

that H13 viruses may have been introduced into domestic poultry from migratory birds and that they may have the potential to become a global cross-species threat.

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References

1. Su S, Bi Y, Wong G, Gray GC, Gao GF, Li S. Epidemiology, evolution, and recent outbreaks of avian influenza virus in China. *J Virol*. 2015;89:8671–6. <http://dx.doi.org/10.1128/JVI.01034-15>
2. Global Consortium for H5N8 and Related Influenza Viruses. Role for migratory wild birds in the global spread of avian influenza H5N8. *Science*. 2016;354:213–7. <http://dx.doi.org/10.1126/science.aaf8852>
3. Kim JY, Park YC. The complete mitogenome of the black-tailed gull *Larus crassirostris* (Charadriiformes: Laridae). *Mitochondrial DNA A DNA Mapp Seq Anal*. 2016;27:1885–6. <http://dx.doi.org/10.3109/19401736.2014.971271> PMID: 25319297
4. Belser JA, Gustin KM, Pearce MB, Maines TR, Zeng H, Pappas C, et al. Pathogenesis and transmission of avian influenza A (H7N9) virus in ferrets and mice. *Nature*. 2013;501:556–9. <http://dx.doi.org/10.1038/nature12391>
5. Gao R, Cao B, Hu Y, Feng Z, Wang D, Hu W, et al. Human infection with a novel avian-origin influenza A (H7N9) virus. *N Engl J Med*. 2013;368:1888–97. <http://dx.doi.org/10.1056/NEJMoa1304459>
6. Lam TT, Wang J, Shen Y, Zhou B, Duan L, Cheung CL, et al. The genesis and source of the H7N9 influenza viruses causing human infections in China. *Nature*. 2013;502:241–4. <http://dx.doi.org/10.1038/nature12515>
7. Zhang Q, Shi J, Deng G, Guo J, Zeng X, He X, et al. H7N9 influenza viruses are transmissible in ferrets by respiratory droplet. *Science*. 2013;341:410–4. <http://dx.doi.org/10.1126/science.1240532>
8. Ke C, Mok CKP, Zhu W, Zhou H, He J, Guan W, et al. Human infection with highly pathogenic avian influenza A(H7N9) virus, China. *Emerg Infect Dis*. 2017;23:1332–40. <http://dx.doi.org/10.3201/eid2308.170600>

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Rat-Bite Fever in Human with *Streptobacillus notomytis* Infection, Japan

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We report a case of rat-bite fever in a 94-year-old woman with *Streptobacillus notomytis* infection. We established an epidemiologic link between exposure to rats and human infection by performing nested PCRs that detected *S. notomytis* in the intraoral swab specimens obtained from rats captured in the patient's house.

Streptobacillus is a genus of gram-negative, filamentous, rod-shaped bacilli belonging to the family *Leptotrichiaceae*. Since 2014, four novel species other than *S. moniliformis* have been reported: *S. hongkongensis* was isolated from 2 human patients, *S. felis* from the lung of a cat, *S. rattii* from black rats, and *S. notomytis* from a spinifex hopping mouse (1–4). We report a case of a human infection with *S. notomytis*.

A 94-year-old woman sought treatment at our hospital for general malaise, anorexia, and bilateral knee pain. At admission, her body temperature was 38°C; physical examination revealed swelling in both knees. Her skin was intact, with no rashes or animal bites. Laboratory tests revealed high leukocyte count (1.42×10^9 cells/L) and elevated level of C-reactive protein (19.5 mg/dL).

Bilateral knee arthrocentesis yielded 25 mL of purulent fluid; Gram stain demonstrated the presence of few, thin, gram-negative bacilli with pyrophosphate calcium crystals and neutrophils (Figure). Bacterial culture yielded transparent, small, smooth colonies on 5% sheep blood agar (Kyokuto, Tokyo, Japan) incubated at 37°C under 5% CO₂ for 48 h. However, the automated bacterial identification method (Vitek 2; bioMérieux, Tokyo, Japan) failed to identify the isolate. We evaluated the isolate (NR2245) by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry using Bruker MALDI BioTyper software version 4.001 library database (Bruker Daltonik GmbH, Bremen, Germany) employing ethanol–formic acid extraction. We identified the isolate as *S. moniliformis*

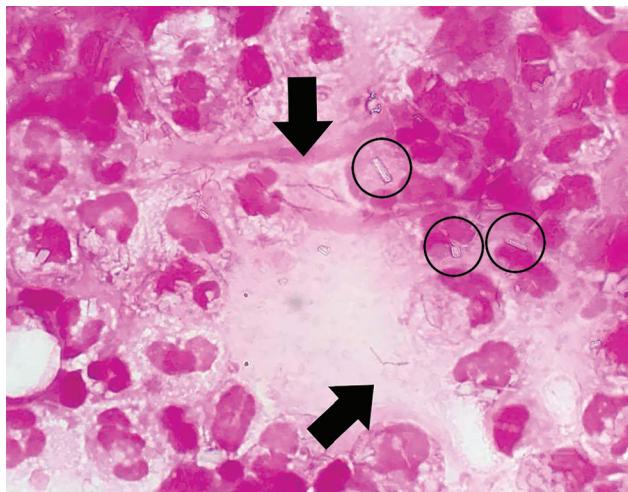


Figure. Gram staining of pus obtained from a patient with rat-bite fever. Circles indicate pyrophosphate calcium crystals. Arrows indicate chain-shaped gram-negative bacilli. Original magnification $\times 1,000$.

