

in white-beaked dolphins. We do not know how the dolphin contracted the infection and whether this remains an isolated case or the beginning of a new zoonosis.

White-beaked dolphins are found in moderate and subarctic waters of the Atlantic Ocean between the eastern coast of North America and northern Europe. They may migrate hundreds of kilometers within days. Therefore, these dolphins may play a role as a reservoir and vector for this morbillivirus, which is infectious for harbor porpoises, bottlenose dolphins, and other cetacean species (10). The reappearance of a morbillivirus represents a serious threat to susceptible marine mammals in northern European and American waters, with potentially devastating consequences and possibly the beginning of a new epidemic.

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## References

- Kennedy S. Morbillivirus infections in aquatic mammals. *J Comp Pathol.* 1998;119:201–25.
- Osterhaus AD, Vedder EJ. Identification of a virus causing recent seal death. *Nature.* 1988;335:20.
- Müller G, Wohlsein P, Beineke A, Haas L, Greiser-Wilke I, Siebert U, et al. Phocine distemper in German seals, 2002. *Emerg Infect Dis.* 2004;10:723–5.
- Domingo M, Ferrer L, Pumarola M, Marco A, Plana J, Kennedy S, et al. Morbillivirus in dolphin. *Nature.* 1990;348:21.
- Birkun A, Kuiken T, Krivokhizhin S, Haines DM, Osterhaus AD, van de Bildt MW, et al. Epizootic of morbilliviral disease in common dolphins (*Delphinus delphis ponticus*) from the Black Sea. *Vet Rec.* 1999;144:85–92.
- Lipscomb TP, Schulman FY, Moffett D, Kennedy S. Morbilliviral disease in an Atlantic bottlenose dolphin (*Tursiops truncatus*) from the 1987–1988 epizootic. *J Wildl Dis.* 1994;30:567–71.
- Kennedy S, Smyth JA, Cush PF, McCullough SJ, Allan GM. Viral distemper now found in porpoises. *Nature.* 1988;336:21.
- Osterhaus A, Groen J, Niesters H, van de Bildt M, Martina B, Vedder L, et al. Morbillivirus in Monk seal mass mortality. *Nature.* 1997;388:838–9.
- Frisk AL, König M, Moritz A, Baumgärtner W. Detection of distemper nucleoprotein RNA by reverse transcription-PCR using serum, whole blood, and cerebrospinal fluid from dogs with distemper. *J Clin Microbiol.* 1999;37:3634–43.
- Barrett T, Visser IK, Mamaev L, Goatley L, van Bresse MF, Osterhaus AD. Dolphin and porpoise morbillivirus are genetically distinct from phocine distemper virus. *Virology.* 1993;193:1010–2.

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## *Bartonella australis* sp. nov. from Kangaroos, Australia

**To the Editor:** During April–May 1999, 3 *Bartonella* isolates (AUST/NH1, AUST/NH2, AUST/NH3) were cultivated and established from the blood of 5 *Macropus giganteus* gray kangaroos from central coastal Queensland, Australia. We used multigene sequencing to evaluate whether these *Bartonella* isolates fulfill the minimum requirements for classification as a new species.

DNA from each *Bartonella* isolate was extracted by using the QIAamp tissue kit (QIAGEN, Hilden, Germany) according to the manufacturer's instructions. Partial PCR amplification and sequencing of the genes encoding the 16S rDNA (*rrs*), citrate synthase (*gltA*),  $\beta$ -subunit of the RNA polymerase (*rpoB*), and cell division

protein (*ftsZ*), as well as for the 16S–23S rDNA intergenic spacer (ITS) were attempted by using previously described primers and conditions (1). *Bartonella* sp. isolates AUST/NH1 to AUST/NH3 exhibited identical sequences for all 4 genes and the spacer studied, and isolate AUST/NH1 was selected as type strain among kangaroo isolates. Similarity rates between strain Aust/NH1 and validated *Bartonella* species (online Appendix Table, available from [www.cdc.gov/EID/content/13/12/1961-appT.htm](http://www.cdc.gov/EID/content/13/12/1961-appT.htm)) ranged from 84.7% to 91.6%, from 97.5% to 98.5%, from 79.6% to 87.2%, from 85.4% to 95.0%, and from 83.5% to 87.1% for the ITS and *rrs*, *gltA*, *rpoB*, and *ftsZ* genes, respectively. Therefore, for each of these 4 genes or the spacer, strain AUST/NH1 exhibited similarity rates with all other species lower than the cutoffs published to classify *Bartonella* isolates within a validated species (1). It may thus be regarded as a new species.

