species can cause disease (symptomatic infection) and death. *C. felis* and *C. meleagridis* infections showed low oocyst shedding (all seven patients had low to moderate oocyst loads in samples). On the contrary, *C. parvum* produced similar clinical manifestations but showed higher oocyst shedding; 46% had high to very high parasite loads. *C. hominis* infections had parasite loads even higher than *C. parvum* infections; 54% of patients had high to very high parasite loads. In immunocompetent persons, *C. hominis* infections produce higher oocyst loads in feces than infections caused by *C. parvum* or zoonotic species (2,9).

The transmission route for the unusual *Cryptosporidium* species is unclear. Because human infection by unusual *Cryptosporidium* species is less common, the principal transmission route for these parasites is likely through direct contact with infected animals. In our study, one of the four immunocompromised patients with *C. felis* was a child who had been in close contact with cats at home. No data on animal contact were available for other patients infected with unusual *Cryptosporidium* species. Cats are found in many homes with no evidence of cryptosporidiosis; therefore, it is difficult to attribute the occasional human *C. felis* infection to contamination by cats. Careful epidemiologic studies are needed to elucidate the transmission route of human infections with unusual *Cryptosporidium* species.

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## *Bartonella henselae* in African Lion, South Africa

**To the Editor:** Four members of the bacterial genus *Bartonella*, *Bartonella henselae*, *B. clarridgeiae*, *B. koehlerae*, and *B. bovis*, have been isolated from felids, mostly domestic cats (1,2). Of these four species, *B. henselae* and *B. clarridgeiae* are recognized human pathogens, which cause many illnesses, including endocarditis, prolonged fever, various ocular infections and, most commonly, cat scratch disease (1).

In 1994, domestic cats (*Felis domesticus*) were found to be a reservoir for *B. henselae*; subsequent surveys have shown that a large proportion of the domestic cat population worldwide has been exposed to, or infected with, bartonellae (1). The epidemiologic features of *Bartonella* infection in other felid species has been explored; a high prevalence of seropositivity has been found in free-ranging and captive wild cats from California and Florida (3), as well as panthers from Florida (4). *B. henselae* has been isolated from a captive cheetah in Zimbabwe (5).

During 2002, blood samples were collected from 65 African lions that inhabited three ranches in the Free State Province of South Africa. These ranches breed and rear lions specifically for game. Although the lions are contained within vast (several $km^2$) enclosures, they are free to move about and interact with one another. The lions have minimal contact with humans or other animals, except carcasses of horses and donkeys that are provided as food. The lions do not receive any other food, food supplements, growth enhancers, or antiparasite prophylaxis. All three ranches are deep in the veld, at least 20 km from any settlements. Blood samples were drawn from the lions as part of an ongoing health surveillance program

conducted by the African Large Predator Research Unit, University of Bloemfontein. Whole blood samples were drawn aseptically from each lion into EDTA tubes, stored at 4°C before being returned to the laboratory, and then frozen at –70°C in the laboratory. Subsequently, blood samples were thawed, and an aliquot was plated onto 10% sheep blood–enriched agar and incubated at 37°C in a 5% $CO_2$ atmosphere for a maximum of 45 days. One culture yielded putative bartonellae (small, smooth, white-gray colonies) after 14 days' incubation. A crude DNA extract was prepared from this isolate and used as a template in previously described polymerase chain reaction–based assays to detect and identify *Bartonella* species which targeted fragments of the 16S rRNA encoding gene and 16S/23S intergenic spacer region (6). Amplification products of the expected size were obtained from the DNA extract. The nucleotide base sequence of each product showed that each shared 100% similarity with sequences of other *B. henselae* isolates held in GenBank. The 16S rRNA gene sequence was identical to that of type II variants.

Antisera from 62 of the 65 samples were tested for the presence of anti-*Bartonella* immunoglobulin G antibodies using an enzyme-linked immunosorbent assay previously evaluated to detect antibodies in domestic cats (7). Eighteen of the samples had matrix scores above the upper limit of the normal range of values observed in uninfected cats, thus indicating past exposure to *Bartonella* species. No serum from the *B. henselae* culture-positive animal was available for testing.

Our findings confirm that lions are susceptible to infection by *B. henselae*, but their role as reservoirs for this species remain unclear. The observed prevalence of infection (1.5%) and exposure rate (29%) in our study are lower than those typically observed in domestic cats, particularly in warmer regions of the world. Nonetheless, our serologic data do suggest that a substantial proportion of the lions are exposed to bartonellae. Although limited, our assessment of the lion *B. henselae* isolate suggests that it is within the genetic spectrum of strains associated with domestic cats, and lions may serve as an extension to this reservoir. The extent of contact between domestic cats, or their ectoparasites, and the farmed lions we studied is likely to be minimal, given the remoteness of the enclosures (the infected lion lived on a cat-free ranch). However, the lions may have contact with other wild-living felids such as the African wild cat (*Felis silvestris lybica*), small spotted cat (*Felis nigripes*), and the caracal (*Caracal caracal*) which are endemic to the region.

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## *Mycobacterium tuberculosis* Transmission from Human to Canine

**To the Editor:** This report is the first known of a case of epidemiologically associated tuberculosis (TB) in a human and a canine caused by the same strain, confirmed by genotyping. In Tennessee, a 71-year-old woman with a 3-week history of a productive, nonbloody cough was evaluated. She lived alone, and standard epidemiologic investigation of family members and other close contacts showed no apparent TB exposure. A TB skin test 20 years earlier had been negative. Chest radiograph showed infiltrates and atelectasis in the upper lobe of the right lung. A TB skin test resulted in a 14-mm area of induration. Sputum stained positive for acid-fast bacilli (AFB) and was positive for *Mycobacterium tuberculosis* by DNA probe and culture. The organism was sensitive to standard antitubercular medications.