Bartonella DNA in Loggerhead Sea Turtles

To the Editor: Bartonella are fastidious, aerobic, gram-negative, facultative, intracellular bacteria that infect erythrocytes, erythroblasts, endothelial cells, monocytes, and dendritic cells, and are transmitted by arthropod vectors or by animal scratches or bites (1–6). Currently, 20 species or subspecies of Bartonella have been characterized, of which 8 are known zoonotic pathogens (7). B. henselae has been recently identified from canine blood (8) and from harbor porpoises (9). Pathogenic bacteria are an important threat in terrestrial and marine environments, and in the case of B. henselae, reservoir hosts may be more diverse than currently recognized.

The purpose of this study was to determine whether sea turtles are infected with Bartonella spp. Blood samples were obtained from 29 free-ranging and 8 captive, rehabilitation loggerhead sea turtles (Caretta caretta) from North Carolina coastal waters. Reptilian erythrocytes are nucleated, and commercial lysis methods clogged filtration columns because of the high DNA content of whole blood. Consequently, DNA was extracted from frozen whole blood by using a modified alkaline lysis method adapted from canine blood (8). Pap31 PCR was performed for Bartonella ITS-PCR–positive samples. Pap31 amplicons were obtained from 5 samples of which 3 were successfully sequenced. Amplification and sequencing of the 16S–23S ITS region detected 2 Bartonella species: a B. henselae–like organisms and 1 more similar to B. vinsonii subsp. berkholffii.

The 3 Pap31 amplicons successfully sequenced confirmed B. henselae infection. Sequences obtained from 1 sample matched B. henselae strains H1-like, the B. henselae SA2-like strain, and B. vinsonii subsp. berkholffii genotypes II and IV, which suggests that this turtle was co-infected with multiple Bartonella spp. and strains. Three other samples yielded amplicons 99%–100% identical with B. henselae strain SA2, and 3 yielded sequences most similar to B. vinsonii subspecies berkholffii genotypes II and IV. Two samples contained an ITS region sequence most similar to B. henselae SA2, but with a 15-bp deletion beginning 617 bases downstream from the 16S rRNA gene.

Four sea turtle blood samples contained partial ITS sequences most similar to B. vinsonii subsp. berkholffii. However these amplicons were much shorter than expected for B. vinsonii subspecies berkholffii genotype II and genotype IV sequences in GenBank. Because Pap31 gene amplification was unsuccessful for these samples, it is unclear whether small amplicons represent distinct strains or nonrandom translocation events is uncertain.

Four sea turtle blood samples contained partial ITS sequences most similar to B. vinsonii subsp. berkholffii. However these amplicons were much shorter than expected for B. vinsonii subspecies berkholffii genotype II and genotype IV sequences in GenBank. Because Pap31 gene amplification was unsuccessful for these samples, it is unclear whether small amplicons represent a species related to B. vinsonii subsp. berkholffii or a new Bartonella sp.
To our knowledge, detection of Bartonella spp. DNA in sea turtle blood represents the first molecular evidence of Bartonella infection in nonmammalian vertebrates. B. henselae infection, now reported in porpoises and sea turtles, may represent an emerging infection of marine animals. According to previous studies, immune status appears to affect disease severity, variation in clinical manifestations, the pattern of histopathologic features, and the relative ease of diagnostic detection of the organism (4,7). Although healthy at the time of sample collection, the captive rehabilitated sea turtles were known to have been sick or injured before sampling, potentially reflecting immunocompromise. Whether detection of Bartonella spp. in blood of sea turtles is a function of prior immunosuppression induced by stressors is not known. Such stressors could include mechanical injury, malnutrition, environmental toxins, parasites, or concurrent bacterial or viral infections. Alternatively, sea turtles may be a natural marine reservoir for B. henselae or for a Bartonella sp. genetically related to B. vinsonii subsp. berkoffii.

In summary, documentation of B. henselae and an organism genetically similar to B. vinsonii subsp. berkoffii in the blood of loggerhead sea turtles provides evidence that this genus is not ecologically limited to terrestrial reservoirs. The geographic distribution, prevalence of infection, carrier potential, mode of transmission, and pathogenicity of bloodborne Bartonella spp. in sea turtles await additional studies.

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References


Human Oestrus sp. Infection, Canary Islands

To the Editor: Myiasis due to Oestrus ovis is a well known zoonosis that affects a variety of animals. Human myiasis has also been described and affects mainly persons in rural areas such as shepherds (1) and farmers (2). Although this disease has been reported in both humans and mammals in Spain (3,4), no human case has been described on the Canary Islands. We describe what we believe is the first confirmed case on the islands and discuss the potential utility of serologic diagnosis for this disease.

A 55-year-old farmer from the island of El Hierro, with a medical history of hypercholesterolemia, Q fever, and murine typhus, but currently not being treated, consulted a physician in August 2005 concerning a wormlike sensation in his nose and sinuses that had lasted 2 days. Three days before noticing this sensation, he had been working in his neighbor’s barn, when he noticed that a passing fly “dropped” something in his nose. He also reported sneezing and watery rhinorrhea. These symptoms were self-treated with nasal anticoagulants, which provided temporary relief. He finally sought medical attention when a severe cough de-