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


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We report a case of rat-bite fever in a 94-year-old woman with Streptobacillus notomitis infection. We established an epidemiologic link between exposure to rats and human infection by performing nested PCRs that detected S. notomitis 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. notomitis from a spinifex hopping mouse (1–4). We report a case of a human infection with S. notomitis.

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).

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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 \textit{S. notomytis} KWG2 (522/522 bp and 758/758 bp, respectively) and 99.6% 5(20/522 bp) and 99.9% (757/758 bp) identity, respectively, to the gene sequence of \textit{S. notomytis} AHL\textsubscript{370–1}.

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.

\textit{S. moniliformis} is known to cause rat-bite fever in humans (6). To study the association between exposure to rats and \textit{S. notomytis} infection, we visited the patient’s house after her death and captured 2 rats (\textit{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% CO\textsubscript{2}; the specimens did not grow \textit{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 \textit{Streptobacillus}-specific primers sbm\textsubscript{T} (5’-GAGAGA-AHL\textsubscript{370–1} and sbmR (5’-GTAACTTCAG-GTYGCAACT-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 \textit{S. notomytis} AHL\textsubscript{370–1}.

Since 2014, a total of 4 novel \textit{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 \textit{S. notomytis} (2); it is possible that \textit{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 \textit{S. notomytis}, not \textit{S. moniliformis} as originally identified (8). By detecting \textit{S. notomytis} from the rats captured in this patient’s house, we support a potential epidemiologic link between rat exposure and human infection.

\textbf{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.

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\begin{figure}[h]
\centering
\includegraphics[width=0.5\textwidth]{Figure}
\caption{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 ×1,000.}
\end{figure}
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