(score: 1.608, 24 h). The database included only 1 entry from *S. moniliformis*, DSM 12112T.

We administered ceftriaxone. Subsequent results of arthrocentesis and blood cultures (BacT/ALERT; bioMérieux) were negative; however, the patient's fever and bilateral knee pain persisted. Transthoracic echocardiography showed no evidence of infective endocarditis. We replaced ceftriaxone with sulbactam and ampicillin on hospital day 16, followed by intraarticular administration of dexamethasone on day 17 for pseudogout (diagnosed by the presence of pyrophosphate calcium crystals). On day 20, we performed bilateral knee lavage; thereafter, the patient's fever and knee pain resolved. The surgery specimen was serous fluid; results of Gram stain and aerobic and anaerobic culture were negative. On day 30, we replaced sulbactam/ampicillin treatment with oral minocycline (100 mg every 12 h) as maintenance therapy; however, pneumonia developed, and the patient died of respiratory failure on day 56. We detected *Acinetobacter baumannii* complex and *Enterococcus faecium* from the sputum; however, we did not detect *Streptobacillus* species.

To identify the isolate from the patient's synovial fluid, we performed 16S rRNA gene sequencing using a universal primer pair: 27F (5'-AGAGTTTGATCC TGGCTCAG-3') and 1492R (5'-GGTACCTGTTACGACTT-3'). The sequence (GenBank accession no. LC360808) showed 100% identity (1,380/1,380 bp) to *S. notomytis* AHL_370-1^T (GenBank accession no. KR001919) and 98.55% (1,360/1,380 bp) identity to *S. moniliformis* DSM12112^T (GenBank accession no. CP001779) in the EzBioCloud 16S database (<http://www.ezbiocloud.net/eztaxon>). We performed PCR and sequencing of housekeeping genes (*groEL* and *gyrB*) using *Streptobacillus* species-specific

primers (5). BLAST search (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>) revealed that the *groEL* (GenBank accession no. LC371754) and *gyrB* (GenBank accession no. LC371753) sequences showed 100% identity to the gene sequence of *S. notomytis* KWG2 (522/522 bp and 758/758 bp, respectively) and 99.6% (20/522 bp) and 99.9% (757/758 bp) identity, respectively, to the gene sequence of *S. notomytis* AHL_370-1^T.

We determined antimicrobial susceptibility pattern by broth microdilution. MIC of penicillin was ≤ 0.06 $\mu\text{g/mL}$; cefazolin, ≤ 0.5 $\mu\text{g/mL}$; ceftriaxone, 0.25 $\mu\text{g/mL}$; vancomycin, ≤ 0.25 $\mu\text{g/mL}$; clarithromycin, 8 $\mu\text{g/mL}$; minocycline, ≤ 0.12 $\mu\text{g/mL}$; and levofloxacin, ≤ 1 $\mu\text{g/mL}$.

S. moniliformis is known to cause rat-bite fever in humans (6). To study the association between exposure to rats and *S. notomytis* infection, we visited the patient's house after her death and captured 2 rats (*Rattus rattus*), from which we collected stool and intraoral and rectal swab samples. On the same day, we brought the specimens at room temperature to our laboratory and performed bacteriological cultures in 5% sheep blood agar, incubated at 37°C under 5% CO₂; the specimens did not grow *Streptobacillus*. We performed nested PCR with DNA extracted from each specimen, amplified the 16S rRNA gene using the universal primer pair 27F and 1492R, and performed nested PCR using the amplicons from the first PCR as templates, with the *Streptobacillus*-specific primers sbmF (5'-GAGAGA-GCTTTCATCCT-3') and sbmR (5'-GTAACCTCAG-GTGCAACT-3') (7). Only 1 rat's intraoral specimen yielded PCR products, and the sequence of the amplicon by nested PCR showed 100% identity (1,089/1,089 bp) to *S. notomytis* AHL_370-1^T.

