**Bartonella clarridgeiae**, a Newly Recognized Zoonotic Pathogen Causing Inoculation Papules, Fever, and Lymphadenopathy (Cat Scratch Disease)

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Shortly after adopting a 6-week-old cat, a veterinarian was bitten on the left index finger. Within 3 weeks, he developed headache, fever, and left axillary lymphadenopathy. Initial blood cultures from the cat and veterinarian were sterile. Repeat cultures from the cut grew *Bartonella*-like organisms with lophotrichous flagella. Sera from the veterinarian were not reactive against *Bartonella henselae*, *B. quintana*, or *B. elizabethae* antigens but were seroreactive (reciprocal titer, 1,024) against the feline isolate. Sequential serum samples from the cat were reactive against antigens of *B. henselae* (titer, 1,024), *B. quintana* (titer, 128), and the feline isolate (titer, 2,048). Phenotypic and genotypic characterization of this and six additional feline isolates, including microscopic evaluation, biochemical analysis, 16S rRNA gene sequencing, DNA-DNA hybridization, and PCR-restriction fragment length polymorphism of the 16S gene, 16S-23S intergenic spacer region, and citrate synthase gene identified the isolates as *B. clarridgeiae*. This is the first report of cat scratch disease associated with *B. clarridgeiae*.

Since the early 1900s, various diverse microbiologic agents have been implicated in the etiology of cat scratch disease (CSD). During the 1980s, it appeared that the long-sought causative agent had been found. A gram-negative bacterium was observed by Wear and colleagues in lymph node sections obtained from CSD patients and stained by the Warthin-Starry silver stain or Brown-Hopps tissue Gram stain (43). In 1988, English et al. (19) isolated a bacterial agent from clinical specimens of CSD patients which was subsequently named *Afipia felis* by Brenner et al. (9). During the early 1990s, two groups independently described a newly recognized gram-negative rod which was named *Bartonella clarridgeiae* (9). During the early 1990s, two groups independently described a newly recognized gram-negative rod which was named *Bartonella clarridgeiae* (9). Recently, investigators performed serologic analysis on samples obtained from patients satisfying the clinical criteria for a presumptive diagnosis of CSD. Comparison of seroreactivity data indicates that an overwhelming number of patients have antibodies to *B. henselae* but are seronegative for *A. felis* (17, 33–36, 40). In addition, Anderson et al. and Bergmans et al. detected *Bartonella henselae* DNA but not *A. felis* DNA in samples of CSD skin test antigen and lymph node aspiration biopsy specimens from CSD patients (1, 2, 4). Although the role of *A. felis* in the clinical syndrome known as CSD has not been clarified, *B. henselae* appears to be the predominant cause of CSD. Seroreactivity to *B. quintana* antigen has been observed in several CSD patients, but *B. quintana* has not been recovered from any patient with this presentation or from any associated cats. *B. clarridgeiae* was recently isolated from a cat owned by a human immunodeficiency virus-positive person bacteremic with *B. henselae* (14, 29). Other currently classified species of *Bartonella* have not been associated with CSD.

A previous study in our laboratory investigating the duration of *Bartonella* bacteremia in cats associated with CSD patients identified a patient (patient 10) fulfilling the diagnostic criteria for classical CSD, yet acute- and convalescent-phase serum samples were minimally reactive against antigens derived from three characterized *Bartonella* species (25). As a result of the subsequent characterization of isolate 94-F40, we describe the isolation of *B. clarridgeiae* from a cat associated with human CSD.

**Case report.** A 6-week-old female domestic shorthair cat was adopted from a North Carolina pet placement group by a 27-year-old male veterinarian. Shortly after acquiring the cat, he sustained a bite wound on his left index finger. A popular lesion approximately 0.5 cm in diameter developed at the site of the bite wound and persisted for approximately 1 month (Fig. 1). The cat was healthy but infested with fleas. Within 3 weeks, the patient developed headache, fever (maximum temperature, 38.5°C) lasting 1 week, and left axillary lymphadenopathy (Fig. 2). Lysis centrifugation blood cultures performed 5 days after the onset of febrile illness and before a 2-week course of doxycycline (500 mg every 12 h) failed to grow bac-
teria. The headache and fever abated during doxycycline therapy, and after 1 month, the axillary lymphadenopathy resolved.

