yanoikuyae* (1). *S. yanoikuyae* is a gram-negative, nonsporulating, strictly aerobic rod-shaped bacterium (2) widely distributed in natural environments, especially in water and soil, and is rarely a human pathogen (3). Although 1 case of *S. yanoikuyae* infection has been reported in the central nervous system (CNS) of a child (4), infections have not been reported in adults. We report a case of *S. yanoikuyae* bacteremia in an older man.

¹These authors contributed equally to this article.

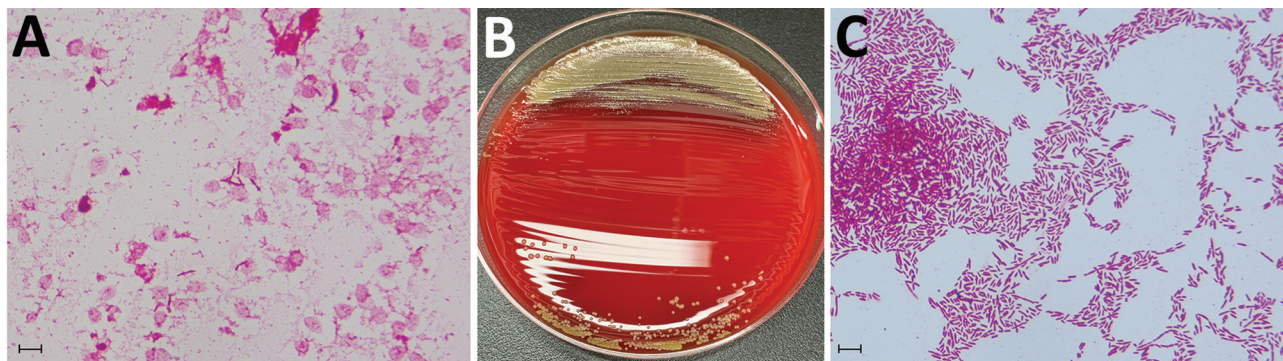


Figure. Identification of *Sphingobium yanoikuyae* bacteremia in 89-year-old man, Japan. A) Gram stain of the organisms growing in a blood sample incubated in a BACTEC Plus Aerobic/F Culture Vial (Becton Dickinson, <https://www.bd.com>). Scale bar is 10 μ m. B) Colonies of *S. yanoikuyae* cultured on Trypticase Soy Agar with 5% Sheep Blood (Becton Dickinson). C) Gram stain of *S. yanoikuyae* bacteria from a colony obtained by subculturing positive blood culture fluid on Trypticase Soy Agar with 5% Sheep Blood at 35°C in an aerobic environment. Scale bar is 10 μ m.

An 89-year-old man from Japan sought care at an emergency department because of fever and chills lasting 1 hour. He had been taking prednisolone (5 mg/day) for 6 years for interstitial pneumonia. He was alert, and his vital signs were as follows: body temperature, 38.6°C; heart rate, 71 beats/min; blood pressure, 112/64 mmHg; respiratory rate, 28 breaths/min; and blood oxygen saturation, 100% while breathing room air. Laboratory findings revealed elevated leukocyte count (16,100 cells/ μ L; reference range 3,300–8,600 cells/ μ L) and C-reactive protein level (4.16 mg/dL; reference range 0–0.14 mg/dL) but were otherwise unremarkable. Chest computed tomography revealed honeycombing and multiple reticular shadows in both lungs, unchanged from 5 months earlier. We suspected