To estimate the genomic G+C content of strain AUST/NH1, we amplified and sequenced its *ftsY* gene as described (2) by using the BartftsYF (5'-ATGACAAAAYCYTTTATMAA-3') and BartftsYR (5'-TCATGAGTGTCTTCCTGC-3') primers. The *ftsY* G+C content was 37.7%; the calculated genomic G+C content was 39.51%. The *ftsY* sequence was deposited in GenBank under accession no. DQ538398.

The phylogenetic relationships among the studied bartonellae were inferred from sequence alignments of each gene and from concatenated gene sequences by using the maximum parsimony and neighbor-joining methods within the MEGA version 2.1 software package (3) and the maximum-likelihood method within the PHYLIP software package (4). Using *rrs*, *gltA*, and *rpoB* sequences, the phylogenetic position of strain AUST/NH1 was supported by bootstrap values <70%. In contrast, by using the ITS, *ftsZ*, and concatenated sequences, strain

AUST/NH1 clustered with a group of *B. tribocorum*, *B. grahamii*, and *B. elizabethae*, with elevated bootstrap values according to the 3 analysis methods (Figure).

The *Bartonella* strains we describe are the first, to our knowledge, obtained from kangaroos and, more generally, from marsupials. Before this study, the only 2 *Bartonella* species found in Australia were *B. henselae* (5) and *B. quintana* (6). We demonstrated that strain AUST/NH1 was reliably associated with a well-established cluster, including the rodent-associated *B. elizabethae*, *B. grahamii*, and *B. tribocorum* (7). Therefore, we are confident that the phylogenetic position of the new *Bartonella*, which was similar according to 3 analysis methods and supported by high bootstrap values, is reliable. Although *B. grahamii* (8) and *B. elizabethae* (9), members of the same phylogenetic cluster as strain AUST/NH1, cause human infections, the pathogenicity of *B. tribocorum* is as yet unknown. Its pathogenicity should therefore be investigated, especially for persons who come in contact with kangaroos.

*B. australis* is a facultative intracellular gram-negative bacterium. It grows on Columbia agar with 5% sheep blood at 32°C to 37°C in a moist atmosphere containing 5% CO<sub>2</sub>. A primary culture was obtained after 7 days, and subculture was obtained after 4 days under the same conditions. Colonies are homogeneous, smooth, round, and gray-white. The 3 strains tested were oxidase negative, catalase negative, and nonmotile. Pathogenicity for humans is, as yet, unknown.

The type strain is strain AUST/NH1. The new species is distinguished from other *Bartonella* species by its 16S rRNA, *gltA*, *rpoB*, *ftsZ* gene sequences, as well as its 16S–23S rRNA ITS sequence. The estimated G+C content is 38%. The type strain exhibits a specific serotype (10) and was susceptible to amoxicillin, ceftriaxone, imipenem, erythromycin, clarithromycin, ofloxacin, ciprofloxacin, rifampin, and tetracycline (unpub. data). The type strain AUST/NH1 has been deposited in the Collection of the World Health Organization Collaborative Center for Rickettsioses, Borrelioses and Tick-borne Infections (CSUR), Marseille,

France, under reference CSUR B1; in the Collection de l'Institut Pasteur (CIP) under reference CIP 108978T; and in the Culture Collection of the University of Göteborg (CCUG), Sweden, under reference CCUG 51999. The strains AUST/NH2 and AUST/NH3 have been deposited in CSUR under references CSUR B2 and CSUR B3, in the CIP under references CIP 108980 and CIP 108979, and in CCUG under references CCUG 52000 and CCUG 52001, respectively.

