ST1 isolates clustered closely with Malaysia strain PR06 (online Technical Appendix 2 Figure 2). This clade (arbitrarily named the Malaysian clade) included most ST1 isolates with resistance to erythromycin and clindamycin. Recombination in a region of ≈200 kbp containing the genes encoding the 2-component virulence regulator CsrRS differentiated the Malaysian clade from a second clade formed by 5 Canadian isolates and the French and Taiwanese ST1 isolates (arbitrarily named the Taiwanese clade) (online Technical Appendix 2 Figure 2). Recombination also explains the aforementioned differences in Alp- and pilus subunit–encoding genes among serotype VI ST1 strains. Isolates NGBS543 and NGBS1605 differed from other ST1 isolates by recombination in a region spanning 107 and 89 kbp, respectively, containing Alp-encoding genes. These 2 isolates also differed between themselves by recombination in the PI-1 locus (online Technical Appendix 2 Figure 2).

Global travel and migration are known contributors to the emergence of bacterial clones in new geographies (*11*). Serotype VI GBS infections have emerged in Malaysia and Taiwan (*3*,*4*). The population of serotype VI GBS isolates in Canada is dominated by 2 ST1 clades, each closely related genetically to the Malaysian or Taiwanese isolates. Although it is tempting to speculate that these 2 ST1 genotypes were introduced into Canada from overseas, the speculation cannot be fully supported by our current limited dataset. Continued monitoring for serotype VI GBS infections is warranted.

Acknowledgments

We thank staff at Public Health Ontario Genome Core for genome sequencing of our strains.

This work was supported by Public Health Ontario through internal grant RRB-17-030 to N.F.

About the Author

Ms. Neemuchwala is a research associate at Public Health Ontario in Toronto, Ontario, Canada. Her research interests include the molecular epidemiology of pathogenic streptococci.

References

1. Le Doare K, Heath PT. An overview of global GBS epidemiology. Vaccine. 2013;31(Suppl 4):D7–12. http://dx.doi.org/10.1016/j.vaccine.2013.01.009
2. Morozumi M, Wajima T, Takata M, Iwata S, Ubukata K. Molecular characteristics of group B *Streptococci* isolated from adults with invasive infections in Japan. J Clin Microbiol. 2016;54:2695–700. http://dx.doi.org/10.1128/JCM.01183-16
3. Eskandarian N, Ismail Z, Neela V, van Belkum A, Desa MN, Amin Nordin S. Antimicrobial susceptibility profiles, serotype distribution and virulence determinants among invasive, non-invasive and colonizing *Streptococcus agalactiae* (group B *Streptococcus*) from Malaysian patients. Eur J Clin Microbiol Infect Dis. 2015;34:579–84. http://dx.doi.org/10.1007/s10096-014-2265-x
4. Lin HC, Chen CJ, Chiang KH, Yen TY, Ho CM, Hwang KP, et al. Clonal dissemination of invasive and colonizing clonal complex 1 of serotype VI group B *Streptococcus* in central Taiwan. J Microbiol Immunol Infect. 2016;49:902–9. http://dx.doi.org/10.1016/j.jmii.2014.11.002
5. Alhhazmi A, Hurteau D, Tyrrell GJ. Epidemiology of invasive group B streptococcal disease in Alberta, Canada, from 2003 to 2013. J Clin Microbiol. 2016;54:1774–81. http://dx.doi.org/10.1128/JCM.00355-16
6. Teatero S, McGeer A, Low DE, Li A, Demczuk W, Martin I, et al. Characterization of invasive group B *Streptococcus* strains from the greater Toronto area, Canada. J Clin Microbiol. 2014;52:1441–7. http://dx.doi.org/10.1128/JCM.03554-13
7. Flores AR, Galloway-Peña J, Sahasrabhojane P, Saldaña M, Yao H, Su X, et al. Sequence type 1 group B *Streptococcus*, an emerging cause of invasive disease in adults, evolves by small genetic changes. Proc Natl Acad Sci U S A. 2015;112:6431–6. http://dx.doi.org/10.1073/pnas.1504725112
8. Teatero S, Athey TB, Van Caeseele P, Horsman G, Alexander DC, Melano RG, et al. Emergence of serotype IV group B *Streptococcus* adult invasive disease in Manitoba and Saskatchewan, Canada, is driven by clonal sequence type 459 strains. J Clin Microbiol. 2015;53:2919–26. http://dx.doi.org/10.1128/JCM.01128-15
9. Clinical and Laboratory Standards Institute. Performance standards for antimicrobial susceptibility testing. 25th informational supplement (M100–S23). Wayne (PA): The Institute; 2015.
10. Teatero S, Neemuchwala A, Yang K, Gomes J, Athey TBT, Martin I, et al. Genetic evidence for a novel variant of the pilus island 1 backbone protein in group B *Streptococcus.* J Med Microbiol. 2017;66:1409–15. http://dx.doi.org/10.1099/jmm.0.000588
11. Morens DM, Fauci AS. Emerging infectious diseases: threats to human health and global stability. PLoS Pathog. 2013;9:e1003467. http://dx.doi.org/10.1371/journal.ppat.1003467

