that can share or not share epidemiologic elements.

Molecular identification of *R. rickettsii* in *A. cajennense* ticks was recorded only in the Paraíba do Sul River basin of southeastern Brazil (*8*), as confirmed in our study. This eco-epidemiologic aspect, its great anthropophily, and its presence in all municipalities surveyed, with absolute frequency greater than other species, demonstrates the possible effect of this tick on epidemic cycle development for the analyzed region, which does not seem to occur in other regions.

R. rickettsii infection of *A. dubitatum* ticks in the 1 focus analyzed might indicate its relevance in specific epidemiologic scenarios. We detected highly similar sequences of different species of *Rickettsia* (LIC2937A) in the same *A. dubitatum* tick specimen (Figure). Other studies have recorded multiple *Rickettsia* infections in 1 tick specimen (*9*,*10*).

Our finding of *C. felis* fleas in 6 of the 7 outbreaks investigated highlights the possible role of this flea in maintaining *Rickettsia* in Rio de Janeiro state. *C. felis* and *C. canis* fleas infected with *R. rickettsii* seem to confirm this potential. Nevertheless, the real epidemiologic value of this report in the BSF cycle deserves to be further investigated.

Our results indicate that dogs and horses are the primary vertebrates in the *Rickettsia* enzootic cycle in the investigated focus, and, considering their common presence in human environments, they must be important in maintaining possible rickettsial vectors to humans. These results contribute to the mapping of BSF-endemic areas and to the understanding of the circulation and epidemiology of *Rickettsia* sp. in an area with one of the highest fatal concentrations of BSF.

Acknowledgments

We thank the Secretaria de Saúde do Estado do Rio de Janeiro for its help in the focus area and for notifying us about the BSF cases.

This study was supported by Fundação de Amparo à Pesquisa do Estado de São Paulo (grant nos. 2010/03554-9 and 2010/52485-0) and Conselho Nacional de Desenvolvimento Cientifico e Tecnológico, Brazil (grant no. 131700/2010-3).

Nicole O. Moura-Martiniano, Erik Machado-Ferreira, Karen M. Cardoso, Flávia S. Gehrke, Marinete Amorim, Andréa C. Fogaça, Carlos A.G. Soares, Gilberto S. Gazêta,[1] and Teresinha T.S. Schumaker[1]

Author affiliations: Universidade de São Paulo, São Paulo, Brazil (N.O. Moura-Martiniano, K.M. Cardoso, F.S. Gehrke, A.C. Fogaça, T.T.S. Schumaker); Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil (E. Machado-Ferreira, C.A.G. Soares); and Fundação Oswaldo Cruz, Rio de Janeiro (M. Amorim, G.S. Gazêta)

