

**Muhammad Masroor Alam,
Adnan Khurshid,
Salmaan Sharif,
Shahzad Shaukat,
Rana Muhammad Suleman,
Mehar Angez,
and Syed Sohail Zahoor Zaidi**

Author affiliation: National Institute of Health,
Chak Shahzad, Islamabad, Pakistan

DOI: <http://dx.doi.org/10.3201/eid1906.120771>

References

1. Grard G, Drexler JF, Fair J, Muyembe JJ, Wolfe ND, Drosten C, et al. Re-emergence of Crimean-Congo hemorrhagic fever virus in Central Africa. *PLoS Negl Trop Dis*. 2011;5:e1350. <http://dx.doi.org/10.1371/journal.pntd.0001350>
2. Mild M, Simon M, Albert J, Mirazimi A. Towards an understanding of the migration of Crimean-Congo hemorrhagic fever virus. *J Gen Virol*. 2010;91:199–207. <http://dx.doi.org/10.1099/vir.0.014878-0>
3. Chinikar S, Ghiasi SM, Hewson R, Moradi M, Haeri A. Crimean-Congo hemorrhagic fever in Iran and neighboring countries. *J Clin Virol*. 2010;47:110–4. <http://dx.doi.org/10.1016/j.jcv.2009.10.014>
4. Burt FJ, Swanepoel R. Molecular epidemiology of African and Asian Crimean-Congo hemorrhagic fever isolates. *Epidemiol Infect*. 2005;133:659–66. <http://dx.doi.org/10.1017/S0950268805003730>
5. Schwarz TF, Nsanze H, Longson M, Nitschko H, Gilch S, Shurie H, et al. Polymerase chain reaction for diagnosis and identification of distinct variants of Crimean-Congo hemorrhagic fever virus in the United Arab Emirates. *Am J Trop Med Hyg*. 1996;55:190–6.
6. Yashina L, Petrova I, Seregin S, Vysheirskii O, Lvov D, Aristova V, et al. Genetic variability of Crimean-Congo hemorrhagic fever virus in Russia and Central Asia. *J Gen Virol*. 2003;84:1199–206. <http://dx.doi.org/10.1099/vir.0.18805-0>
7. Suleiman MN, Muscat-Baron JM, Harries JR, Satti AG, Platt GS, Bowen ET, et al. Congo/Crimean hemorrhagic fever in Dubai. An outbreak at the Rashid Hospital. *Lancet*. 1980;316:939–41. [http://dx.doi.org/10.1016/S0140-6736\(80\)92103-0](http://dx.doi.org/10.1016/S0140-6736(80)92103-0)
8. Hewson R, Gmyl A, Gmyl L, Smirnova SE, Karganova G, Jamil B, et al. Evidence of segment reassortment in Crimean-Congo hemorrhagic fever virus. *J Gen Virol*. 2004;85:3059–70. <http://dx.doi.org/10.1099/vir.0.80121-0>
9. Hoogstraal H. The epidemiology of tick-borne Crimean-Congo hemorrhagic fever in Asia, Europe, and Africa. *J Med Entomol*. 1979;15:307–417.

10. Altaf A, Luby S, Ahmed AJ, Zaidi N, Khan AJ, Mirza S, et al. Outbreak of Crimean-Congo haemorrhagic fever in Quetta, Pakistan: contact tracing and risk assessment. *Trop Med Int Health*. 1998;3:878–82. <http://dx.doi.org/10.1046/j.1365-3156.1998.00318.x>

Address for correspondence: Syed Sohail Zahoor Zaidi, Department of Virology, National Institute of Health, Chak Shahzad, Park Rd, Islamabad-44000, Pakistan; email: zaidis@pak.emro.who.int

Shewanella haliotis Associated with Severe Soft Tissue Infection, Thailand, 2012

To the Editor: Marine bacteria of the family Shewanellaceae, genus *Shewanella*, are gram-negative, motile bacilli that grow aerobically or anaerobically and produce hydrogen sulfide (1). Organisms belonging to a *Shewanella* species were first isolated in 1931 by Derby and Hammer from dairy products and classified as *Achromobacter putrefaciens* (2). Members of *Shewanella* species usually are found in marine environments in warm climates or during summer in temperate climates (3). In humans, most *Shewanella* species infections occur in skin and soft tissues (4). One species (*S. algae*) and possibly a second (*S. putrefaciens*) have been isolated from human samples on multiple occasions (5). A third species, *S. haliotis*, was implicated in human infections during 2010 (6) and *S. xiamenensis* was reported as the fourth infectious species among humans during 2011 (7). *S. haliotis* is a novel bacterial species that was isolated from the gut microflora of abalones (*Haliotis discus han-nai*) in 2007 (8). We report the second

description, to our knowledge, of *S. haliotis* involved in human disease.