sepsis and administered intravenous ceftriaxone (2 g/24 h) after obtaining 2 sets of blood samples for culture. On day 2, the patient's fever subsided. On day 5, a blood culture sample yielded positive results after incubation in an aerobic BACTEC Plus Aerobic/F Culture Vial in a BACTEC FX system (Becton Dickinson, <https://www.bd.com>). Gram staining revealed small gram-negative rods (Figure, panel A) that we were unable to identify by using mass spectrometry (MALDI Biotyper; Bruker Daltonics, <https://www.bruker.com>). We subsequently cultured the positive blood culture fluid on Trypticase Soy Agar with 5% Sheep Blood (Becton Dickinson) at 35°C in an aerobic environment and identified *S. yanoikuyae* by using mass spectrometry of bacteria isolated on day 6 (Figure, panels B, C). Genetic analysis of a 1,402 nt 16S rRNA sequence revealed 99.5% homology with *S. yanoikuyae* (Appendix, <https://wwwnc.cdc.gov/EID/article/30/5/23-1514-App1.pdf>). We performed antimicrobial susceptibility testing by using the dilution method and a Neg MIC NF1J panel (Beckman Coulter, <https://www.beckmancoulter.com>) in accordance with Clinical and Laboratory Standards Institute (CLSI) criteria for other non-Enterobacterales bacteria (Table) (5). We determined the ceftriaxone MIC by using the Neg MIC EN 2J panel for Enterobacterales bacteria and Pos MIC 1J panel for gram-positive cocci (both Beckman Coulter). Although *S. yanoikuyae* was susceptible to ceftriaxone, we preferred to use antimicrobial drugs that were effective against glucose nonfermenting bacteria, which is the fermentation pattern exhibited by *Sphingomonas* spp. On day 6, we switched the antimicrobial to ceftazidime (1 g/8 h). We did not detect *S. yanoikuyae* in blood cultures at follow-up on days 6 and 11, indicating treatments were effective, and the patient's condition remained stable. However, severe aspiration

Table. Drug susceptibility pattern for *Sphingobium yanoikuyae* isolated from an 89-year-old man's blood sample in study of *S. yanoikuyae* bacteremia, Japan*

Antimicrobial drug	MIC \dagger , μ g/mL	Breakpoint MIC \ddagger , μ g/mL
Piperacillin/tazobactam	\leq 4/4	16/4
Ceftriaxone	4	8
Ceftazidime	2	8
Cefepime	\leq 1	8
Aztreonam	$>$ 16	8
Imipenem	1	4
Meropenem	4	4
Gentamicin	\leq 1	4
Tobramycin	\leq 1	4
Amikacin	\leq 4	16
Minocycline	\leq 1	4
Ciprofloxacin	\leq 0.25	1
Levofloxacin	\leq 0.5	2
Trimethoprim/sulfamethoxazole	\leq 1/19	2/38

*Drug susceptibility data according to Clinical and Laboratory Standards Institute criteria (5). MIC values for antimicrobial drugs, except ceftriaxone, were determined by using a Neg MIC NF1J panel (Beckman Coulter, <https://beckmancoulter.com>). The MIC value of ceftriaxone was determined by using Neg MIC EN 2J Enterobacterales and Pos MIC 1J gram-positive cocci panels (both Beckman Coulter).

\dagger MIC for the isolate from 89-year-old case-patient.

\ddagger Breakpoints for other non-Enterobacterales susceptible strains.

pneumonia developed on day 16, and he died of respiratory failure on day 17.

Within the genus *Sphingomonas*, *S. paucimobilis* is the most frequently reported cause of human infection (6), predominantly causing bacteremia, septicemia, peritonitis, lung infections, pneumonia, or urinary tract infections; 24 of 52 (46%) cases in published literature were of nosocomial origin (7). Thus, *Sphingomonas* spp. might be a chief cause of nosocomial infection in addition to other glucose nonfermenting bacteria. The *S. yanoikuyae* infection reported previously in a child was a nosocomial infection after head surgery (4). Although this case in an older man was not a nosocomial infection, he had been taking prednisolone for 6 years, which might have increased his infection risk.

No antimicrobial regimen has been established for treating *S. yanoikuyae* infections. The child who had a CNS infection received 28 days of intravenous meropenem and 5 days of intrathecal amikacin (4). A novel bacteria strain, CC4533, isolated from a contaminated Tris-acetate-phosphate agar plate used to grow *Chlamydomonas reinhardtii*, showed 99.55% DNA sequence identity to *S. yanoikuyae*; drug susceptibility testing indicated CC4533 was resistant to polymyxin B, penicillin, and chloramphenicol and sensitive to neomycin (8). We treated our patient with intravenous ceftriaxone and then ceftazidime. Cefepime, a 4th-generation cephalosporin, can penetrate the cerebral spinal fluid and has an additional quaternary ammonium group enabling penetration through the outer membrane of gram-negative bacteria, increasing effectiveness against β -lactamase-producing gram-negative bacilli (9). We selected ceftazidime, a 3rd-generation cephalosporin, because our clinical findings did not suggest a CNS infection, and *S. yanoikuyae* did not produce β -lactamase.