Initial lysis centrifugation cultures from the cat and the patient failed to yield bacteria. Two subsequent blood cultures from the cat (1.5 and 4 months later) grew *Bartonella*-like organisms. Acute-phase and 1- and 5-month convalescent-phase serum samples from the patient were analyzed by IFA for *Bartonella* species-specific immunoglobulin G (IgG) (Table 1). He did not seroconvert to *B. henselae*, *B. quintana*, or *B. elizabethae* antigens but was seroreactive at a reciprocal titer of 1,024, and after 1 month, the axillary lymphadenopathy resolved. The headache and fever abated during doxycycline therapy.

**MATERIALS AND METHODS**

**Bacterial strains.** The type strains of *B. henselae* (Houston 1; ATCC 49882), *B. elizabethae* (F9251; ATCC 49927), *B. vinsonii* subsp. *vinsonii* (Baker; ATCC VR-152), and *B. claridgeiae* (ATCC 51734) were obtained from the American Type Culture Collection (Rockville, Md.). The type strains of *B. quintana* (NCTC 12862) and *B. doshiae* (NCTC 12860) and *B. berkhoffii* type strain (ATCC 51672) were isolated from the College of Veterinary Medicine, North Carolina State University, Raleigh, N.C.

**Isolation of bacteria.** Aseptically collected blood was cultured by using an Isolator tube (10 ml) for the veterinarian’s sample and the Pediatric Isolator (1.5 ml) for all samples from the cat (Wampole Laboratories, Cranbury, N.J.). The samples were processed in accordance with the manufacturer’s recommendations and plated on Trypticase soy agar (TSA) containing 5% rabbit blood (BBB, Becton Dickinson, Cockeysville, Md.). Inoculated plates were incubated at 35°C in 5% CO2 with humidity.

**Microscopic and biochemical analysis, *Bartonella* organisms were visualized by light microscopy following Gram or Gimenez staining. To determine whether flagella were present, 6-day-old subcultures were gently scraped from agar plates in phosphate-buffered saline. Samples were applied to grids, negatively stained with 2% phosphotungstic acid, and examined by using a transmission electron microscope (18). Motility was assessed by incubation of the isolate in M agar and hanging drop slides. A drop of a saline suspension of bacteria was placed on single-well Teflon-coated microscope slides. A coverslip was placed over the well, and the preparation was examined.

**Commercial bacterial identification systems (UniScept 20E, An-IDENT, and API-ZYM [Analytab, Sherwood Medical, Plainview, N.Y.]) were used in conjunction with standard microbiological methods to characterize the isolate (30).**

**Microimmunofluorescent serology.** Vero cell cultures were inoculated with *Bartonella* organisms that were initially cultivated on solid media. Infected cells were harvested between 3 and 8 days postinoculation when >80% infected and were used as a whole-cell antigen in the IFA. Sera were digested in 0.5% bovine serum albumin in phosphate-buffered saline before being applied to Teflon-coated microscope slides in 5-μl aliquots. The protocol has been described in detail previously (7).

**Cellular fatty acid composition.** Organisms were cultivated on TSA-rabbit blood at 35°C in 5% CO2 for 4 to 9 days. Cells were harvested from an average of three plates and saponified with heat. The liberated fatty acids were methylated with [32P]dCTP as previously described (8). Radioactively labeled DNA was heat denatured, combined with sheared, unlabeled DNA, and allowed to reassociate at 55°C (optimal incubation temperature) and/or 70°C (stringent incubation temperature). Double-stranded DNA was detected in a scintillation counter, and relative binding ratios were calculated. Divergence in related sequences was approximately 1% for each degree of decreased thermal stability in a heterologous reassociated DNA duplex compared with the homologous reassociated DNA duplex. Divergence was calculated to the nearest 0.5%.

**Extraction of DNA used for PCR amplification.** DNA used for PCR amplification. DNA used for PCR amplification of the 16S gene and the 16S-23S rRNA intergenic spacer (ITS) region was extracted in the following manner. Subcultures of the blood isolates and type strains were grown on TSA-rabbit blood plates, recovered in glucose-Tris-EDTA, and kept on ice until subjected to proteinase K digestion. The bacterial lysate was purified with hexadeccytrimethylammonium bromide-NaCl at 65°C, and genomic DNA was precipitated with isopropanol. The resulting pellet was washed in ethanol, air dried, and reconstituted in Tris-EDTA (pH 8). DNA used in the evaluation of the citrate synthase gene was extracted by an alternative method. Eight to 10 isolated colonies from 

