from the lack of knowledge among the travelers themselves or among their pretravel health care providers (*5,9*). In recent years, the World Health Organization and the GeoSentinel Surveillance Network recommended that persons planning to visit rabies-endemic areas receive preexposure prophylaxis before traveling (*6,10*). Understanding the factors influencing acceptance of vaccination could help governments develop and institute strategies for disease prevention. Thus, the Taiwan government should enhance tour leaders' knowledge about rabies, especially regarding the high mortality rate. Education of tour leaders could, in turn, increase vaccination rates and help with prevention and management of rabies.

The results of this study are relevant for countries other than Taiwan because many Asian tourists participate in group tours. We suggest that governments place more emphasis on tour leaders' education concerning travel medicine. Such education could not only improve the quality of group tours but also help prevent travel-related infectious diseases.

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Chiao-Yu Huang,[1] Hsien-Liang Huang,[1] Shao-Yi Cheng, Chia-Wen Lu, Long-Teng Lee, Tai-Yuan Chiu, and Kuo-Chin Huang

Author affiliations: National Taiwan University Hospital, Taipei City, Taiwan (C.-Y. Huang, H.-L. Huang, S.-Y. Cheng, C.-W. Lu, L.-T. Lee, T.-Y. Chiu, K.-C. Huang); Cardinal Tien Hospital, New Taipei City, Taiwan (H.-L. Huang); Fu-Jen Catholic University, New Taipei City (H.-L. Huang); and China Medical University, Taichung, Taiwan (K.-C. Huang)

[1]These authors contributed equally to this article.

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Address for correspondence: Kuo-Chin Huang, Department of Family Medicine, National Taiwan University Hospital, 7 Chung-Shan South Rd, Taipei, Taiwan 100; email: bretthuang@ntu.edu.tw

Corynebacterium ulcerans in Ferrets

To the Editor: Infection with *Corynebacterium ulcerans* occurs sporadically throughout the world, and in the United Kingdom it has emerged as the most common cause of diphtheria-like disease (*1*). *C. ulcerans*, along with *C. diphtheriae* and *C. pseudotuberculosis*, can be lysogenized by diphtheria toxin–encoding bacteriophages; this process enables the organism to induce its characteristic sequela (the diphtheritic membrane) in the host. *C. ulcerans* in the environment has been a source of mastitis in cattle and a cause of diphtheria in humans who consume unpasteurized, contaminated milk. The organism has been isolated from various domestic, wild, and laboratory animals; additional definitive sources are dogs, cats, and pigs (*2*). *C. ulcerans* has been isolated from bonnet macaques with mastitis and from the cephalic implants of purpose-bred macaques used in cognitive neuroscience experiments (*3,4*). We report isolation of *C. ulcerans* from cephalic implants in 4 ferrets (*Mustela putorius furo*) and the oropharynx of 1 ferret, all used in imaging experiments in Massachusetts, USA, during 2007–2008.

All ferrets described here were purpose-bred, domestic ferrets, purchased from a commercial vendor. The index case occurred in a ferret with a cephalic implant. Microbiological culture of a purulent discharge

from the implant margin yielded a polymicrobial infection that included an organism identified as *C. ulcerans* by the API Coryne strip system (bioMérieux, Durham, NC, USA) (Table). This isolate and additional isolates from mixed infections of the implants of 3 other ferrets were subsequently identified as *C. ulcerans* by our diagnostic laboratory (Division of Comparative Medicine, Massachusetts Institute of Technology, Cambridge, MA, USA) and by the Centers for Disease Control and Prevention (Atlanta, GA, USA) by use of the API Coryne strip system. The oropharyngeal isolate was originally identified by our laboratory as *C. pseudotuberculosis* (99.5%); the same test performed at the Centers for Disease Control and Prevention yielded ambiguous results (*C. ulcerans* [87.3%] and *C. pseudotuberculosis* [12.5%]).

Three isolates (2 implant isolates and the oropharyngeal isolate) were subsequently characterized by MALDI-TOF-MS (matrix-assisted laser desorption–ionization time-of-flight mass spectroscopy) Bruker Daltonics, Fremont, CA, USA) and by 16S rRNA sequencing (*5*) and partial *rpoB* (*6*) gene sequencing (Table). The conserved primers C2700F and C3130R from the *rpoB* gene were used to amplify the PCR products (*6*). All were confirmed to be *C. ulcerans*. The presence of toxin genes for diphtheria toxin (*tox*) (*7*) and phospholipase D (*pld*) (*3*) were evaluated by PCR. Diphtheria toxin production was evaluated by a modified Elek test (*4*). None of the isolates produced diphtheria toxin or contained the diphtheria toxin gene; all isolates were phospholipase-D positive for the 720-bp product.

To determine the source of the isolates, we tested the ferret isolates along with 3 select isolates from our macaque colony by BOX PCR and random amplified polymorphic DNA analysis. Neither type of analysis of the ferret and macaque *C. ulcerans* strains identified any common patterns (data not shown). Ferrets and macaques were housed in separate rooms in the same vivarium; animal care technicians were dedicated to 1 of the 2 species during any particular month. The prevalence of *C. ulcerans* in our macaque population and the precedence of its isolation from those animals more than a decade ago strongly suggests that the isolates are of macaque origin (*3,4*). More exhaustive comparison of the ferret isolates with archived macaque isolates might provide a match. The possibility also exists that newly acquired ferrets arrived infected with *C. ulcerans* or contracted it from an animal technician, veterinarian, or researcher. These possible sources of *C. ulcerans* infection have not been investigated.