Address for correspondence: Nahuel Fittipaldi, Public Health Ontario Laboratory, 661 University Ave, Ste 17-100, Toronto, ON M5G 1M1, Canada; email: nahuel.fittipaldi@oahpp.ca

Psychrobacter sanguinis Wound Infection Associated with Marine Environment Exposure, Washington, USA

Jesse Bonwitt, Michael Tran, Angela Droz, Anna Gonzalez, William A. Glover

Author affiliations: Centers for Disease Control and Prevention, Atlanta, Georgia, USA (J. Bonwitt); Durham University, Durham, England (J. Bonwitt); Washington State Department of Health, Shoreline, Washington, USA (J. Bonwitt, M. Tran, W.A. Glover); Harrison Medical Center, Bainbridge Island, Washington, USA (A. Droz); Kitsap Public Health District, Bremerton, Washington, USA (A. Gonzalez)

DOI: https://doi.org/10.3201/eid2410.171821

We report a 26-year-old man with *Psychrobacter sanguinis* cellulitis of a wound sustained during ocean fishing in Washington, USA, in 2017. *Psychrobacter* spp. are opportunistic pathogens found in a wide range of environments. Clinicians should be aware of *Psychrobacter* spp. and perform 16S rRNA sequencing if this pathogen is suspected.

In February 2017, a 26-year-old man sought treatment at an urgent care facility (Harrison Medical Center, Bainbridge Island, Washington, USA) for a hand laceration and reported tingling in his fingers, hand, and forearm. The laceration was a healing 6-cm diagonal cut across the dorsum of the hand with surrounding erythema and cellulitis without active bleeding. Vital signs (blood pressure, pulse, respiration, and temperature) were within reference ranges. The patient reported that his wound occurred while he was cutting squid bait when he was ocean fishing for crabs in Puget Sound (Pacific Ocean), Washington, USA. The squid bait was purchased frozen from an independent fishing retail store. The patient did not report any other pertinent medical history (e.g., immunosuppression). We cleaned and dressed his wound, administered tetanus vaccine (Adacel; Sanofi Pasteur Inc., Swiftwater, Pennsylvania, USA) prophylactically, and treated him as an outpatient with oral cephalexin and topical bacitracin zinc. He fully recovered.

We submitted a wound swab sample to the hospital laboratory for bacterial culture. The cultures yielded rare colonies of coagulase-negative *Staphylococcus* spp. and light growth of a gram-negative rod. In a subsequent attempt to identify the unknown gram-negative rod by VITEK 2 (bioMérieux Inc., Durham, NC, USA), the results suggested *Brucella* spp. The isolate was sent to Washington State Public Health Laboratories (Shoreline, Washington, USA) for confirmatory testing, but the isolate tested negative for *Brucella* spp. by PCR. No leftover squid bait was available for sampling. Gram staining of the isolate revealed gram-negative coccobacilli arranged in pairs with rare cells that retained crystal violet stain. When culturing at 35°C was performed, medium-sized, convex, sticky, nonhemolytic colonies formed on blood agar and pinpoint colonies with pitting on chocolate agar. Colonies were catalase, oxidase, and urease positive. The isolate could not be identified by matrix-assisted laser desorption/ionization mass spectrometry (MALDI Biotyper CA System, research-use-only version 4.1.8; Bruker Daltonics Inc., MA, USA). Sequencing of 16S rRNA performed by the Centers for Disease Control and Prevention (Atlanta, Georgia, USA) identified the bacterium as *Psychrobacter sanguinis* (GenBank accession no. MH178035).