**TABLE 1. Blood culture results and seroreactivity of the veterinarian and his cat at various time points**

<table>
<thead>
<tr>
<th>Time of sample collection</th>
<th>Blood culture result</th>
<th>IFA serology (reciprocal titer)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>94-F40 B. henselae B. quintana B. elizabethae</td>
</tr>
<tr>
<td><strong>Veterinarian</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>11/18/93</td>
<td>Negative</td>
<td>1,024 &lt;16 &lt;16 16</td>
</tr>
<tr>
<td>12/20/93</td>
<td>ND*</td>
<td>1,024 &lt;16 &lt;16 16</td>
</tr>
<tr>
<td>4/12/94</td>
<td>ND</td>
<td>1,024 &lt;16 &lt;16 16</td>
</tr>
<tr>
<td><strong>Cat</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>11/18/93</td>
<td>Negative</td>
<td>ND b 512 ND ND ND ND</td>
</tr>
<tr>
<td>1/6/94</td>
<td>ND</td>
<td>2,048 1,024 128 128 ND</td>
</tr>
<tr>
<td>1/31/94</td>
<td>Positive</td>
<td>2,048 1,024 128 128 ND</td>
</tr>
<tr>
<td>4/7/94</td>
<td>Positive</td>
<td>ND ND ND ND ND ND</td>
</tr>
<tr>
<td>a ND, not done.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>b Several samples from the cat were of insufficient volume to test.</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**FIG. 1.** Inoculation papule from the cat bite.

**FIG. 2.** Axillary lymphadenopathy in the patient.

Six feline *Bartonella* isolates obtained during previous studies at the College of Veterinary Medicine were included in the genotypic analysis (25).

**Isolation of bacteria.** Aseptically collected blood was cultured by using an Isolator tube (10 ml) for the veterinarian’s sample and the Pediatric Isolator (1.5 ml) for all samples from the cat (Wampole Laboratories, Cranbury, N.J.). The samples were processed in accordance with the manufacturer’s recommendations and plated on Trypticase soy agar (TSA) containing 5% rabbit blood (BBB, Becton Dickinson, Cockeysville, Md.). Inoculated plates were incubated at 35°C in 5% CO2 with humidity.
subcultures were harvested with a 10-μ1 loop and placed into 1 N NaOH for 30 min. An equal volume of 1 M Tris-HCl, pH 8.4, was added to adjust the pH. The lysate was diluted 1:10 with sterile PCR grade H2O, and 1, 5, or 10 μl of the DNA preparation was used per PCR.

**PCR amplification.** PCR amplification of the 16S rRNA gene was accomplished by using eubacterial primers P0-C and PC-5A as reported elsewhere (7, 45). The 16S-23S ITS region was amplified by using the primers and cycling parameters described by Roux and Raoult (38). Citrate synthase amplicons were produced by using primers BHCS.78I (GGG GAC CAG CTC ATG TGG G) and BHCS.1137 (AAT GCA AAA AGA ACA GTA AAC A). Amplification of the citrate synthase gene was carried out in 50-μl reaction volumes. A standard PCR mixture consisted of the following: 1 μl of template DNA, 1 U of Taq polymerase, 5 μl of 10× Taq buffer, 3 μl of MgCl2 (25 mM), 0.3 μl of deoxyribonucleoside triphosphates (100 μM each), 50 pmol of each primer, and sterile distilled water to a final volume of 50 μl. Cycling parameters were 30 cycles of denaturation at 95°C for 20 s, annealing of primers at 60°C for 30 s, and primer extension at 72°C for 1 min. All PCRs were performed in a GeneAmp 9600 thermal cycler (Perkin-Elmer Cetus, Norwalk, Conn.).

**Restriction endonuclease digestion of PCR-amplified DNA.** 16S amplicons from the novel isolate and type strains were digested by restriction endonucleases DdeI, HaeIII, and AluI in accordance with the manufacturer’s (New England BioLabs, Beverly, Mass.) recommendations. PCR-amplified DNA from the ITS region was digested with HaeIII, AluI, and aTaqI. Four microliters of template DNA and 10 U of enzyme were used in each reaction. Digestions were performed at 37°C (DdeI, HaeIII, and AluI) or 65°C (aTaqI) for 2 h, and products were separated by electrophoresis through 2% NuSieve agarose (FMC BioProducts, Rockland, Maine) at 200 V. Restriction endonuclease digestion of the PCR-amplified 600-base portion of the citrate synthase gene was performed with aTaqI (Life Technologies, Bethesda, Md.) at 95°C for 2 h. Products derived from the digestion of the citrate synthase gene were electrophoresed through 2% agarose gels at 100 V for 2.5 h. All gels were stained with ethidium bromide and viewed by using UV light to assess differences (21).

