Feline Bartonellosis

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KEYWORDS

- *Bartonella* • Cat • Feline • Bartonellosis
- Vector • Flea • Bacteremia

CAUSE

Bartonella are small, fastidious, vector-transmitted gram-negative bacteria in the family Bartonellaceae of the α-2 subgroup of the Proteobacteria.[1] These bacteria are highly adapted to mammalian reservoir hosts, in which a long-term asymptomatic bacteremia often occurs. The type species is *B bacilliformis*, an intracellular parasite of human erythrocytes and endothelial cells that causes severe hemolytic anemia and cutaneous angioproliferative lesions in human beings. It is endemic to some countries in South America and is transmitted among human beings by *Lutzomyia* sp sandflies.[1,2] In addition to the type species, the *Bartonella* species includes organisms that originally comprised the genera *Rochalimaea* and *Grahamella*.[1,3] The *Bartonellas* are phylogenetically close to the *Rickettsiae* and bacteria of the species *Brucella*, *Agrobacterium*, and *Afipia*.[4–6] At least 22 species of *Bartonella* are officially named, and numerous other species are pending formal naming. Approximately 14 *Bartonella* species are considered zoonotic, and of these zoonotic species, several are transmitted to human beings via companion animals, including some transmitted by cats.

The primary zoonotic *Bartonella* species associated with cats is *B henselae,* which causes bacteremia in healthy cats, and has been detected by polymerase chain reaction (PCR) in tissues of numerous other mammalian species, including dogs, seals, whales, horses, and wild felids.[7–12] *B henselae* causes cat scratch disease (CSD), bacillary angiomatosis, bacillary peliosis, relapsing fever with bacteremia, meningitis, encephalitis, neuroretinitis, endocarditis, and multiple additional clinical entities in human beings.[13–17] *B clarridgeiae* causes bacteremia in healthy cats,[18,19] and was serologically associated with a CSD-like condition in 2 people.[20,21] It was also associated with aortic valve endocarditis in a dog,[22] and was detected by PCR in the liver of a dog with hepatopathy.[12] *B koehlerae*[23] was isolated from 4 healthy cats, and has been associated with human endocarditis.[24] *B koehlerae* did not cause clinical signs in cats inoculated experimentally, but was associated with endocarditis in a dog.[25,26] It has not been established that *B quintana* is zoonotic. *B quintana* caused trench fever in World War I and is now known to cause endocarditis, bacillary angiomatosis,

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bacillary peliosis, and chronic lymphadenomegaly in people. Human beings are considered the reservoir host for *B quintana*, and it is transmitted among human beings by the human body louse.[27,28] *B quintana* has been identified in tissues of domestic cats and other animals, but whether *B quintana* should be considered zoonotic is not yet defined.[29,30] *Candidatus* B rochalimae was associated with febrile disease in one human being, and has been detected in wild foxes.[31,32] This organism was also detected in a dog with endocarditis.[33] Cats inoculated experimentally with *candidatus* B rochalimae exhibited no clinical signs of illness.[34] Dogs and foxes are considered likely reservoir hosts for *candidatus* B rochalimae.

This article focuses on feline bartonellosis, in particular on *B henselae*, as it is the feline-associated *Bartonella* for which the most information is known. *B henselae* is an important zoonotic agent with the cat as the primary mammalian reservoir.

EPIDEMIOLOGY

Feline *B henselae* infection was first reported in 1992.[35] Since then, natural infection of cats with 5 *Bartonella* species (*B henselae*, *B clarridgeiae*, *B koehlerae*, *B quintana*, and *B bovis* [formerly *B weissii*])[21,23,30,36–38] has been reported, although feline infections with species other than *B henselae* or *B clarridgeiae* are rarely reported.[21,23,36,38] Seroepidemiologic studies of cats indicate that exposure to *Bartonella* species, most frequently *B henselae*, occurs worldwide. Seroprevalence is greatest in warm, humid climates, particularly in older cats, feral cats, and cats infested with fleas.[39–44] *B henselae* bacteremia occurs in approximately 5% to 40% of cats in the United States on average, also with a higher prevalence in warmer, more humid regions with high flea prevalence.[19,41,45] In some cat colonies, *Bartonella* seroprevalence is as high as 90%.[44] In one study, most cats belonging to people with CSD had *B henselae* bacteremia.[46] Approximately 10% of cats with *Bartonella* bacteremia in the United States were infected with *B clarridgeiae.* Approximately 30% of cats in studies in France and in the Philippines with *Bartonella* bacteremia were infected with *B clarridgeiae*.[43,47,48] *B koehlerae* was isolated from 2 cats from one household in California, 1 cat in France and 1 cat in Israel and *B bovis* (formerly *B weissii*) was isolated from a cat in Utah and one in Illinois.[23,24,38,49] Domestic cats are considered the primary mammalian reservoir and vector for human infections with *B henselae*. Cats may be the reservoir for *B clarridgeiae*, and cattle are the reservoir for *B bovis*. The reservoir for *B koehlerae* is believed to be the cat. Human beings are considered the primary reservoir for *B quintana*.

Wild felids are also exposed to *Bartonella* infection. Eighteen percent of panthers in Florida, 28% of mountain lions in Texas, 30% to 53% of free-ranging and captive wild felids in California, 17% of African lions, and 31% of African cheetahs had serum antibodies to *B henselae*.[50–52] *Bartonella* species were also identified by culture or PCR testing in wild African lions and cheetahs.

B henselae are genetically diverse. There are 2 primary 16S rRNA types of *B henselae*, and at least 2 subgroups within each type.[53] Coinfection of cats with *B henselae* 16S rRNA types I and II, and with *B henselae* and *B clarridgeiae* is reported.[18,54,55] There are regional differences in prevalence of infection of cats with different rRNA types of *B henselae*.[42,43,47,54] Other molecular methods also show remarkable molecular diversity among *Bartonella* isolates.[56–65] There is evidence of genomic variation in *B henselae* during the course of infection in cats.[56–64] Such variation likely enhances the ability of *B henselae* to persist in infected cats for prolonged periods. Genetic variation makes vaccine development difficult, although it is useful in epidemiologic