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Address for correspondence: Karthikeyan
Paranthaman, Specialist Registrar in Public
Health, Public Health Department, Room 9
Richards Building, Old Road Campus, Oxford
OX3 7LF, UK; email: karthik.paranthaman@
oxfordshirepct.nhs.uk

Novel Relapsing
Fever Spirochete in
Bat Tick

To the Editor: Tick-borne relapsing
fever in western North America is a
dimension caused by spirochetes in
the genus Borrelia that are trans-
mitted 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 para-
eters 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) pro-
vided evidence that the argasid bat
tick, Carios kelleyi, feeds upon hu-
mans. Subsequently, Loftis et al. (5)
used PCR analysis and DNA sequenc-
ing to detect in C. kelleyi an unidenti-
fied Borrelia species that was closely
related to B. turicatae and B. parkeri.
We report the partial molecular char-
acterization of another novel tick-
borne relapsing fever spirochete in C.
kelleyi, which expands our knowledge
for this group of pathogenic spiro-
chetes and their potential vertebrate
hosts and tick vectors.

C. kelleyi were collected Au-
ghust 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 nympha 1 C. kel-
leyi, 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, Madi-
son, 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 ob-
tained. 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 ob-
tained 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
nymphal 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 se-
quence from tick 3 had 85.1%–89.1%
identity compared with glpQ sequenc-
es from B. hermsii, B. turicatae, and B.
parkeri. This finding suggests the pres-
ence of at least 2 relapsing fever group
spirochetes in C. kelleyi that await fur-
ther characterization.

We found a novel Borrelia in bat
ticks that is closely related to, but dis-
tinct 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

Figure. Phylogram comparing the novel spirochete in the bat tick Carios kelleyi with
Borrelia parkeri, B. turicatae, and B. hermsii based on the concatenated partial 16S
rRNA-flaB-glpQ DNA sequences in the Carios spirochete (1,992 bp total) (produced
with ClustalV software from DNASTAR [Madison, WI, USA]). Scale bar represents the
number of base substitutions per 100 aligned bases. GenBank accession numbers for the
C. kelleyi spirochete sequences used to construct the tree are EF688575, EF688576, and EF688577.
Spiro, spirochete.
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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James S. Gill,*
Amy J. Ullmann,†
Amanda D. Loftis,‡
Tom G. Schwan,§
Sandra J. Raffel,§
Merry E. Schrumpf,§ and Joseph Piesman†

*Iowa State University, Ames, Iowa, USA; †Centers for Disease Control and Prevention, Fort Collins, Colorado, USA; ‡Centers for Disease Control and Prevention, Atlanta, Georgia, USA; and §Rocky Mountain Laboratories of National Institutes of Health, Hamilton, Montana, USA

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Address for correspondence: James S. Gill, 313 N Mt Vernon Dr, Iowa City, IA 52245, USA; email: bugmangill@yahoo.com

Kl 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 coronaviruses; 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...