are needed to determine the role of nasal carriage in *B. holmesii* bacteremia. That no *B. holmesii* infections occurred after rituximab was stopped suggests that rituximab played a role in the recurrent infections. In cases of recurrent infection or bacteremia, nasal carriage should be assessed, and the interruption of rituximab should be considered by physicians.

Acknowledgments

We thank Alain Le Coustumier for his advice concerning antimicrobial treatment and Institut Pasteur Fondation, Institut National de Veille Sanitaire, and Le Centre National de la Recherche Scientifique for financial support.

Liem Binh Luong Nguyen, Loïc Epelboin, Jean Gabarre, Marylin Lecso, Sophie Guilhot, François Bricaire, Eric Caumes, and Nicole Guiso

Author affiliations: Groupe Hospitalier Pitié-Salpêtrière, Paris, France (L.B.Luong Nguyen, L. Epelboin, J. Gabarre, M. Lecso, F. Bricaire, E. Caumes); Université Paris, Paris (L. Epelboin, F. Bricaire, E. Caumes); and Institut Pasteur, Paris (S. Guilhot, N. Guiso)

DOI: http://dx.doi.org/10.3201/eid1910.130345

References


After tick identification, DNA was extracted from ticks by using QIAamp DNeasy kits (QIAGEN, Hilden, Germany). Two PCR targets were assessed within each sample; the primer pair Rp.CS.877p and RpCS.1258n was selective for a 396-bp fragment of a highly conserved gene encoding the citrate synthase (gltA) shared by all *Rickettsia* spp. (6); the Rr190–70p and Rr190–701n primer pair amplified a 629–632-bp fragment of the gene encoding the 190-kD antigenic outer membrane protein A (ompA), common to all SFG rickettsiae (6,7). DNA extracted from 2 *A. variegatum* tick cell lines (AVL/CTVM13 and AVL/CTVM17), previously amplified and sequenced by using primers for *Rickettsia* 16S rRNA, ompB, and sca4 genes revealing >98% similarity with *R. africae* (8), was used as a positive control. Negative controls consisted of DNA from 2 male and female laboratory-reared *Rhipicephalus appendiculatus* ticks and distilled water. DNA of positive samples was recovered, and confirmation of amplicon authenticity was obtained through sequence analysis by using nucleotide BLAST (www.ncbi.nlm.nih.gov/BLAST).

A total of 39 ticks were collected in Uganda (32 adult males, 5 females, and 2 nymphs), and 141 were collected in Nigeria (80 males, 59 females, and 2 nymphs); all were identified as *A. variegatum* (online Technical Appendix Table, wwwnc.cdc.gov/EID/articlepdfs/19/10/13-0389-Techapp1.pdf). SFG rickettsiae DNA was amplified in 26 (67%) of 39 ticks from Uganda and 88 (62%) of 141 ticks from Nigeria by using the ompA gene primers; amplicons of the gltA genes were obtained in 16 (41%) of 39 ticks and 84 (60%) of 141 ticks, respectively (online Technical Appendix Table). Overall, 81 (45%) of 180 ticks were positive by gltA and ompA PCRs (online Technical Appendix Table). DNA sequences of the 22 gltA and ompA products from Uganda and the 22 from Nigeria showed 100% similarity with published sequences of *R. africae* (GenBank accession nos. U59733 and RAU43790, respectively). For both countries, ticks positive for *Rickettsia* spp. and SFG rickettsiae DNA were male and female specimens (online Technical Appendix Table). Among females, both unengorged and engorged specimens contained DNA from rickettsiae and SFG rickettsiae (online Technical Appendix Table).

These findings represent a novelty for Uganda. With reference to Nigeria, our results contrast with the prevalence of 8% recorded in a similarly sized sample (n = 153) of *A. variegatum* ticks collected from cattle in the same part of the country (3); this discrepancy might be the result of previous targeting of the rickettsial 16S rDNA gene. In the study reported here, the SFG-specific ompA PCR proved to be more sensitive than gltA for detecting rickettsiae DNA, as has also been reported in previous work (9). Although finding *R. africae* DNA in engorged female and nymphal tick specimens might be attributable to prolonged rickettsiemia in cattle (10), the presence of *R. africae* in distinctly unengorged female ticks indicates the potential for *A. variegatum* ticks to act as a reservoir of this SFG rickettsia (2).