In September 2012, a 52-year-old woman, living in Bangkok, Thailand, was hospitalized after experiencing drowsiness for 2 hours. She had a low-grade fever, chills, and swelling, erythema, and tenderness in her left leg. During the previous week, she had handled fresh seafood in a market and had eaten cooked mackerel. She denied having eaten uncooked food or wading into flooded areas or the sea. She had undergone orthotopic liver transplantation 6 months previously to excise hepatocellular carcinoma related to Child-Pugh class C hepatitis C cirrhosis; since that procedure, she had been under treatment with immunosuppressive drugs. She also had diabetes, hypertension, and nephrotic syndrome. Physical examination revealed that in addition to above-named symptoms, multiple blisters were noted (Figure, panel A). Her oral temperature was 37.8°C, blood pressure 80/40 mm Hg, pulse was 110 bpm, and respiratory rate was 24 breaths/minute. A complete blood count showed a leukocyte count of 2,250 cells/μL (91.2% neutrophils). Despite adequate rehydration, monitored by central venous pressure, the patient required norepinephrine to stabilize her vital signs. The clinical diagnosis of her condition was septic shock with suspected necrotizing fasciitis.

After tissue and blood samples were collected and submitted for microbiological analysis, shock resuscitation and an emergency fasciotomy (Figure, panel B) were performed, and antimicrobial drug treatment with meropenem and vancomycin was started. Surgeons did not confirm the suspected necrotizing fasciitis. Two sets of blood cultures and fluid culture sampled from the left leg identified *S. algae* by conventional biochemical methods. The MICs of antimicrobial drugs were determined by Etest (bio-Mérieux, Solna, Sweden). This strain was susceptible to ciprofloxacin (0.25



Figure. *Shewanella haliotis* severe soft tissue infection of woman in Thailand, 2012. The patient sought treatment for painful erythematous swelling of the left leg. A) Arrow indicates affected area. B) Postsurgical fasciotomy wound with necrotic tissue.

mg/L), piperacillin-tazobactam (1.0 mg/L), ceftriaxone (1.0 mg/L), and meropenem (0.38 mg/L). The patient had fever for the first 2 days of hospitalization. After 2 weeks of treatment, the antimicrobial drug was switched to oral ciprofloxacin; treatment was continued after dressing and debridement of the fasciotomy wound.

The organism produced yellowish-brown mucoid colonies on sheep blood agar and chocolate agar after 18 hours of incubation at 35°C under CO₂ atmosphere. MacConkey agar showed non-lactose-fermenting colonies that were oxidase-positive, motile, and produced hydrogen sulfide on triple sugar iron agar. Growth at 42°C with 6.5% NaCl suggested that this organism was *S. algae*. Because phylogenetically related *Shewanella* species may be misidentified by routine biochemical tests, the strain was confirmed by using 16S rRNA gene sequencing.

Molecular characterization of 16S rRNA gene sequencing was performed by using PCR with *Shewanella* species consensus primers (online Technical Appendix Table, wwwnc.cdc.gov/EID/article/19/6/12-1607-Techapp.pdf) and direct sequencing from PCR product (JX968803). Phylogenetic analysis of the 16S rRNA gene sequence showed clustering with *S. haliotis* (NR_044134T) and 99.9% similarity and 1 base difference (online Technical Appendix Figure). By using BLAST (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>) analysis, JX968803 showed the closest match (99.9%; 1 base difference) with Alteromonadaceae bacterium PH39 (AF513471).

The strain was confirmed as *S. haliotis* by using additional biochemical tests and API 20 NE System (bioMérieux, Durham, NC, USA). It was positive for ornithine decarboxylase, gelatinase, reduction of nitrates to nitrites, tolerance to 6% NaCl, and assimilation of caprate and malate, but negative for citrate utilization, arginine dihydrolase, lysine decarboxylase, urease, indole production, assimilation of mannose, glucose, arabinose, mannitol, maltose, adipate, and acidification of glucose. This strain was resistant to polymyxin B (300 µg/disc).

