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 Costumier 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 Leco, Sophie Guillot, François Bricaire, Eric Caumes, and Nicole Guiso

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

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

References


Rickettsia africae in Amblyomma variegatum Ticks, Uganda and Nigeria

To the Editor: *Rickettsia africae* is the most widespread spotted fever group (SFG) rickettsia in sub-Saharan Africa, where it causes African tick-bite fever (1), an acute, influenza-like syndrome. The number of cases in tourists returning from safari in sub-Saharan Africa is increasing (1). In western, central, and eastern sub-Saharan Africa, *R. africae* is carried by *Amblyomma variegatum* (Fabricius, 1794) ticks (2); usually associated with cattle, this 3-host tick also can feed on a variety of hosts, including humans (2). *R. africae* has not been reported in Uganda and rarely reported in Nigeria (3,4). Our objective was to determine the potential risk for human infection by screening for rickettsial DNA in *A. variegatum* ticks from cattle in Uganda and Nigeria.

In February 2010, ticks were collected from zebu cattle (*Bos indicus*) from 8 villages in the districts of Karamoja (Adektar [1°81′N–33°22′E], Awimom [1°66′N–33°04′E], Kalobo [1°88′N–33°25′E], Odidip [1°90′N–33°30′E], Odikara [1°91′N–33°30′E], and Ollilimo [1°75′N–33°38′E], and Dokolo (Alek [2°09′N–33°16′E], and Angeta [1°87′N–33°10′E]) in Uganda and, in June 2010, in 3 villages (Mangar [9°14′N–8°93′E], Ruff [9°43′ N–9°10′E], and Tambes [9°38′N–9°38′E]) in the Plateau State in Nigeria (Figure). This convenience sample was obtained as part of other ongoing research projects in both countries. Ticks were preserved in 70% ethanol and identified morphologically to the species level by using taxonomic keys (5). Because the anatomic features do not enable an objective assessment of the feeding status of adult male ticks, engorgement level was determined only in female tick specimens and nymphs.

Another Dimension

Thoughtful essays, short stories, or poems on philosophical issues related to science, medical practice, and human health. Topics may include science and the human condition, the unexpected side of epidemic investigations, or how people perceive and cope with infection and illness. This section is intended to evoke compassion for human suffering and to expand the science reader’s literary scope. Manuscripts are selected for publication as much for their content (the experiences they describe) as for their literary merit.
After tick identification, DNA was extracted from ticks by using QIAamp DNAeasy 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-kDa 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 engorged and unengorged 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).
This study extends the known geographic range of *R. africae* in *A. variagatum* 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 rickettsioses 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, Tim 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 and Biological Sciences Research Council umbrella of the Stamp Out Sleeping Sickness Programme, the UK Biotechnology and Biological Sciences Research Council, and the European Union’s seventh framework programme, the UK Biotechnology and Biological Sciences Research Council, and the European Union’s seventh framework programme, the UK Biotechnology and Biological Sciences Research Council. 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 and Biological Sciences Research Council umbrella of the Stamp Out Sleeping Sickness Programme, the UK Biotechnology and Biological Sciences Research Council, and the European Union’s seventh framework programme, the UK Biotechnology and Biological Sciences Research Council. 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 and Biological Sciences Research Council umbrella of the Stamp Out Sleeping Sickness Programme, the UK Biotechnology and Biological Sciences Research Council, and the European Union’s seventh framework programme, the UK Biotechnology and Biological Sciences Research Council.

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 Trypanosomiasis Research, Jos, Nigeria (A. Igweh)

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

**References**