**DNA sequencing of the 16S rRNA gene.** Dideoxy terminator sequence reactions of purified PCR products were performed in a PE 9600 in preparation for use in an ABI 373A automated DNA sequencer (Applied Biosystems Inc., Foster City, Calif.) (7). The 16S rRNA nucleotide sequence of the *Bartonella*-like isolate was compared with sequences from the Ribosomal Database Project (31) for *B. henselae*, *B. quintana*, *B. elizabethae*, *B. vinsonii* subsp. *vinsonii*, *B. vinsonii* subsp. *berkhoffii*, *B. claridgeiae*, *B. bacilliformis*, *B. garinii*, *B. duchiae*, and *B. taylorii*. Phylogenetic analysis was performed by using the Genetic Data Environment (39) on a Sun Sparstation II (Sun Microsystems, Mountain View, Calif.). A dendrogram prepared from 16S rDNA sequences was based on the maximum-likelihood method (20).

**Nucleotide sequence accession number.** The 16S rRNA gene sequence for isolate 94-F40 was deposited in the GenBank, EMBL, and DDBJ databases under accession number U64691.

**RESULTS**

**Blood culture isolates.** The blood culture obtained from the patient remained negative for 63 days. Blood was obtained from the associated cat on three occasions at approximately 2.5-month intervals. The initial culture was sterile; however, two subsequent blood cultures grew a *Bartonella*-like organism (designated isolate 94-F40) within 10 to 23 days of incubation. The bacterial colonies were smooth with tan to pale pink pigmentation and slightly raised centers. Colonies were loosely adherent to, but not embedded in, the medium. There was no hemolysis of the blood agar.

**Biochemical testing.** Isolate 94-F40 was negative in oxidase, catalase, urease, and Voges-Proskauer tests. It utilized arginine and hydrolyzed indoxyl-acetate. Positive reactions were obtained for the production of arginine aminopeptidase, alanine aminopeptidase, glycine aminopeptidase, esterase, esterase, lipase, leucine arylamidase, and naphthol-AS-BI-phosphohydrolase.

**Microscopic analysis.** Isolate 94-F40 stained faintly as a gram-negative rod but was easier to visualize when cultivated in Vero cells and stained by the Gimenez technique. The isolate was tinctorially similar to other *Bartonella* species by both the Gram and Gimenez methods. After 1 week of incubation, motility was not detected in M agar; however, twitching motion was seen in a hanging drop preparation. Negative staining with 2% phosphotungstic acid revealed the presence of lophotrichous flagella when examined with a transmission electron microscope (Fig. 3).

**Seroreactivity of patient and cat.** An acute-phase and two convalescent-phase serum samples from the patient analyzed by IFA were not reactive against *B. henselae*, *B. quintana*, or *B. elizabethae* but did react with isolate 94-F40. Sequential serum samples from the cat reacted with antigens of *B. henselae*, *B. quintana*, and isolate 94-F40 (Table 1).

**Cellular fatty acid analysis.** Isolate 94-F40 clustered among other feline *Bartonella* isolates and *Bartonella* type strains as described previously (25).

**DNA hybridization.** Radiolabeled DNA from *Bartonella*-like isolate 94-F40 was tested with other isolates obtained from cats and the type strains of *Bartonella* species (Table 2). Strain 94-F40 DNA was 89% related to *B. claridgeiae* DNA and 34 to 47% related to DNAs of the other *Bartonella* type strains.

