

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](mailto:brooklyn.noble@biomerieux.com)

## *Sphingobium yanoikuyae* Bacteremia, Japan

Yayoi Miyamatsu,<sup>1</sup> Ryutarō Tanizaki,<sup>1</sup> Satoko Yamada

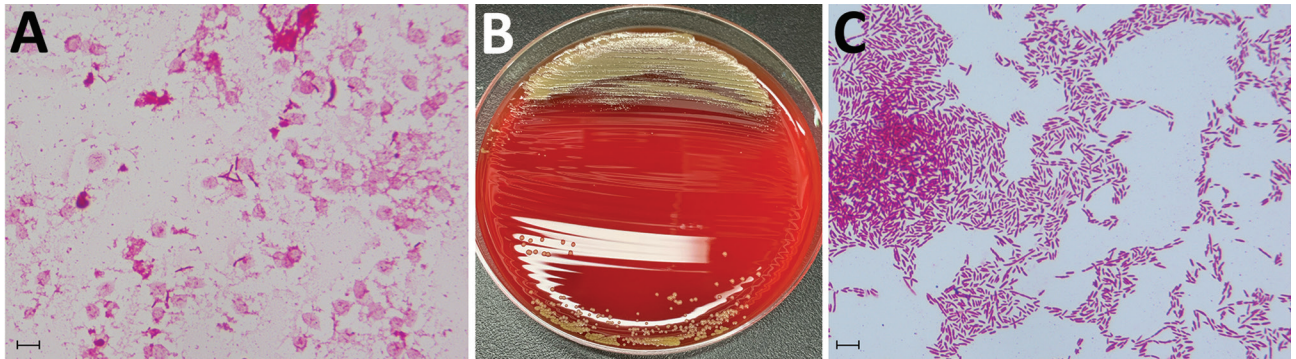
Author affiliation: Ise Municipal General Hospital, Ise, Japan

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.

<sup>1</sup>These authors contributed equally to this article.



**Figure.** Identification of *Spingobium 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  $\mu$ 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  $\mu$ 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/ $\mu$ L; reference range 3,300–8,600 cells/ $\mu$ 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 *Spingobium yanoikuyae* isolated from an 89-year-old man's blood sample in study of *S. yanoikuyae* bacteremia, Japan\*

Antimicrobial drug	MIC $\dagger$ , $\mu$ g/mL	Breakpoint MIC $\ddagger$ , $\mu$ 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  $\beta$ -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  $\beta$ -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  $\leq 4$  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](mailto: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  
GAAGAACACCAGTGGCGAAGGCGGCTCACTGGACTGGTATTGACGCTGAGGTGCGA  
AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGA  
TAACTAGCTGTCAGGGCACATGGTGTTTTGGTGGCGCAGCTAACGCATTAAGTTATC  
CGCCTGGGGAGTACGGTCGCAAGATTA AAACTCAAAGGAATTGACGGGGGCCTGCA  
CAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGCAGAACCTTACCAACGTTT  
GACATCCCTATCGCGGATCGTGGAGACACTTTCCTTCAGTTCGGCTGGATAGGTGAC  
AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCTGAGATGTTGGGTAAAGTCCCGCAA  
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  
CTGACTTGAATAGCCGCCTACGTGCGCTTTACGCCAGTAATTCGAACAACGCTAG  
CTCCCTCCGTATTACCGCGGCTGCTGGCACGGAGTTAGCCGGAGCTTATTCTCCCGG  
TACTGTCATTATCATCCCGGGTAAAAGAGCTTTACAACCCTAAGGCCTTCATCACTC  
ACGCGGCATTGCTGGATCAGGCTTTCGCCATTGTCCAATATTCCCTACTGCTGCCTC  
CCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAGTGTGGCTGATCATCCTCTCAGACCA  
GCTAAGGATCGTCGCCTTGGTGAGCCTTACCTACCAACTAGCTAATCCTACGCGG

GCTCATCCTTGGGCGATAAATCTTTGGACTTACGTCATCATCCGGTATTAGCTTCCGT  
TTCCAGAAGTTATTCCGAACCCAAGGGCAGATTCCCACGCGTTACGCACCCGTGCGC  
CACTATCTCCGAAGAGATCGTTCGACTTGCATGTATTAGGCATGCCGCCAGCGTTCG  
TTCTGAGCAGTTCAAAAAA