**Figure.** Location of areas studied for *Rickettsia africae* in *Amblyomma variegatum* ticks in Nigeria (A) and Uganda (B), 2010.
This study extends the known geographic range of *R. africae* in *A. variegatum* ticks in sub-Saharan Africa. The number of potentially infective ticks recorded in Uganda and central Nigeria suggests that persons in rural areas of northern Uganda and central Nigeria might be at risk for African tick-bite fever. Awareness of this rickettsiosis should be raised, particularly among persons who handle cattle (e.g., herders and paraveterinary and veterinary personnel). Physicians in these areas as well as those who care for returning travelers, should consider African tick-bite fever in their differential diagnosis for patients with malaria and influenza-like illnesses.

Acknowledgments

We thank Abraham Goni Dogo for helping with tick collections in Nigeria, Lesley Bell-Sakyi and Pilar Alberdi for providing positive controls, Tom Connelley for providing laboratory-reared ticks to be used as negative controls, Cristina Socolovschi for her valuable suggestions on the molecular proceedings, and Albert Mugenyi for his indispensable assistance with map design.

The research leading to these results received funding from the UK Department for International Development under the umbrella of the Stamp Out Sleeping Sickness Programme, the UK Biotechnology and Biological Sciences Research Council under the Combating Infectious Diseases in Livestock for International Development scheme, and the European Union’s Seventh Framework Program (FP7/2007-2013) under grant agreement no. 221948, Integrated Control of Neglected Zoonoses.

Vincenzo Lorusso, Karolina Anna Gruszka, Ayodele Majekodunmi, Augustine Igweh, Susan C. Welburn, and Kim Picozzi

Author affiliations: University of Edinburgh, Edinburgh, Scotland, UK (V. Lorusso, K.A. Gruszka, A. Majekodunmi, S. Welburn, K. Picozzi); and Nigerian Institute for Trypanosomiases Research, Jos, Nigeria (A. Igweh)

DOI: http://dx.doi.org/10.3201/eid1910.130389

References


Address for correspondence: Kim Picozzi, Division of Pathway Medicine, Edinburgh University Medical School, The Chancellor’s Bldg, 49 Little France Crescent, Edinburgh EH16 4SB, Scotland, UK; email: kim.picozzi@ed.ac.uk

Ongoing Measles Outbreak in Orthodox Jewish Community, London, UK

To the Editor: Measles outbreaks have been reported in Orthodox and ultra-Orthodox Jewish communities across Europe and Israel (1–5). We describe an ongoing outbreak within the largest European Orthodox Jewish community (including a Charedi population of 17,587), based in London, focused in Hackney (6). Vaccination coverage within this community is lower than in the general population of London, causing low herd immunity and outbreaks of vaccine-preventable diseases. Vaccination coverage data within the community cannot be extrapolated, because membership is not classified as an ethnicity and not collected within health electronic recording systems. However, general practice surgeries in Hackney known to have high proportions of Orthodox Jewish patients have considerably lower vaccination coverage (55%–75% of patients 24 months of age had received measles, mumps, rubella [MMR] vaccine in the 3rd quarter of 2012) compared with the London average (87.3%) (7). Health beliefs, family size (the average Charedi household size is 6.3 persons), and underutilization of immunization services contribute to low coverage (8,9).

The outbreak clinical case definition was taken from Public Health England’s guidance (10). It also included membership in the Orthodox community.
**Rickettsia africae in Amblyomma variegatum Ticks, Uganda and Nigeria**

Technical Appendix

Technical Appendix Table. Results of PCR screening of Amblyomma variegatum ticks, Uganda and Nigeria, 2010*

<table>
<thead>
<tr>
<th>Study area</th>
<th>No. ticks Identified</th>
<th>gltA</th>
<th>ompA</th>
<th>gltA and ompA</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>M  F  N</td>
<td>M  F  N</td>
<td>M  F  N</td>
<td>M  F  N</td>
</tr>
<tr>
<td>Nigeria, n = 141</td>
<td>80  59 (28)  2 (1)</td>
<td>84/141  45/80  38 (19)/59 (28)  1 (1)/2 (1)</td>
<td>88/141  44/80  44 (22)/59 (28)  0/2(1)</td>
<td>68/141  32/80  36 (18)/59 (28)  0/2(1)</td>
</tr>
<tr>
<td>Total, n = 180</td>
<td>112  64 (32)  4 (1)</td>
<td>100/180  57/112  42 (22)/64 (32)  1 (1)/4 (1)</td>
<td>114/180  68/112  46 (24)/64 (32)  0/4 (1)</td>
<td>81/180  43/112  38 (18)/64 (32)  0/4(1)</td>
</tr>
</tbody>
</table>

*M, male; F, female; N, nymph. Numbers in parentheses indicate engorged female ticks and nymphs.