**TABLE 2. DNA relatedness of *Bartonella*-like strain 94-F40 and other feline isolates to *Bartonella* type strains**

<table>
<thead>
<tr>
<th>Source of unlabeled DNA</th>
<th>Result obtained with labeled 94-F40 DNA</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>RBR, 55°C</td>
</tr>
<tr>
<td><em>Bartonella</em>-like strain 94-F40 (ATCC 700095)</td>
<td>100</td>
</tr>
<tr>
<td><em>Bartonella</em>-like strain Lea</td>
<td>86</td>
</tr>
<tr>
<td><em>Bartonella</em>-like strain Bishop</td>
<td>87</td>
</tr>
<tr>
<td><em>Bartonella</em>-like strain Snowy</td>
<td>88</td>
</tr>
<tr>
<td><em>Bartonella</em>-like strain Jazz</td>
<td>86</td>
</tr>
<tr>
<td><em>Bartonella claridgeiae</em> ATCC 51734</td>
<td>89</td>
</tr>
<tr>
<td><em>Bartonella henselae</em> ATCC 49882</td>
<td>47</td>
</tr>
<tr>
<td><em>Bartonella quintana</em> ATCC VR-358</td>
<td>46</td>
</tr>
<tr>
<td><em>Bartonella vinsonii</em> subsp. <em>berkhoffii</em> ATCC 51672</td>
<td>46</td>
</tr>
<tr>
<td><em>Bartonella vinsonii</em> subsp. <em>vinsonii</em> ATCC VR-152</td>
<td>43</td>
</tr>
<tr>
<td><em>Bartonella elizabethae</em> ATCC 49927</td>
<td>40</td>
</tr>
<tr>
<td><em>Bartonella bacilliformis</em> ATCC KC 583 (NCTC 12138)</td>
<td>35</td>
</tr>
<tr>
<td><em>Bartonella garinii</em> NCTC 12860</td>
<td>25</td>
</tr>
<tr>
<td><em>Bartonella duchiae</em> NCTC 12862</td>
<td>37</td>
</tr>
</tbody>
</table>

*All reactions were run in duplicate.*

b RBR, relative binding index.

c D, divergence.
tested. Four of the six isolates from other cats were assayed, and they were 86 to 88% related to 94-F40. The type strain of *B. taylorii* was unavailable (21a), and the type strains of *B. peromysci* and *B. talpae* are no longer extant.

**PCR-RFLP analysis.** Restriction fragment length polymorphism (RFLP) analysis performed on the PCR-amplified 16S gene and the 16S-23S ITS region demonstrated unique restriction patterns. Endonuclease digestion of the 16S gene with *Dde*I resulted in fragments of approximately 410 and 210 bp for each type strain. In all type strains except 94-F40, a third fragment migrated at approximately 380 bp. Other species-specific products ranged from 100 to 280 bp. Digestion of the ITS region with *Hae*III did not yield any fragment common to all type strains. Examples of restriction profiles are shown in Fig. 4. Comparison of the products generated by endonuclease digestion of the citrate synthase gene revealed a band of 300 bp in all of the species tested. *B. quintana* had a band at 120 bp, *B. henselae* had a species-specific band at approximately 150 bp, and isolate 94-F40 had a band at 400 bp.

**DNA sequence of the 16S rRNA gene.** DNA sequence analysis of the 16S rRNA gene disclosed several areas of variability among the *Bartonella* species currently listed in GenBank. Strain 94-F40 had 99.8% sequence similarity with *B. clarridgeiae*, 97.3% with *B. henselae*, 97.7% with *B. quintana*, 97.9% with *B. elizabethae*, 97.2% with *B. bacilliformis*, 98.1% with *B. vinsonii* subsp. *vinsonii*, and 97.2% with *B. vinsonii* subsp. *berkhoffii*. The 16S rRNA gene sequences from recently described *Bartonella* species isolated from rodents in England, *B. taylorii, B. grahamii*, and *B. doshiae* (6), were 97.7, 99.4, and 99.7% similar to isolate 94-F40, respectively. A phylogenetic tree depicting the relationship among these *Bartonella* species is shown in Fig. 5.

**DISCUSSION**

*B. clarridgeiae* isolated from a cat induced fever, lymphadenopathy, and an inoculation papule (classic CSD) in a human. Our patient failed to develop IFA seroreactivity to *B. henselae, B. quintana,* and *B. elizabethae,* despite overwhelming clinical evidence supporting a diagnosis of CSD. We were unable to confirm bacteremia in the patient; however, blood cultures from the cat responsible for inflicting the puncture wound on the patient’s finger yielded a *Bartonella* organism on two of three culture attempts. Although the lysis centrifugation blood culture technique enhances recovery of *Bartonella* isolates, anecdotal reports indicate that *Bartonella* is more difficult to culture from human blood than from feline blood. Our inability to obtain a positive culture from the cat on the initial attempt may be due to the fact that we were able to collect only 0.75 ml, as opposed to the recommended 1.5 ml, in the Pediatric Isolator system. At this dilution, the lysis solution contained in the tube may have lysed not only the blood cells but also the bacteria. Alternatively, as we observed during a recent transmission study, bacteremia in experimentally infected cats appears to be relapsing in nature (27).