No breakpoints have been established for *Sphingobium* sp. bacteria; thus, we evaluated antimicrobial susceptibility according to CLSI criteria for other non-Enterobacterales bacteria (5). According to the dilution method, MIC values for ceftriaxone were >2 by using the Enterobacterales panel and ≤ 4 by using the gram-positive cocci panel. The ceftriaxone MIC for the isolate from this patient was 4, which is below the CLSI breakpoint of 8 for other non-Enterobacterales bacteria (5), indicating that the isolate was susceptible to ceftriaxone.

In conclusion, no standard antimicrobial treatment regimen has been established for *S. yanoikuyae*. Ceftriaxone and ceftazidime were effective treatments for *S. yanoikuyae* infection in this patient. Increased antimicrobial susceptibility data are needed to establish appropriate treatments for *S. yanoikuyae*.

Acknowledgments

We thank Editage (<http://www.editage.com>) for reviewing and editing this manuscript for English language.

About the Author

Dr. Miyamatsu is a physician in the Department of Internal Medicine and General Medicine, Ise Municipal General Hospital, Ise, Japan. Her primary research interest is general internal medicine.

References

1. Takeuchi M, Hamana K, Hiraishi A. Proposal of the genus *Sphingomonas* sensu stricto and three new genera, *Sphingobium*, *Novosphingobium* and *Sphingopyxis*, on the basis of phylogenetic and chemotaxonomic analyses. *Int J Syst Evol Microbiol*. 2001;51:1405–17. <https://doi.org/10.1099/00207713-51-4-1405>
2. Yabuuchi E, Yano I, Oyaizu H, Hashimoto Y, Ezaki T, Yamamoto H. Proposals of *Sphingomonas paucimobilis* gen. nov. and comb. nov., *Sphingomonas parapaucimobilis* sp. nov., *Sphingomonas yanoikuyae* sp. nov., *Sphingomonas adhaesiva* sp. nov., *Sphingomonas capsulata* comb. nov., and two genospecies of the genus *Sphingomonas*. *Microbiol Immunol*. 1990;34:99–119. <https://doi.org/10.1111/j.1348-0421.1990.tb00996.x>
3. Ammendolia MG, Bertuccini L, Minelli F, Meschini S, Baldassarri L. A *Sphingomonas* bacterium interacting with epithelial cells. *Res Microbiol*. 2004;155:636–46. <https://doi.org/10.1016/j.resmic.2004.05.009>
4. Guner Ozenen G, Sahbudak Bal Z, Bilen NM, Yildirim Arslan S, Aydemir S, Kurugol Z, et al. The first report of *Sphingomonas yanoikuyae* as a human pathogen in a child with a central nervous system infection. *Pediatr Infect Dis J*. 2021;40:e524. <https://doi.org/10.1097/INF.0000000000003301>
5. Clinical and Laboratory Standards Institute. Performance standards for antimicrobial susceptibility testing; thirty-third edition (M100-ED33). Wayne (PA): The Institute; 2023.
6. Laupland KB, Paterson DL, Stewart AG, Edwards F, Harris PNA. *Sphingomonas paucimobilis* bloodstream infection is a predominantly community-onset disease with significant lethality. *Int J Infect Dis*. 2022;119:172–7. <https://doi.org/10.1016/j.ijid.2022.03.060>
7. Ryan MP, Adley CC. *Sphingomonas paucimobilis*: a persistent gram-negative nosocomial infectious organism. *J Hosp Infect*. 2010;75:153–7. <https://doi.org/10.1016/j.jhin.2010.03.007>
8. Mitra M, Nguyen KM, Box TW, Gilpin JS, Hamby SR, Berry TL, et al. Isolation and characterization of a novel *Sphingobium yanoikuyae* strain variant that uses biohazardous saturated hydrocarbons and aromatic compounds as sole carbon sources. *F1000Res*. 2020;9:767. <https://doi.org/10.12688/f1000research.25284.1>
9. Bui T, Preuss CV. Cephalosporins. Treasure Island (FL): StatPearls Publishing; 2023 [cited 2024 Feb 3]. <https://www.ncbi.nlm.nih.gov/books/NBK551517>

Address for correspondence: Ryutaro Tanizaki, Department of Internal Medicine and General Medicine, Ise Municipal General Hospital, 3038, Kusubecho, Ise, Mie 516-0014, Japan; email: rtanizaki@hospital.ise.mie.jp

EID cannot ensure accessibility for supplementary materials supplied by authors. Readers who have difficulty accessing supplementary content should contact the authors for assistance.