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#### References

1. La Scola B, Zeaiter Z, Khamis A, Raoult D. Gene-sequence-based criteria for species definition in bacteriology: the *Bartonella* paradigm. *Trends Microbiol.* 2003;11:318–21.
2. Fournier PE, Suhre K, Fournous G, Raoult D. Estimation of prokaryote genomic G+C content by sequencing universally-conserved genes. *Int J Syst Evol Microbiol.* 2006;56:1205–9.
3. Kumar S, Tamura K, Jakobsen IB, Nei M. MEGA2: molecular evolutionary genetics analysis software. *Bioinformatics.* 2001;17:1244–5.
4. Retief JD. Phylogenetic analysis using PHYLIP. *Methods Mol Biol.* 2000;132:243–58.
5. Fournier PE, Robson J, Zeaiter Z, McDougall R, Byrne S, Raoult D. Improved culture from lymph nodes of patients with cat scratch disease and genotypic characterization of *Bartonella henselae* isolates in Australia. *J Clin Microbiol.* 2002;40:3620–4.
6. Rathbone P, Graves S, Miller D, Odorico D, Jones S, Hellyar A, et al. *Bartonella (Rochalimaea) quintana* causing fever and

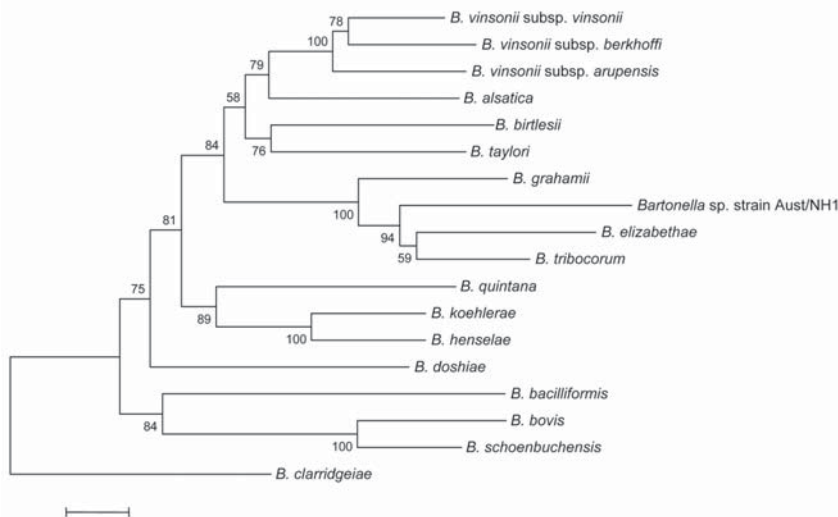


Figure. Unrooted dendrogram showing the phylogenetic position of *Bartonella* sp. strain AUST/NH1 among *Bartonella* species inferred from the comparison of concatenated sequences from the *rrs*, *gltA*, intergenic spacer, *rpoB*, and *ftsZ* genes by the neighbor-joining method. We included only species for which all 5 genes were available. Bootstrap values are indicated at the nodes. The scale bar indicates nucleotide sequence divergence of 0.5%.

- bacteremia in an immunocompromised patient with non-Hodgkin's lymphoma. *Pathology*. 1996;28:80-3.
7. Houpijian P, Raoult D. Molecular phylogeny of the genus *Bartonella*: what is the current knowledge? *FEMS Microbiol Lett*. 2001;200:1-7.
  8. Kerkhoff FT, Bergmans AMC, van der Zee A, Rothova A. Demonstration of *Bartonella grahamii* DNA in ocular fluids of a patient with neuroretinitis. *J Clin Microbiol*. 1999;37:4034-8.
  9. Daly JS, Worthington MG, Brenner DJ, Moss WC, Hollis DG, Weyant RS, et al. *Rochalimaea elizabethae* sp. nov. isolated from a patient with endocarditis. *J Clin Microbiol*. 1993;31:872-81.
  10. Bonhomme CJ, Nappez C, Raoult D. Microarray for serotyping of *Bartonella* species. *BMC Microbiol*. 2007;7:59.