We performed antimicrobial susceptibility testing under aerobic conditions at 35°C using disk diffusion testing. Despite the absence of standardized break points for *Psychrobacter* spp., the large zone sizes indicated that the isolate was susceptible to cefazolin, cefepime, cefoxitin, ceftriaxone, ciprofloxacin, meropenem, penicillin, and tetracycline. The isolate tested negative for β-lactamase.

Psychrobacter are psychrotrophic (i.e., cold tolerant), gram-negative bacteria of the family *Moraxellaceae* (*1*). *Psychrobacter* spp. have been isolated from marine species (crustaceans, fish, and marine mammals); marine environments (seabed and seaweed); food products (seafood, cheese, and meat); storks; pig digestive tracts; and lamb lungs (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi). *Psychrobacter* spp. might also be a component of the human microbiota; studies have demonstrated the presence of *P. arenosus*, *P. faecalis*, *P. phenylpyruvicus*, and *P. pulmonis* in the human gut (*2*).

Only a subset of *Psychrobacter* spp. are considered medically relevant opportunistic pathogens on the basis of a limited number of published case reports (*1*,*3*). Clinical manifestations depend on the infection site and include bacteremia (*4*,*5*), meningitis (*6*,*7*), surgical wound infection (*8*), and ocular infection (*9*). Of these cases, only 1 was associated with exposure to a marine environment; in that case, the patient experienced *P. phenylpyruvicus* bacteremia after consuming a raw geoduck clam that was possibly imported from the Pacific Northwest (*5*).

P. sanguinis was reported as a new species in 2012, after retrospective isolation from the blood of 4 patients in New York, USA (*10*). *P. sanguinis* infection was subsequently reported in a patient with meningitis in France (*7*), and an organism closely related to *P. sanguinis* (98% identity of 16S rRNA) was reported in a patient with meningitis in Mexico (*6*). One of these patients acquired the infection nosocomially, but the source of the infections could not be determined, and exposure to marine environments was not reported for either case. Both patients were treated with antimicrobial drugs; 1 patient fully recovered, and the other died from complications, including septic shock. *P. sanguinis* has previously been described as broadly susceptible (*7*); however, *Psychrobacter* spp. have displayed penicillin resistance (*1*).

We describe a case of *P. sanguinis* infection in a healthy person after wound exposure to squid bait and seawater of the Pacific Northwest Coast. The source of the infection could not be determined, but isolation of *Psychrobacter* spp. from a wide range of environments suggests the infection could have occurred from exposure to the marine environment. Contamination of the wound by human gut microbiota cannot be excluded but is unlikely, given that only 2 types of bacteria were isolated from the wound. The wound displayed cellulitis, a presentation consistent with infection by an opportunistic pathogen; this finding, therefore, expands the clinical spectrum of *P. sanguinis* infection. Clinicians and laboratorians should be aware of the opportunistic potential of *Psychrobacter* spp. and the limitations of commercial identification systems for confirming these agents.

Acknowledgments

We thank the staffs of the Microbiology Department of the Harrison Medical Center and the Special Bacteriology Reference Laboratory of the US Centers for Disease Control and Prevention.

About the Author

Dr. Bonwitt is a veterinarian and Epidemic Intelligence Service officer in the Division of Scientific Education and Professional Development, Center for Surveillance, Epidemiology and Laboratory Services, Office of Public Health Scientific Services, Centers for Disease Control and Prevention, Atlanta, Georgia, USA, assigned to the Washington State Department of Health. His research interests are zoonotic and emerging infectious diseases and qualitative research at the animal–human interface.

