were conducted by using MEGA version 4.1 (www.megasoftware.net). The partial lppA gene nucleotide sequences of isolates GN407 and GN408 were submitted to GenBank under accession nos. HQ699892 and HQ699893, respectively.

PCR amplifications of the 2 joint fluids and their cultures were positive for M. leachii. When we compared the complete 16S rRNA gene and the partial lppA gene, the 2 isolates from the same epizootic shared 100% nt identity. For 16S rRNA gene, the isolates shared 99.9%, 99.9%, and 99.7% nt identities to M. leachii PG50, M. capricolum subsp. capricolum, and M. mycoides subsp. mycoides small colony, respectively. For partial lppA gene, the isolates shared 99.6%, 95.1%, and 69.6% nt identities to M. leachii PG50, M. mycoides subsp. mycoides small colony, and M. capricolum subsp. capricolum, respectively.

Intraarticular inoculation of the passage cultures successfully reproduced the polyarthritis in calves 1 month of age. Thus, there are notable similarities between our findings and those reported in Australia (3). Multidisciplinary procedures, including clinical assessment and comprehensive laboratory investigations of affected calves, were used to identify the etiologic agent. The results showed that the outbreak of the serious polyarthritis in calves was caused by M. leachii.

Our detection of M. leachii in China confirms a wider geographic presence of this type of Mycoplasma spp. in cattle and suggests M. leachii is common and potentially distributed worldwide. Currently, the source of M. leachii infection and its means of spread have not been established. However, our epidemiologic and clinical investigations indicated clear evidence of seminal infection because all calves with arthritis were from dams that were fertilized by using the same batch of semen, and cows in the same herd that were fertilized by using a different batch of semen delivered healthy calves. More epidemiologic, molecular, and pathogenic studies are required to determine the relevance, distribution, importance, and diversity of M. leachii in cattle.

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We report Bartonella species in fleas collected from cats and dogs in Tahiti, French Polynesia. In October 2009, fleas were collected from 1 cat and 9 dogs in Papeete, capital of Tahiti Island, French Polynesia. Fleas collected were kept in 70% ethanol and sent to the military veterinary service in Marseille, France; these fleas were later sent to Unité de Recherche sur les Maladies Infectieuses et Tropicales Emergentes in Marseilles, France; these fleas were kept in 70% ethanol and sent to French Polynesia. Fleas collected in Tahiti Island, Papeete, the capital of Tahiti, were collected from 1 cat and 9 dogs in Papeete in October 2009. These positive samples were confirmed after intergenic spacer PCR amplification and sequencing with sequences at 100% identity with Bartonella clarridgeiae (GenBank accession no. EU589237).

B. clarridgeiae was first isolated from the pet cat of an HIV-positive patient in the United States (6). However, Bartonella clarridgeiae has never been isolated or detected by molecular methods in humans, and thus its implication as a human pathogen remains controversial. The presence of Bartonella clarridgeiae antibodies has been reported in a suspected case of CSD and in a patient with a chest-wall abscess (4). However, Bartonella clarridgeiae has been detected on fleas from various continents, including Europe, Asia, North America (1), Africa, New Zealand, and recently from New Caledonia (7).

In France, several studies have reported the molecular detection of Bartonella clarridgeiae in the blood of a cat or in cat fleas (C. felis), indicating the potential role of fleas as vectors of this organism (8,9). Prevalence of this bacterium in cat fleas may vary and be as high as 67.9% in cat fleas from France (3). Moreover, DNA of Bartonella henselae and Bartonella clarridgeiae has been reported from cat fleas from New Zealand (10). Similarly, co-infection with Bartonella clarridgeiae and Bartonella henselae has been reported in domestic cats from Europe and Asia (1). In our study, all Bartonella spp.–positive fleas harbored Bartonella clarridgeiae only; all were obtained from cats and none from dogs, similar to findings reported from New Zealand (10), although Bartonella clarridgeiae has been reported from a flea on a dog in Taiwan (2).

Papeete, the capital of Tahiti, is located in the South Pacific Ocean, and remains one of the most visited areas by tourists from all over the world. There are many stray cats and dogs in Tahiti that may be infected with Bartonella species and thus serve as a reservoir for these pathogens. Our result confirms the presence of Bartonella clarridgeiae in Tahiti and is a warning of the presence of fleaborne bartonellosis and the potential risk of Bartonella clarridgeiae or other flea-borne diseases for humans exposed to cat fleas.

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Bocavirus in Children with Respiratory Tract Infections

To the Editor: Four species of human bocavirus (HBoV1–4) have been identified since 2005 (1–4). Several reports have documented that HBoV1 are prevalent in respiratory tract samples. Although there may be many asymptomatic carriers, HBoV1 has been shown to cause respiratory tract diseases (1,5,6). HBoV2 has mainly been detected in fecal samples and has been linked to gastroenteritis (3,7,8). HBoV3 and HBoV4 have recently also been detected in fecal samples (3,4), although no link to disease has been established for these 2 species.

In this study, we identified and characterized 3 HBoV species (HBoV1–3) detected in respiratory samples. Nasopharyngeal aspirates were collected from 1,238 children (784 boys and 454 girls) with acute lower respiratory tract infections hospitalized in Beijing Children’s Hospital from March 2008 through July 2010. Patients’ ages ranged from 1 month to 9 years (median 10.0 months, mean 32.1 months).

Viral nucleic acid was extracted from nasopharyngeal aspirates by using the NucliSens easyMAG system (bioMérieux, Marcy l’Etoile, France). We screened for HBoV1–4 by nested PCR with touch-down procedure using primers targeting the viral proteins (VP) 1/2 region (4). For HBoV-positive samples, we then quantified viral loads by real-time PCR (online Technical Appendix, www.cdc.gov/EID/content/17/9/110078-Techapp.pdf).

Each positive sample was assessed for HBoV1, -2, and -3 in children <5 years old was 124/131 (94.7%), 4/5 (80%), and 4/5 (80%), respectively. Additional respiratory viruses were co-detected in 120/141 (85.1%) HBoV-positive patients (Table). An unanticipated finding was that real-time PCR only detected 1/5 positive sample for HBoV2 (viral load 4.87 × 10^4 copies/mL) and 2/5 positive samples for HBoV3 (viral load 2.59 × 10^4 and 4.1 × 10^2 copies/mL). In contrast, we detected viral loads of 8.35 × 10^4 to 1.28 × 10^6 copies/mL in 5 randomly selected HBoV1–positive samples.

The clinical diagnoses of patients providing HBoV-positive samples included pneumonia (63.1%), bronchitis (14.9%), bronchopneumonia (12.8%), and acute asthmatic bronchopneumonia (9.2%). No clinically significant differences were found between the signs and symptoms of patients with HBoV1, -2, and -3 (cough, sputum production, fever, runny nose, wheezing, and diarrhea).

For patients positive for HBoV3, the major diagnoses were pneumonia (2/5), bronchopneumonia (2/5), and acute asthmatic bronchopneumonia (1/5). Main signs and symptoms included cough (5/5), wheezing (4/5), sputum production (3/5), fever (3/5), runny nose (1/5), and diarrhea (1/5). For patients positive for HBoV2, the diagnoses were pneumonia (5/5) and bronchopneumonia (1/5), and main signs and symptoms included cough (5/5), sputum production (4/5), wheezing (3/5), fever (3/5), and runny nose (2/5) (Table).

HBoV2 and HBoV3 were detected sporadically during the study. HBoV3 was detected in samples collected in...