When strain 94-F40 was cultivated in Vero cells and used as antigen in an IFA, the patient was seropositive for the isolate obtained from his cat. Serum obtained from the cat was reactive with antigens of *B. henselae, B. quintana,* and strain 94-F40. Given the high seroprevalence of *B. henselae* in the domestic cat population throughout the world (3, 11–13, 16, 22, 23, 32, 41), it is probable that the cat had been previously exposed to *B. henselae,* as well as *B. clarridgeiae.* However, extensive cross-reactivity, which is highly variable in degree, occurs among cats, dogs, and humans exposed to *Bartonella* species (3, 11, 12, 24). Therefore, in this instance, the feline IgG antibody response to *B. clarridgeiae* may be less specific than the human IgG response to the organism.

Genotypic analysis, including DNA sequencing and PCR-RFLP, of portions of the rRNA and citrate synthase genes identified isolate 94-F40 as *B. clarridgeiae.* DNA-DNA hybridization is considered by most to be the ultimate determinant of taxonomic relationships among organisms. Under optimal conditions, the DNA relatedness to isolate 94-F40 was 86 to 89%...
for B. clarridgeiae and the other four feline B. clarridgeiae isolates obtained in our laboratory. Under stringent conditions, relatedness values ranged from 86 to 93%. The generally accepted definition of a bacterial species is a group of strains with at least 70 and 55% relatedness under optimal and stringent DNA reassociation conditions, respectively, and 5% or less divergence within related sequences (8, 42). Data obtained from isolate 94-F40 and our other feline strains satisfy these guidelines and confirm their identity as B. clarridgeiae.

Several recent reports (16, 36, 46) have indicated that 5 to 16% of patients with clinically defined CSD are seronegative for B. henselae. It is possible that some of these seronegative cases of CSD may be due to infection with B. clarridgeiae and the lack of seroreactivity is a result of failure to use the proper antigen for diagnosis. In fact, prevalence of bacteremia with B. henselae is probably more widespread than currently recognized.

During a continuing study investigating the prevalence of feline Bartonella infections, we obtained six additional feline isolates with the same genotype as isolate 94-F40. Of these isolates, two were obtained from cats (cats P and R) with a historical association with CSD (25). Other investigators have also reported the recovery of unique Bartonella isolates (23) or DNA (5) from cat blood. Bergmans and coworkers submitted a partial 16S rRNA gene sequence (GenBank accession no. Z69039) derived from bacterial DNA extracted from cat blood (5). Comparison of the 471 nucleotides with corresponding sequences of isolate 94-F40 and B. henselae revealed 100 and 98% similarity, respectively. The cat was associated with a case of CSD in The Netherlands. These data identify B. clarridgeiae as an etiologic agent of CSD and broaden its geographic distribution outside the United States. The type strain of B. clarridgeiae was isolated from the cat of a human immunodeficiency virus-positive patient with B. henselae bacteremia (14, 29). We documented B. henselae and B. clarridgeiae coinfection in a naturally exposed cat used as a blood donor during a transmission study (28). Blood transfusions from this cat transmitted B. henselae to recipients on one occasion and B. clarridgeiae on another. In light of these observations, we propose that cats may be coinfected with more than one species of Bartonella. Although the predominant species involved in CSD is B. henselae, B. clarridgeiae may be responsible for cases of CSD, particularly in patients seronegative for B. henselae.

The relevance of B. clarridgeiae in other clinical presentations, such as bacillary angiomatisos (BA), is unknown. In 1991, Cockerell et al. reported the isolation of a Bartonella-like organism from an excised lesion of BA (15). The isolate possessed flagella and appeared to be related to B. bacilliformis by cellular fatty acid analysis. The patient denied having contact with cats, but his pet parakeet frequently perched on the affected arm. Inasmuch as people have become infected with B. henselae without apparent exposure to cats and B. clarridgeiae is the only Bartonella species aside from B. bacilliformis to be identified with flagella, it is possible that the etiologic agent in this case was B. clarridgeiae. Unfortunately, retrospective analysis of the strain is not possible. The isolate was lost during subculture attempts, and genomic DNA became contaminated.

Given the prevalence of B. clarridgeiae among cats and the pathogenicity of closely related species to people, additional studies to assess the role of B. clarridgeiae as a cause of CSD, BA, and other disease manifestations in humans appear to be justified.

ACKNOWLEDGMENTS

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