More than 50 species of *Shewanella* have been reported. The route of *Shewanella* infection is associated with direct contact with the organism through seawater or ingestion of raw seafood (9). Japan reported 1 case of *S. haliotis* infection in an elderly patient in whom *Vibrio vulnificus* infection was initially suspected (6), and various clinical manifestations of *S. algae* infection have been reported (5). Community- and hospital-acquired infection with *Shewanella* species from contaminated medical devices have also been reported (10). *S. haliotis* and *S. algae* are closely related organisms; discriminating between them on the basis of biochemical tests is difficult. Molecular characterization of

S. haliotis soft tissue infection in the absence of typical exposures.

16S rRNA gene sequencing can be used to differentiate the 2 species. In summary, this case suggests that immune-compromised persons in tropical climates could be susceptible to *S. haliotis* soft tissue infection in the absence of typical exposures.

Acknowledgments

We thank the staff of the Gastroenterology Unit, Department of Medicine, Liver Transplant Unit, Center of Excellence in Clinical Virology, Faculty of Medicine, Chulalongkorn University and Hospital, and the Thai Red Cross Society. We also thank Petra Hirsch for reviewing the manuscript.

This work was supported by the Higher Education Research Promotion and National Research University Project of Thailand, Office of the Higher Education Commission (HR1155), Thailand Research Fund (DPG5480002), Center of Excellence in Clinical Virology, Chulalongkorn University, Integrated Innovation Academic Center, Chulalongkorn University Centenary Academic Development Project (CU56-HR01), and King Chulalongkorn Memorial Hospital.

**Kittiyod Poovorawan,
Tanittha Chatsuwat,
Narisorn Lakananurak,
Jira Chansaenroj,
Piyawat Komolmit,
and Yong Poovorawan**

Author affiliation: Chulalongkorn University, Bangkok, Thailand

DOI: <http://dx.doi.org/10.3201/eid1906.121607>

References

- Ivanova EP, Flavier S, Christen R. Phylogenetic relationships among marine Alteromonas-like proteobacteria: emended description of the family Alteromonadaceae and proposal of Pseudoalteromonadaceae fam. nov., Colwelliaceae fam. nov., Shewanellaceae fam. nov., Moritellaceae fam. nov., Ferrimonadaceae fam. nov., Idiomarinaceae fam. nov. and Psychromonadaceae fam. nov. *Int J Syst Evol Microbiol.* 2004;54:1773–88. <http://dx.doi.org/10.1099/ijs.0.02997-0>

2. Derby HA, Hammer BW. Bacteriology of butter. IV. Bacteriological studies on surface taint butter. Iowa Agric Exp Station Res Bull. 1931;145:387–416.
3. Holt HM, Gahrn-Hansen B, Bruun B. *Shewanella* algae and *Shewanella putrefaciens*: clinical and microbiological characteristics. Clin Microbiol Infect. 2005;11:347–52. <http://dx.doi.org/10.1111/j.1469-0691.2005.01108.x>
4. Goyal R, Kaur N, Thakur R. Human soft tissue infection by the emerging pathogen *Shewanella* algae. J Infect Dev Ctries. 2011;5:310–2. <http://dx.doi.org/10.3855/jidc.1436>
5. Janda JM, Abbott SL. The genus *Shewanella*: from the briny depths below to human pathogen. Crit Rev Microbiol. 2012;10. <http://dx.doi.org/10.3109/1040841X.2012.726209>
6. Tadera K, Shimonaka A, Ohkusu K, Morii D, Shimohana J, Michinaka T, et al. A case report of *Shewanella haliotis* showing a phlegmonous inflammation of right lower leg with sepsis [in Japanese]. JSCM. 2010;20:239–44.
7. Zong Z. Nosocomial peripancreatic infection associated with *Shewanella xiamenensis*. J Med Microbiol. 2011;60:1387–90. <http://dx.doi.org/10.1099/jmm.0.031625-0>
8. Kim D, Baik KS, Kim MS, Jung BM, Shin TS, Chung GH, et al. *Shewanella haliotis* sp. nov., isolated from the gut microflora of abalone, *Haliotis discus hannai*. Int J Syst Evol Microbiol. 2007;57:2926–31. <http://dx.doi.org/10.1099/ijms.0.65257-0>
9. Myung DS, Jung YS, Kang SJ, Song YA, Park KH, Jung SI, et al. Primary *Shewanella* algae bacteremia mimicking *Vibrio* septicemia. J Korean Med Sci. 2009;24:1192–4. <http://dx.doi.org/10.3346/jkms.2009.24.6.1192>
10. Oh HS, Kum KA, Kim EC, Lee HJ, Choe KW, Oh MD. Outbreak of *Shewanella* algae and *Shewanella putrefaciens* infections caused by a shared measuring cup in a general surgery unit in Korea. Infect Control Hosp Epidemiol. 2008;29:742–8. <http://dx.doi.org/10.1086/589903>

