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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About the Author
Dr. Yu is a chief of the Monitoring and Early Warning Platform for Cross-species and Virus-induced Diseases in Livestock and Poultry at the Institute of Poultry Science, Shandong Academy of Agricultural Sciences, Jinan, China. His research interests include the epidemiology and evolutionary mechanisms of influenza viruses, the pathogenesis of influenza viruses, and the innate host antiviral immune response.

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Address for correspondence: Zhijun Yu, Shandong Academy of Agricultural Sciences, Institute of Poultry Science, No. 1 Jiaoxiao Rd, Jinan, 250023, China; email: zhijun0215@gmail.com

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


Author affiliations: Nara Medical University, Nara, Japan (Y. Ogawa, K. Kasahara, S.T. Lee, (R. Nakano, H. Yano) K. Mikasa); Osaka Gyoumeikan Hospital, Osaka, Japan (T. Ito, H. Hasegawa, S. Hirose, S. Santo, A. Yoshida)

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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. ratti 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 × 10⁹ 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 intact, with no rashes or animal bites. Laboratory tests revealed high leukocyte count (1.42 × 10⁹ cells/L) and elevated level of C-reactive protein (19.5 mg/dL).

Bacterial culture yielded intact, with no rashes or animal bites. Laboratory tests revealed high leukocyte count (1.42 × 10⁹ cells/L) and elevated level of C-reactive protein (19.5 mg/dL).
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 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′-AGAGTTTGATCCTGGCTCAG-3′) and 1492R (5′-GGTTACCTTGTTACGACTT-3′). The sequence (GenBank accession no. LC360808) showed 100% identity (1,380/1,380 bp) to S. notomytis AHL_370–1T (GenBank accession no. KR001919) and 98.55% (1,360/1,380 bp) identity to S. moniliformis DSM12112T (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% (520/522 bp) and 99.9% (757/758 bp) identity, respectively, to the gene sequence of S. notomytis AHL_370–1T.

We determined antimicrobial susceptibility pattern by broth microdilution. MIC of penicillin was ≤0.06 µg/mL; cefazolin, ≤0.5 µg/mL; ceftriaxone, 0.25 µg/mL; vancomycin, ≤0.25 µg/mL; clarithromycin, 8 µg/mL; minocycline, ≤0.12 µg/mL; and levofloxacin, ≤1 µg/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-GCTTTCGATCCT-3′) and sbmR (5′-GTAACCTTCAG-GTGCAAATCATT-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_370–1T.

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.

**About the Author**
Dr. Ogawa is a medical doctor at Nara Medical University Hospital. His primary research interest is HIV and the epidemiology of infectious diseases, with a focus on resistant pathogens.
Perceptions of Zika Virus Risk during 2016 Outbreak, Miami-Dade County, Florida, USA

Imelda K. Moise, Joseph Kangmennaang, Tricia Caroline S.G. Hutchings, Ira M. Sheskin, Douglas O. Fuller

Author affiliations: University of Miami, Coral Gables, Florida, USA
(I.K. Moise, T.C.S.G. Hutchings, I.M. Sheskin, D.O. Fuller); University of Waterloo, Waterloo, Ontario, Canada (J. Kangmennaang)

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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

References

Address for correspondence: Kei Kasahara, Center for Infectious Diseases, Nara Medical University, Shijo-cho 840, Kashihara, Nara, Japan; email: kassan@naramed-u.ac.jp