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## Q Fever in Migrant Workers, Scotland

**To the Editor:** Q fever is a zoonosis caused by infection with *Coxiella burnetii* and is most commonly associated with occupational exposure to animal-slaughtering facilities. *C. burnetii* is an obligate intracellular bacterium and causes highly variable disease, ranging from asymptomatic infection to fatal chronic infective endocarditis. In June 2006, the United Kingdom experienced its largest outbreak of Q fever with 138 cases associated with a slaughterhouse near Stirling in Scotland. The slaughterhouse had been processing post-parturition ewes in the lairage (place for keeping livestock temporarily) at the end of May. These animals were thought to be among the most likely to shed the organism (1). Further investigation showed that a ewe had aborted in

the lairage toward the end of May. Although the sheep lairage was the most likely source of the infection, no microbiologic evidence confirmed this, as *C. burnetii* was not isolated from environmental samples.

The outbreak was neither remarkable for its putative mode of transmission nor for the industry involved, but both the number and nationalities of migrant workers infected was noteworthy. Since 2004, 12 member states have joined the European Union and this has led to an influx of immigrants to the United Kingdom. The increase in migrant numbers has partly been a result of the government's managed migration policy, expanding migration to fill vacancies in skilled and low-wage occupations. Employers have difficulty recruiting UK workers because of the jobs' physical demands, long hours that limit social activities, and low pay. They therefore recruit international workers with a good work ethic and reliability; central and Eastern European workers are compared favorably with UK nationals (2). Migrants from Eastern and central Europe are now more likely to be found in low-wage occupations in agriculture, construction, hospitality, and au pair employment. Of the 138 cases of Q fever, 48 were immigrants from the following countries: Slovakia (41), Poland (3), Czech Republic (2), and Lithuania (2). Unsurprisingly, epidemiologic case interviews were beset with linguistic and logistic problems.

The diagnosis of Q fever relies predominantly on its serologic legacy since asymptomatic seroconversion

occurs in up to 60% of patients (3). Analysis of our cohort found that non-UK patients were significantly less likely than their UK counterparts to have symptoms (fever, muscle pain, joint pain, headache, and cough) and to subsequently have Q fever confirmed (Table,  $p < 0.001$ ). Twenty-two patients (15 UK, 7 non-UK) did not complete epidemiologic questionnaires and were therefore not included in this analysis.

Furthermore, analysis of cases registered with general practitioners (GPs) identified a significant difference (Table,  $p < 0.001$ ) between UK and non-UK patients with the latter group less likely to be registered with a GP. Although most UK residents were registered with a general practice, only 11 of 43 non-UK cases were registered. Information on GP registration was not known for 17 patients, and these were not included in the analysis.

Although the investigating health board took stringent steps to ensure follow-up of all patients, we believe that some asymptomatic non-UK patients may have permanently returned to their native countries with undiagnosed illness, and subsequently, cannot be traced. This unfortunate scenario has potentially catastrophic implications for these patients because proper follow-up clinical management of Q fever is necessary to prevent possible endocarditis (4), unnecessary surgery, and premature death.

Persons with known occupational hazards have benefited from an effective Q fever vaccine; abattoir workers and farmers are routinely vaccinated

Table.  $\chi^2$  analysis of Q fever symptoms and GP registration by nationality\*

Characteristic	No. (%) UK natives		All
	Yes	No	
Symptoms			
No	19 (28.4)	25 (15.6)	44
Yes	56 (46.6)	16 (25.4)	72
All	75	41	116
GP registered			
No	1 (21.3)	32 (11.7)	33
Yes	77 (56.7)	11 (31.3)	88
All	78	43	121

\*Expected nos. in parentheses. GP, general practitioner; UK, United Kingdom.