the exact tissue type of each sample, only that tonsils, adenoids, or both combined could be present, the 5.5% rate we found was about one third the rate found in tonsil lymphocytes and about one tenth the rate found in adenoid lymphocytes.

A seasonal effect may contribute to the large discrepancies found in HBoV prevalences. Apparently, viruses can persist in tonsillar tissue well after the symptomatic phase of illness. In children with no signs of acute respiratory infection, Drago et al. (7) reported that 45.5% of samples contained viral nucleic acid. Depending on the duration of persistence, asymptomatic children, sampled shortly after the season of the virus in question, would be more likely to have detectable virus in their tonsillar tissue. The Longtin et al. study samples were collected from December through April; our study samples were collected from June through September. If the HBoV is seasonal, as has been suggested (3), it may have been circulating in the target population before samples were taken and persisted only in tonsillar tissues. Thus, if tonsillar tissue from asymptomatic children was obtained within the persistence period after the HBoV season, samples would be HBoV positive; those obtained shortly after the persistence period would have a much lower rate.

Differences in patient age in the 3 studies may also have contributed to the different rates observed. The Longtin et al. group was substantially younger (median age 23 months) than the Lu et al. group (median age 5 years) or our group (median age 5.9 years). Preliminary seroepidemiology reports indicate the presence of HBoV antibodies in >50% of children 2–3 years of age (8,9).

The detection of HBoV in the tonsillar tissues we tested showed a higher rate of infection than would be expected in an asymptomatic population. However, the rate was far lower than that previously reported for tonsillar tissues (1,4).

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DOI: 10.3201/eid1507.090102

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Bartonella rochalimae and Other Bartonella spp. in Fleas, Chile

To the Editor: Fleas are involved in the natural cycle of different Bartonella spp. Among the 20 currently recognized Bartonella spp., 13 species or subspecies have been implicated in human disease. Recently, B. rochalimae was identified in a patient who had received numerous insect bites and subsequently had bacteremia, fever, and splenomegaly after visiting Peru (1). A recent study in Taiwan suggested that rodents could be a reservoir for B. rochalimae (2), but the vector or other mechanism of infection remains unknown. We amplified B. rochalimae, B. claridgeiae, and B. henselae from fleas (Pulex irritans and Ctenocephalides felis) collected in Chile and dis-
cuss the role of these fleas as possible vectors of infection.

From 2005 through 2008, we collected 82 fleas from cats and dogs in pounds in Chile: 34 P. irritans, 37 C. felis, and 11 C. canis. Fleas were kept in 70% ethanol and sent to the Special Pathogens Laboratory of the Área de Enfermedades Infecciosas of the Hospital San Pedro, La Rioja, Spain, to be examined for Bartonella spp. Fleas were then rinsed in distilled water and dried on sterile filter paper under a laminar-flow hood. Each flea was crushed with a sterile pestle, and DNA was extracted by lysis with 0.7 M ammonium hydroxide. PCR was used to detect Bartonella DNA (according to the defining criteria for Bartonella spp.); primers targeted the RNA polymerase \(\beta\)-subunit–encoding gene (\(rpoB\)) and the citrate synthase gene (\(gltA\)) (3–5).

PCR primers for a fragment of the 16/23S rRNA intergenic region and the heat-shock protein-encoding gene (\(groEL\)) were also used (6,7). Positive controls (\(B. henselae\) strain Marseille, kindly supplied by Unité des Rickettsies, Faculté de Médecine, Université de la Méditerranée, Marseille, France) and negative controls (sterile water instead of template DNA) were used. PCR products were purified, and both strands of each amplicon were subjected to sequence analysis. Nucleotide sequence homologies were searched using BLAST (www.ncbi.nlm.nih.gov/blast/Blast.cgi). These 4 specimens also differed from those described for all known Bartonella spp. and phylogenetically was most closely related to \(B. clarridgeiae\) (8). The sequence of the protein encoded by \(rpoB\) in these 3 specimens (protein id ABH09235) had 3 aa changes (121I→V, 233K→I, and 274N→E) with respect to the deduced sequence of the \(rpoB\) protein for \(B. rochalimae\). The importance of these changes remains unknown. The remaining nucleotide sequence was recently submitted to GenBank under accession no. FJ147196, designated \(B. rochalimae\) because isolation of uncultured Bartonella sp. was reported in 2007 (1). These 4 specimens also yielded positive PCR products for \(gltA\) (380 bp) and 16/23S rRNA (≈175 bp). Subsequent nucleotide sequence analysis showed 100% homology with the corresponding partial nucleotide sequences from \(B. rochalimae\).

In 2002, Parola et al. (9) amplified Bartonella DNA by using PCR with \(Pulex\) spp. fleas collected from persons in Peru and suggested the existence of a new Bartonella sp. The nucleotide sequence of the 16S-23S ribosomal RNA intergenic spacer obtained from 1 genotype (clone F17688) was nearly identical to the corresponding sequence of \(B. rochalimae\). This finding suggests that \(Pulex\) spp. fleas could be vectors.

Cat scratch disease has been reported in Chile, and \(B. henselae\) has been found in cats in Chile (10). Thus, our finding of \(B. henselae\) and \(B. clarridgeiae\) in \(C. felis\) fleas from Chile confirms the risk for exposure of humans in contact with cat fleas. Furthermore, our finding of \(B. rochalimae\) fleas from dogs in Chile supports the possibility that \(P. irritans\) fleas could be vectors for \(B. rochalimae\). These findings are of public health importance because they identify possible vectors of these human pathogens.

Acknowledgments

We are grateful to Lourdes Romero and Josune García for their contribution to this work.

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DOI: 10.3201/eid1507.081570

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