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**Novel Relapsing Fever Spirochete in Bat Tick**

To the Editor: Tick-borne relapsing fever in western North America is a zoonosis caused by spirochetes in the genus *Borrelia* that are transmitted by argasid ticks of the genus *Ornithodoros* (1). Human disease occurs in many focal areas and is associated with infections of *Borrelia hermsii*, *B. turicatae*, and possibly *B. parkeri* (2,3). Although the ecologic parameters that maintain *B. hermsii* and *B. turicatae* differ, human infections usually occur in rustic cabins (*B. hermsii*) and caves (*B. turicatae*) inhabited by ticks and their terrestrial vertebrate hosts (1). Recently, Gill et al. (4) provided evidence that the argasid bat tick, *Carios kelleyi*, feeds upon humans. Subsequently, Loftis et al. (5) used PCR analysis and DNA sequencing to detect in *C. kelleyi* an unidentified *Borrelia* species that was closely related to *B. turicatae* and *B. parkeri*. We report the partial molecular characterization of another novel tick-borne relapsing fever spirochete in *C. kelleyi*, which expands our knowledge for this group of pathogenic spirochetes and their potential vertebrate hosts and tick vectors.

*C. kelleyi* were collected August 18, 2005, from a house in Jones County, Iowa, built in 1857. Bats had been excluded from the attic since 1992. Nine months before ticks were collected, bats were prevented from roosting under the eaves. DNA was extracted from 31 nymphaal *C. kelleyi*, as described previously (6). For each tick, regions of the glpQ, flaB, and 16S rRNA genes were amplified and sequenced as described (3,7,8). Sequences were assembled by using the SeqMan program in the Lasergene software package (DNASTAR, Madison, WI, USA).

Fourteen (45.1%) of 31 ticks were positive by PCR for ≥1 of the genes tested. Partial DNA sequences were determined from tick no. 16, for which amplicons for all 3 genes were obtained. The partial flaB sequence had 4 bases different from the 300-base sequence (98.66% identity) reported previously (GenBank accession no. AY763104) for another *Borrelia* sp. found in *C. kelleyi* (5). We constructed a 1,992-bp concatenated sequence that contained 1,273 bp of the 16S rRNA, 351 bp of flaB, and 368 bp of glpQ. This concatenated sequence was aligned with homologous, trimmed DNA sequences of the same length obtained from representative full-length sequences determined previously for *B. hermsii*, *B. turicatae*, and *B. parkeri* (3,9) (Figure). This *C. kelleyi* spirochete was more closely related to *B. turicatae* and *B. parkeri* than to *B. hermsii* but was clearly distinct from all 3 species (DNA sequence identities of 98.89%, 98.75%, and 95.98% to *B. turicatae*, *B. parkeri*, and *B. hermsii*, respectively).

A glpQ amplicon from another nymphaal tick (no. 3) was sequenced (GenBank accession no. EF688578) and was unique in the database; it was also considerably different from the glpQ sequence determined from tick 16, with 325 of 368 bases matching (88.3% identity). The *Borrelia* glpQ sequence from tick 3 had 85.1%–89.1% identity compared with glpQ sequences from *B. hermsii*, *B. turicatae*, and *B. parkeri*. This finding suggests the presence of at least 2 relapsing fever group spirochetes in *C. kelleyi* that await further characterization.

We found a novel *Borrelia* in bat ticks that is closely related to, but distinct from, the other known species of tick-borne relapsing fever spirochetes in North America. The human health implications of the new relapsing fever group spirochetes are not yet known. The willingness of *C. kelleyi* to feed on humans and the fact that infection with bacteria closely related to true relapsing fever spirochetes occurs in...
these ticks suggest that human habitation near bats and their associated tick colonies could pose a public health risk. Growth in laboratory animals or culture could help isolate these novel organisms for further studies to establish the distribution and public health implications of this newly identified *Borrelia* sp.

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### KI and WU Polyomaviruses in Children, France

**To the Editor:** Two new members of the *Polyomaviridae* family, provisionally named *Karolinska Institutet virus* (KIPyV) and *Washington University virus* (WUPyV), have been recently discovered (1,2). These new polyomaviruses were identified by screening human respiratory secretions with molecular tools. KIPyV and WUPyV are genetically related to the BK virus and the JC virus, the 2 known members of the family *Polyomaviridae* that affect humans.

In France, from November 2006 through June 2007, nasopharyngeal aspirates were obtained from 537 children who were <5 years of age and who had acute respiratory tract disease. The aspirates were tested for respiratory syncytial virus (RSV); influenza virus types A and B; parainfluenza virus types 1, 2, and 3; and adenoviruses (AdVs) by direct immunofluorescence assay. The aspirates were also tested for human metapneumovirus (HMPV) by an enzyme immunoassay (HMPV EIA, Biotrin, Lyon, France) and for the human bocavirus (HBoV) by PCR (3). Samples were placed on MRC5 cell monolayers for virus isolation.

Nucleic acid extracts were tested for KIPyV and WUPyV DNA by PCR. KIPyV detection was performed by using a nested PCR approach that targeted the VP1 capsid gene as described by Allander et al. (1). For WUPyV detection, primers targeted the predicted 3’ end of the large T antigen coding region as described by Gaynor et al. (2). The amplification specificity was assessed by sequencing the PCR product; sequences were deposited in GenBank (WUPyV isolates, accession no. AM778536–48; KIPyV isolates, accession no. AM849808–10).

At least 1 type of virus was identified for 271 (50.5%) children. The viruses found were RSVs in 175 (32.6%), HBoVs in 54 (10.0%), HMPVs in 50 (9.3%), rhinoviruses/enteroviruses in 11 (2%), influenza A viruses in 8 (1.5%), human AdVs in 6 (1.1%), and parainfluenza type 3 viruses in 4 (0.7%) samples. Aspirates were not tested for coronavirus; detection of rhinoviruses/enteroviruses was likely low because cell culture is less sensitive than molecular assays.

A total of 13 (2.4%) samples were positive for WUPyV; of these 4 (30.8%) were co-infected with another virus. The 13 children with samples positive for WUPyV had a median age