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 *Shewanella sulfide (S. putrefaciens)*. 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. halotis*, was implicated in human infections during 2010 (6) and *S. xiamenensis* was reported as the fourth infectious species among humans during 2011 (7). *S. halotis* is a novel bacterial species that was isolated from the gut microflora of abalones (*Haliotis discus hannai*) in 2007 (8). We report the second description, to our knowledge, of *S. halotis* 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 (bioMérieux, Solna, Sweden). This strain was susceptible to ciprofloxacin (0.25
S. haliotis gene sequence showed clustering withlogenetic analysis of the 16S rRNA- from PCR product (JX968803). PhyTechapp.pdf) and direct sequencing cdc.gov/EID/article/19/6/12-1607-Technical Appendix Table, wwwnc.la species consensus primers (online formed by using PCR withShewanel-16S rRNA gene sequencing was per- rRNA gene sequencing. The strain was confirmed by using 16S identified by routine biochemical tests,latedNaCl suggested that this organism wasS. algae. Because phylogenetically re-nowned hydrogen sulfide on triple sugar 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 wasS. algae. Because phylogenetically re-identified 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 withShewanella 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). Phylogenic analysis of the 16S rRNA gene sequence showed clustering withS. 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 (bio-Mérieux, 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 whomVibrio vulnificus infection was initially suspected (6), and various clinical manifestations of S. algae infection have been reported (5). Community- and hospital-acquired infection withShewanella 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 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.

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

References

Mmurine 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 (Table). Both patients were treated with a 17-kDa 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×/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 zooneses 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 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).
Technical Appendix

Specific *Shewanella* Consensus Primer Sets for 16S rRNA Gene Sequencing and Phylogenetic Analysis

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Technical Appendix Figure. Phylogenetic analysis of *Shewanella* spp. 16S rRNA gene sequencing (1,077 base pairs). Closed circle indicates the strain in this study compared with the *S. haliotis* prototype species (NR_044134) and other representative species. Numbers at branch nodes are bootstrap values. Scale bar represents number of nucleotide substitutions per site.