An organism recently isolated from the lung, liver, and kidney tissue of a ferret that died of sepsis has been designated as a novel species, *C. mustelae* (*8*). *C. mustelae* is 96.78% related to *C. ulcerans* in 16S rRNA gene sequence similarity and is the first member of the genus to be implicated in disease of ferrets. *C. ulcerans* must now also be considered a potential pathogen of ferrets, although the mixed nature of these implant infections precludes definitive etiologic statements. Implant infection and oropharyngeal carriage in ferrets potentially represent additional zoonotic sources of this organism, underscoring the need for accurate and complete characterization of coryneform bacteria. Notably, the API Coryne test was unable to definitively identify the oropharyngeal isolate, a result reported by our group for other studies and by other investigators (*4*). The results of additional characterization modalities were all concordant. The *C. ulcerans* isolates from this study were nontoxigenic, and their potential for causing classical diphtheria is unlikely (Table). In contrast, a non–diphtheria toxin–producing *C. ulcerans* skin infection mimicking cutaneous diphtheria in a 29-year-old man was recently reported (*9*). Although the source of *C. ulcerans* was not definitively determined, nontoxigenic *C. ulcerans* was later isolated from the oral cavity of the patient's pet cat. Identity of these 2 isolates was not confirmed by molecular identification techniques (*9*). In another case, strain identity was

Table. Identification of *Corynebacterium ulcerans* strains isolated from ferrets*

MIT accession no.	CDC API code	CDC interpretation (confidence limit, %)	Isolate source	CDC MALDI-TOF-MS (score)†	16S rRNA (confidence limit, %), GenBank accession no.	*rpoB* (confidence limit, %), GenBank accession no.
07–3331	0101326‡	*C. ulcerans* (87.3), *C. pseudotuberculosis* (12.5)	Oropharynx	*C. ulcerans* (2.13)	*C. ulcerans* (99.5) KF564646	*C. ulcerans* (99.5) KF539859
08–0584	0111326	*C. ulcerans* (99.7)	Cephalic implant	*C. ulcerans* (2.35)	*C. ulcerans* (99.5) KF564647	*C. ulcerans* (99.5) KF539860
07–3276	0111326	*C. ulcerans* (99.7)	Cephalic implant	*C. ulcerans* (2.24)	*C. ulcerans* (99.7) KF564645	*C. ulcerans* (99.5) KF539858

*Identification was performed by use of the API Coryne strip system (bioMérieux, Durham, NC, USA), MALDI-TOF-MS (matrix-assisted laser desorption–ionization time-of-flight mass spectroscopy) (Bruker Daltonics; Fremont, CA, USA), and gene sequencing. Percentages after the API identification refer to confidence limits. Percentages after the gene sequencing results refer to percentage identities with a reference strain (*4*). MIT, Massachusetts Institute of Technology; CDC, Centers for Disease Control and Prevention.
†2.000–2.299, secure genus identification, probable species identification; 2.300–3.000, highly probable species identification (*4*).
‡The API code generated at MIT was 0101320, interpreted as *C. pseudotuberculosis* (99.5%).

established between a toxigenic isolate cultured from a woman with clinical diphtheria and the same organism cultured from her asymptomatic cat (*2*). Toxigenic and nontoxigenic isolates of *C. diphtheriae* have been reported to cause the cutaneous form of this disease (*10*).

Robert P. Marini, Pamela K. Cassiday, Jaime Venezia, Zeli Shen, Ellen M. Buckley, Yaicha Peters, Nancy Taylor, Floyd E. Dewhirst, Maria L. Tondella, and James G. Fox

Author affiliations: Massachusetts Institute of Technology, Cambridge, Massachusetts, USA (R.P. Marini, J. Venezia, Z. Shen, E.M. Buckley, Y. Peters, N. Taylor, J.G. Fox); Centers for Disease Control and Prevention, Atlanta, Georgia, USA (P.K. Cassiday, M.L. Tondella); The Forsyth Institute, Cambridge (F.E. Dewhirst); and Harvard School of Dental Medicine, Boston, Massachusetts, USA (F.E. Dewhirst)

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Address for correspondence: James G. Fox, Massachusetts Institute of Technology, Division of Comparative Medicine, Building 16-825C, 77 Massachusetts Ave, Cambridge, MA 02139, USA; email: jgfox@mit.edu

Bat Lyssaviruses, Northern Vietnam

To the Editor: Bats have been associated with a wide diversity of viruses, including lyssaviruses, which can cause rabies. Currently, 12 distinct species of lyssaviruses have been classified worldwide; 3 of these were isolated from bats in northern and central Asia (*1*). In addition, 3 putative novel bat lyssaviruses (Boklob, Ikoma, and Leida) have recently been described and are awaiting taxonomic assessment (*1*,*2*). Surveys for lyssaviruses in bat reservoirs in several countries in Southeast Asia, such as the Philippines, Cambodia, and Thailand, showed that bat lyssaviruses are naturally circulating in insectivorous and frugivorous bats (*3*–*5*).

Rabies is endemic to Vietnam, and ≈100 human deaths caused by rabies are reported annually; most are attributable to canine rabies (*6*). Although bat-associated rabies cases have not been reported in humans or animals in Vietnam, this finding might be caused by lack of a suitable reporting system. The limited understanding of the extent of lyssavirus circulation in Vietnam and its potential effect on public and animal health prompted this surveillance study.

This study was approved by the ethics committee of The National Institute of Hygiene and Epidemiology, and all capture and experimental procedures complied with institute guidelines for bat capture and use. During May–September 2011, a total of 926 bats were collected from 6 northern provinces in Vietnam (online Technical Appendix Figure, wwwnc.cdc.gov/EID/article/20/1/13-0813-Techapp1.pdf). Bats were classified by using a gross morphology key (*7*). Blood and brain samples were obtained after anesthetizing bats by intramuscular injection with 0.05–0.1 mg ketamine hydrochloride.

All bat brains were tested for lyssavirus by using reverse transcription