Address for correspondence: Yong Poovorawan, Center of Excellence in Clinical Virology, Department of Pediatrics, Faculty of Medicine, Chulalongkorn University, Bangkok 10330 Thailand; email: Yong.P@chula.ac.th

The opinions expressed by authors contributing to this journal do not necessarily reflect the opinions of the Centers for Disease Control and Prevention or the institutions with which the authors are affiliated.

Murine Typhus in Humans, Yucatan, Mexico

To the Editor: *Rickettsia typhi* is the causal agent of murine typhus, a febrile illness affecting humans worldwide (1). In Mexico, recent studies demonstrated a 14% prevalence of antibodies against typhus group rickettsiae in healthy adult blood donors in Mexico City, and a recent nonfatal case of endemic typhus was reported in Yucatan (2,3).

In May 2011, a 42-year-old woman and her 12-year-old son sought care at the clinical service of the Autonomous University of Yucatan. They had malaise, headache, fever (39°C), fibromyalgia, sore throat, and fatigue and an erythematous rash on the chest that after 6 days spread to the abdomen and extremities.

Dengue fever was diagnosed, and the patients were treated empirically with acyclovir, methanesulfonamide, N-(4-nitro-2-phenoxyphenyl) and clarithromycin. Dengue could not be confirmed by laboratory testing.

Murine typhus was diagnosed on the basis of PCR amplification and immunofluorescent assay for antibodies to *R. typhi*. *Rickettsia* species was determined by sequencing of rickettsial genes. Three serum samples were collected from the woman (8, 12, and 16 days after illness onset) and 1 from the boy (8 days) in 3.8% sodium citrate as anticoagulant, and DNA was extracted immediately by QIAamp DNA Blood Mini Kit (QIAGEN Valencia, CA, USA) in accordance with the manufacturer's instructions. Single-step PCR amplification was performed by using genus-specific primers for the rickettsial 17-kDa protein and citrate synthase (*gltA*) genes as reported (4).

Sequences of the citrate synthase and 17-kDa PCR products were compared at the National Center for Biotechnology Information BLAST software (5). Three PCR amplicons

of both genes were fully sequenced and compared with sequences in GenBank. The 17-kDa and citrate synthase fragment sequences (GenBank accession nos. JX198507 and JX458814) showed 99% and 100% identity, respectively, with *R. typhi* strain Wilmington strain (GenBank accession no. AE017197.1) (Table).

Immunofluorescent assay was performed by using *R. rickettsii* and *R. typhi* antigen fixed on slides. We examined the serum samples for IgG and IgM, assessing reactivity of γ chain-specific and m heavy chain-specific secondary conjugates, respectively, with rickettsial antigens. All 3 samples from the woman and the sample from the boy contained antibodies to *R. typhi* (Table). Both patients were treated with 100 mg of oral doxycycline 2 \times /day for 7 days (boy), and 10 days (woman); symptoms improved in 72 hours for the child. The woman's symptoms resolved completely in 5 days.

Typhus has been endemic in Mexico since before the conquest period (6). Socioeconomic aspects play a major role in zoonotic diseases, such as rickettsioses, especially in their distribution in urban and suburban areas because of factors such as marginalized communities, animal breeding, education levels, poverty, and social exclusion from health systems.

Overcrowding resulting from migration from rural areas to large urban centers contributes to increased zoonoses in urban areas. Also contributing is the ecologic imbalance of flora and fauna associated with deteriorating sanitary conditions in areas where mammals involved in the cycle of *R. typhi*, such as rodents and opossum, may live in the same habitat as humans and colonize backyards, waste deposit area, and areas around the neighborhoods where they can find food. The concurrence and presence of mammals, vectors, and humans may contribute to maintaining transmission of endemic typhus in a reduced area, with the possibility to cause outbreaks