References

1. Vaneechoutte M, Dijkshoorn L, Nemec A, Kämpfer P, Wauters G. *Acinetobacter*, *Chryseobacterium*, *Moraxella*, and other nonfermentative gram-negative rods. In: Jorgensen JH, Pfaller MA, Carroll KC, Funke G, Landry ML, Richter SS, et al., editors. Manual of clinical microbiology. 11th ed. Washington: AMS Press; 2015. p. 813–37.
2. Lagier J-C, Khelaifia S, Alou MT, Ndongo S, Dione N, Hugon P, et al. Culture of previously uncultured members of the human gut microbiota by culturomics. Nat Microbiol. 2016;1:16203. http://dx.doi.org/10.1038/nmicrobiol.2016.203
3. Deschaght P, Janssens M, Vaneechoutte M, Wauters G. *Psychrobacter* isolates of human origin, other than *Psychrobacter phenylpyruvicus*, are predominantly *Psychrobacter faecalis* and *Psychrobacter pulmonis*, with emended description of *P. faecalis*. Int J Syst Evol Microbiol. 2012;62:671–4. http://dx.doi.org/10.1099/ijs.0.032631-0
4. Caspar Y, Recule C, Pouzol P, Lafeuillade B, Mallaret MR, Maurin M, et al. *Psychrobacter arenosus* bacteremia after blood transfusion, France. Emerg Infect Dis. 2013;19:1118–20. http://dx.doi.org/10.3201/eid1907.121599
5. Leung WK, Chow VC, Chan MC, Ling JM, Sung JJ. *Psychrobacter* bacteraemia in a cirrhotic patient after the consumption of raw geoduck clam. J Infect. 2006;52:e169–71. http://dx.doi.org/ 10.1016/j.jinf.2005.08.031
6. Ortiz-Alcántara JM, Segura-Candelas JM, Garcés-Ayala F, Gonzalez-Durán E, Rodríguez-Castillo A, Alcántara-Pérez P, et al. Fatal *Psychrobacter* sp. infection in a pediatric patient with meningitis identified by metagenomic next-generation sequencing in cerebrospinal fluid. Arch Microbiol. 2016;198: 129–35. http://dx.doi.org/10.1007/s00203-015-1168-2
7. Le Guern R, Wallet F, Vega E, Courcol RJ, Loïez C. *Psychrobacter sanguinis*: an unusual bacterium for nosocomial meningitis. J Clin Microbiol. 2014;52:3475–7. http://dx.doi.org/10.1128/JCM.01197-14
8. Stepanović S, Vuković D, Bedora-Faure M, K'ouas G, Djukić S, Svabić-Vlahović M, et al. Surgical wound infection associated with *Psychrobacter phenylpyruvicus*-like organism. Diagn Microbiol Infect Dis. 2007;57:217–9. http://dx.doi.org/10.1016/j.diagmicrobio.2006.08.002
9. Gini GA. Ocular infection caused by *Psychrobacter immobilis* acquired in the hospital. J Clin Microbiol. 1990;28:400–1.
10. Wirth SE, Ayala-del-Río HL, Cole JA, Kohlerschmidt DJ, Musser KA, Sepúlveda-Torres LC, et al. *Psychrobacter sanguinis* sp. nov., recovered from four clinical specimens over a 4-year period. Int J Syst Evol Microbiol. 2012;62:49–54. http://dx.doi.org/10.1099/ijs.0.029058-0

Address for correspondence: Jesse Bonwitt, Centers for Disease Control and Prevention, 1600 Clifton Rd NE, Atlanta, GA 30329-4027, USA; email: jbonwitt@cdc.gov

Diagnosis of *Haemophilus influenzae* Pneumonia by Nanopore 16S Amplicon Sequencing of Sputum

Jangsup Moon,[1] Yoonhyuk Jang,[1] Narae Kim, Wan Beom Park, Kyung-Il Park, Soon-Tae Lee, Keun-Hwa Jung, Manho Kim, Sang Kun Lee, Kon Chu

Author affiliations: Seoul National University Hospital, Seoul, South Korea (J. Moon, Y. Jang, N. Kim, W.B. Park, S.-T. Lee, K.-H. Jung, M. Kim, S.K. Lee, K. Chu); Seoul National University Hospital Healthcare System Gangnam Center, Seoul (K.-I. Park)

DOI: https://doi.org/10.3201/eid2410.180234

We used deep sequencing of the 16S rRNA gene from sputum to identify *Haemophilus influenzae* in a patient with community-acquired pneumonia. This method may be more effective than conventional diagnostic tests in pneumonia patients because of its speed and sensitivity.

Pathogen identification in patients with community-acquired pneumonia primarily relies on culture-based techniques (*1*,*2*). Sequencing-based approaches for pathogen identification are being applied to pneumonia patients (*3*). MinION (Oxford Nanopore Technologies, Oxford, UK), a nanopore sequencer, is gaining attention in metagenomics research because of its capability for long-read sequencing and real-time analysis, along with its small size (*4*,*5*). Recently, the first use of MinION for real-time metagenomic sequencing of bronchoalveolar lavage (BAL) specimens in pneumonia patients was reported (*6*). We report successfully detecting a respiratory pathogen by deep sequencing of 16S amplicons of sputum using MinION.

[1]These authors contributed equally to this article.