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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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*), β-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) 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 phylogenic 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_2. 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.

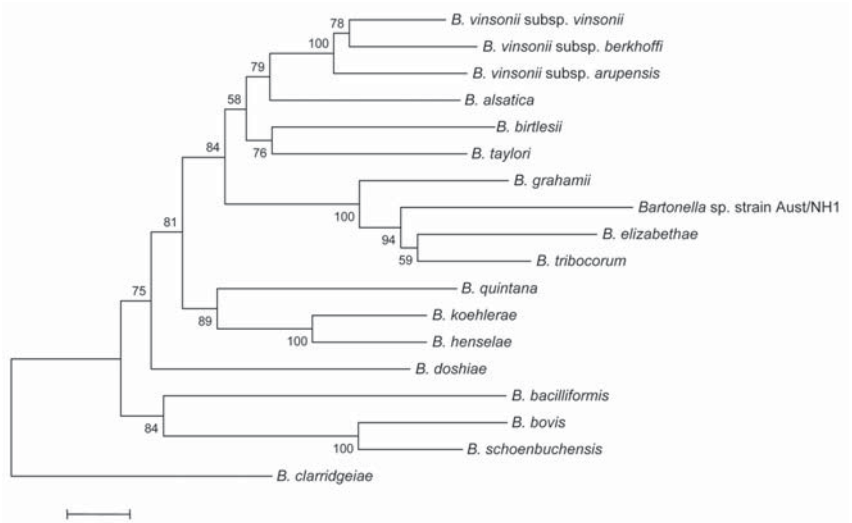

Figure. Unrooted dendrogram showing the phylogenetic position of *Bartonella* sp. strain AUST/NH1 among *Bartonella* species inferred from the comparison of concatenated sequences from the *rrs*, *gltA*, intergenic spacer, *rpoB*, and *ftsZ* genes by the neighbor-joining method. We included only species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

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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. χ^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.

Appendix Table. *Bartonella* spp. and sequences used to validate *Bartonella* isolates (AUST/NH1, AUST/NH2, AUST/NH3) from 5 *Macropus giganteus* gray kangaroos, Australia, 1999*

Species	Strain	GenBank accession no.				
		16S rRNA	16S-23S rRNA	*gltA*	*rpoB*	*ftsZ*
B. alsatica	IBS 382^T	AJ002139	AF312506	AF204273	AF165987	AF467763
B. bacilliformis	KC584^T	Z11683	L26364	U280276	AF165988	AF007266
B. birtlesii	IBS 325^T	AF204274	AY116640	AF204272	AF165989	AF467762
B. bovis	91–4^T	AF199502	AY116638	AF293394	AF166581	AF467761
B. capreoli	IBS 193^T	AF293389	NA	AF293392	NA	NA
B. chomelii	A828^T	AY254309	NA	AY254309	NA	NA
B. clarridgeiae	Houston-2^T	U64691	AF167989	U84386	AF165990	AF141018
B. doshiae	R18^T	Z31351	AJ269786	AF207827	AF165991	AF467754
B. elizabethae	F9251^T	L01260	L35103	U28072	AF165992	AF467760
B. grahamii	V2^T	Z31349	AJ269785	Z70016	AF165993	AF467753
B. henselae	Houston-1^T	M73229	L35101	L38987	AF171070	AF061746
B. koehlerae	C-29^T	AF076237	AF312490	AF176091	AY166580	AF467755
B. peromysci		U71322	U77057	NA	NA	NA
B. quintana	Fuller^T	M11927	L35100	Z70014	AF165994	AF061747
B. schoenbuchensis	R1^T	AJ278187	AY116639	AJ278783	AY167409	AF467765
B. talpae†		NA	NA	NA	NA	NA
B. taylorii	M6^T	Z31350	AJ269784	AF191502	AF165995	AF467756
B. tribocorum	IBS 506^T	AJ003070	AF312505	AJ005494	AF165996	AF467759
B. vinsonii subsp. *arupensis*	OK 94–513	AF214558	AF312504	AF214557	AY166582	AF467758
B. vinsonii subsp. *berkhoffii*	93-CO1	L35052	AF312503	AF143445	AF165989	AF467764
B. vinsonii subsp. *vinsonii*	Baker^T	M73230	L35102	Z70015	AF165997	AF467757
B. australis	AUST/NH1^T	DQ538394	DQ538396	DQ538395	DQ538397	DQ538399

*Superscript T, type strain; NA, not available.
†No sequence available for this species.