Since 2014, a total of 4 novel *Streptobacillus* species have been reported. Whether these new species have recently emerged or existed previously is uncertain. In 2014, Eisenberg et al. identified 2 isolates recovered from rats in 2008 as *S. notomytis* (2); it is possible that *S. notomytis* may have been prevalent but underrecognized in Japan because identification is difficult by conventional methods (2). Fukushima et al. reported that 16S rRNA sequencing identified an isolate obtained from a rat-bite fever patient as *S. notomytis*, not *S. moniliformis* as originally identified (8). By detecting *S. notomytis* from the rats captured in this patient's house, we support a potential epidemiologic link between rat exposure and human infection.

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References

1. Woo PC, Wu AK, Tsang CC, Leung KW, Ngan AH, Curreem SO, et al. *Streptobacillus hongkongensis* sp. nov., isolated from patients with quinsy and septic arthritis, and emended descriptions of the genus *Streptobacillus* and *Streptobacillus moniliformis*. *Int J Syst Evol Microbiol*. 2014;64:3034–9. <http://dx.doi.org/10.1099/ijms.0.061242-0>
2. Eisenberg T, Glaeser SP, Ewers C, Semmler T, Nicklas W, Rau J, et al. *Streptobacillus notomytis* sp. nov., isolated from a spinifex hopping mouse (*Notomys alexis* Thomas, 1922), and emended description of *Streptobacillus* Levaditi et al. 1925, Eisenberg et al. 2015 emend. *Int J Syst Evol Microbiol*. 2015;65:4823–9. <http://dx.doi.org/10.1099/ijsem.0.000654>
3. Eisenberg T, Glaeser SP, Nicklas W, Mauder N, Contzen M, Aledelbi K, et al. *Streptobacillus felis* sp. nov., isolated from a cat with pneumonia, and emended descriptions of the genus *Streptobacillus* and of *Streptobacillus moniliformis*. *Int J Syst Evol Microbiol*. 2015;65:2172–8. <http://dx.doi.org/10.1099/ijms.0.000238>
4. Eisenberg T, Imaoka K, Kimura M, Glaeser SP, Ewers C, Semmler T, et al. *Streptobacillus rattii* sp. nov., isolated from a black rat (*Rattus rattus*). *Int J Syst Evol Microbiol*. 2016; 66:1620–6. <http://dx.doi.org/10.1099/ijsem.0.000869>
5. Eisenberg T, Ewers C, Rau J, Akimkin V, Nicklas W. Approved and novel strategies in diagnostics of rat bite fever and other *Streptobacillus* infections in humans and animals. *Virulence*. 2016;7:630–48. <http://dx.doi.org/10.1080/21505594.2016.1177694>
6. Eisenberg T, Nicklas W, Mauder N, Rau J, Contzen M, Semmler T, et al. Phenotypic and genotypic characteristics of members of the genus *Streptobacillus*. *PLoS One*. 2015;10:e0134312. <http://dx.doi.org/10.1371/journal.pone.0134312>
7. Elliott SP. Rat bite fever and *Streptobacillus moniliformis*. *Clin Microbiol Rev*. 2007;20:13–22. <http://dx.doi.org/10.1128/CMR.00016-06>
8. Fukushima K, Yanagisawa N, Imaoka K, Kimura M, Imamura A. Rat-bite fever due to *Streptobacillus notomytis* isolated from a human specimen. *J Infect Chemother* 2018;24:302–304. Epub 2017 Nov 27.

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Perceptions of Zika Virus Risk during 2016 Outbreak, Miami-Dade County, Florida, USA

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We conducted a survey on Zika virus perceptions and behaviors during the 2016 outbreak in Miami-Dade County, Florida, USA. Among women, Zika knowledge was associated with having a bachelor's degree. Among men, knowledge was associated with knowing someone at risk. Interventions during future outbreaks could be targeted by sex and education level.

Misconceptions about arboviruses transmitted by *Aedes* spp. mosquitoes, such as Zika virus, can lead to misplaced reactions and affect local public health officials' abilities to contain outbreaks (1–3). Despite media campaigns on Zika virus, misperceptions persisted during the 2016 outbreak among some subgroups in Miami, Florida, USA (4). More than 4 in 10 Americans mistakenly thought that Zika virus infection was fatal and that symptoms were noticeable (5).

We conducted a structured bilingual (English, Spanish) telephone survey with a random sample of adults in late spring (May 1–June 30, 2016), when the Zika virus outbreak began in Florida. We applied the basic concepts of the Health Belief Model (HBM) in an attempt to understand perceptions of Zika virus risk and prevention practices in Miami-Dade County, Florida, the epicenter of the 2016 Zika virus outbreak (6).

The HBM provided the framework enabling effective structuring of messages to influence behavioral change in the context of health communication strategies for Zika virus prevention and control. According to the HBM, persons are influenced by their perceived susceptibility to a disease and the severity of that disease (7). To use the HBM, participants must have the ability to implement a desired behavior, self-efficacy (i.e., confidence in their ability to implement that action), and cues to action (which could lead to health behavior changes) (7). Because Zika virus infection mainly affects pregnant