Sphingobium yanoikuyae Bacteremia, Japan

Appendix

16S rRNA Sample Sequences

Sample_518F Signal G:1282 A:1220 C:1612 T:1227

Lane: 45 Base Spacing: 14.643044 964 bases in 11647 scans

GGGGAAAAGGTTTTTCGGATTACTGGGCGTAAGCGCACGTAGGCGGCTATTCAAGT
CAGAGGTGAAAGCCCAGGGGCTCAACCCCGGAACTGCCTTTGAACTAGATAGCTTG
AATCCAGGAGAGGTGAGTGGAATTCGAGTGTAGAGGTGAAATTCGTAGATATTCG
GAAGAACACCAGTGCGCAAGGCGGCTCACTGGACTGGTATTGACGCTGAGGTGCGA
AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGA
TAACTAGCTGTCAGGGCACATGGTGTTTTGGTGGCGCAGCTAACGCATTAAGTTATC
CGCCTGGGGAGTACGGTCGCAAGATTA AAACTCAAAGGAATTGACGGGGGCCTGCA
CAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGCAGAACCTTACCAACGTTT
GACATCCCTATCGCGGATCGTGGAGACACTTTCCTTCAGTTCGGCTGGATAGGTGAC
AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCTGAGATGTTGGGTTAAGTCCCGCAA
CGAGCGCAACCCTCGCCTTTAGTTGCCAGCATTAGTTGGGTACTCTAAAGGAACCG
CCGGTGATAAGCCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTACGC
GTTGGGCTACACACGTGCTACAATGGCGACTACAGTGGGCAGCCACCTCGCGAGAG
GGAGCTAATCTCCAAAAGTCGTCTCAGTTCGGATCGTTCTCTGCAACTCGAGAGCGT
GAAGGCGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGGAATACCGTTCCC
AGGCCTTGTACACACCGCCCGTCACACCATGGGAGTTGGATTCACTCGAAGGCGTTG
AGCTAACCGTAAGGAGGCAGGCGACCACAGTGGGTTTAGCGACTGGGGTGAGCTAG
AGGGA

Sample_800R Signal G:1287 A:1340 C:2903 T:1931

Lane: 43 Base spacing: 14.576325 706 bases in 8462 scans

2GGCCCTTTTTCGCCCTCAGCGTCATAACCAGTCCAGTGAGCCGCCTTCGCCACTGGTG
TTCTTCCGAATATCTACGAATTCACCTCTACACTCGGAATTCACCTCACCTCTCCTG
GATTCAAGCTATCTAGTTTCAAAGGCAGTTCGGGGTTGAGCCCCGGGCTTTCACCT
CTGACTTGAATAGCCGCTACGTGCGCTTTACGCCAGTAATTCGAACAACGCTAG
CTCCCTCCGTATTACCGCGGCTGCTGGCACGGAGTTAGCCGGAGCTTATTCTCCCGG
TACTGTCATTATCATCCCGGGTAAAAGAGCTTTACAACCCTAAGGCCTTCATCACTC
ACGCGGCATTGCTGGATCAGGCTTTCGCCATTGTCCAATATTCCCTACTGCTGCCTC
CCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAGTGTGGCTGATCATCCTCTCAGACCA
GCTAAGGATCGTCGCCTTGGTGAGCCTTACCTACCAACTAGCTAATCCTACGCGG

GCTCATCCTTGGGCGATAAATCTTTGGACTTACGTCATCATCCGGTATTAGCTTCCGT
TTCCAGAAGTTATTCCGAACCCAAGGGCAGATTCCCACGCGTTACGCACCCGTGCGC
CACTATCTCCGAAGAGATCGTTCGACTTGCATGTATTAGGCATGCCGCCAGCGTTCG
TTCTGAGCAGTTCAAAAAA