DOI: http://dx.doi.org/10.3201/eid2003.131013

References

1. Horta MC, Labruna MB, Pinter A, Linardi PM, Schumaker TTS. *Rickettsia* infection in five areas of the state of São Paulo, Brazil. Mem Inst Oswaldo Cruz. 2007;102:793–801. http://dx.doi.org/10.1590/S0074-02762007000700003
2. Silveira I, Pacheco RC, Szabó MPJ, Ramos HGC, Labruna MB. *Rickettsia parkeri* in Brazil. Emerg Infect Dis. 2007;13:1111–3. http://dx.doi.org/10.3201/eid1307.061397
3. Aragão H, da Fonseca F. Ixodological notes. VIII. List and key to the representatives of the Brazilian ixodological fauna [in Portuguese]. Mem Inst Oswaldo Cruz. 1961;59:115–29. http://dx.doi.org/10.1590/S0074-02761961000200001
4. Aljanabi SM, Martinez I. Universal and rapid salt-extraction of high quality genomic DNA for PCR-based techniques. Nucleic Acids Res. 1997;25:4692–3. http://dx.doi.org/10.1093/nar/25.22.4692
5. Labruna MB, Whitworth T, Horta MC, Bouyer DH, Mcbride JW, Camargo LM, et al. *Rickettsia bellii* and *Rickettsia amblyommii* in *Amblyomma* ticks from the State of Rondônia, Western Amazon, Brazil. J Med Entomol. 2004;41:1073–81. http://dx.doi.org/10.1603/0022-2585-41.6.1073
6. Labruna MB, Mcbride JW, Bouyer DH, Camargo LMA, Camargo EP, Walker DH. Molecular evidence for a spotted fever group *Rickettsia* species in the tick *Amblyomma longirostre* in Brazil. J Med Entomol. 2004;41:533–7. http://dx.doi.org/10.1603/0022-2585-41.3.533
7. Regnery RL, Spruill CL, Plikaytis BD. Genotypic identification of rickettsiae and estimation of intraspecies sequence divergence for portions of two rickettsial genes. J Bacteriol. 1991;173:1576–89.
8. Guedes E, Leite RC, Prata MCA, Pacheco RC, Walker DH, Labruna MB. Detection of *Rickettsia rickettsii* in the tick *Amblyomma cajennense* in a new Brazilian spotted fever–endemic area in the state of Minas Gerais. Mem Inst Oswaldo Cruz. 2005;100:841–5. http://dx.doi.org/10.1590/S0074-02762005000800004
9. Ferrari FAG, Goddard J, Paddock CD, Varela-Stokes A. *Rickettsia parkeri* and *Candidatus Rickettsia andeanae* in Gulf Coast ticks, Mississippi, USA. Emerg Infect Dis. 2012;18:1705–7. http://dx.doi.org/10.3201/eid1810.120250
10. Varela-Stokes AS, Paddock CD, Engber B, Toliver M. *Rickettsia parkeri* in *Amblyomma maculatum* ticks, North Carolina, USA, 2009–2010. Emerg Infect Dis. 2011;17:2350–3. http://dx.doi.org/10.3201/eid1712.110789

Address for correspondence: Nicole O. Moura-Martiniano. Lab. de Referência Nacional em Vetores das Riquetsioses, Instituto Oswaldo Cruz–Fiocruz, Av. Brasil 4365, Pav. Lauro Travassos, anexo posterior/sala 08, Manguinhos, Rio de Janeiro, Rio de Janeiro, CEP: 21.045-900, Brazil; email: nicmoura@ioc.fiocruz.br

[1]These authors contributed equally to this article.

Atypical *Streptococcus suis* in Man, Argentina, 2013

To the Editor: *Streptococcus suis* is a major swine pathogen and an emerging zoonotic agent that causes mainly meningitis and septic shock (*1*,*2*). Among the 35 described

serotypes classified by differences in capsular antigens, serotype 2 is the most frequently isolated from humans worldwide, and serotype 14 cases are also increasing in some countries (*1*). In Southeast Asia, this pathogen affects not only workers in close contact with pig/pork by-products but also the general population, probably because of the widespread presence of backyard types of pig production, open meat markets, and some special dishes prepared with raw meat or blood (*3*). We report a case of peritonitis caused by an atypical *S. suis* serotype 21 strain in a patient in Argentina.

A 62-year-old man from Santa Fe Province in Argentina, who had a history of tobacco and alcohol abuse, was hospitalized in 2013 as an emergency patient with symptoms of acute abdominal distress. Ten days before admission, abdominal distention, accompanied by intense upper abdominal pain, developed in the patient. The patient's family reported that he had been having gastrointestinal bleeding 4 days before admission, and he was suspected of having diabetes.

At admission, a physical examination indicated jaundice, hepatosplenomegaly, and ascites. A neurologic examination indicated that the patient was conscious, but disoriented, and that his vital signs were stable. The patient had a temperature of 38.9°C, a pulse rate of 130 beats/min, and blood pressure of 110/70 mm Hg. Other laboratory results were a leukocyte count of 2,900 cells/μL (70% neutrophils), a platelet count of 94,000/μL, a serum hemoglobin concentration of 13.20 g/dL, a glucose concentration of 195 mg/dL, a blood urea nitrogen level of 42 mg/dL, a creatinine level of 0.96 mg/dL; a serum bilirubin level of 3.01 mg/dL, an alanine aminotransferase level of 35 U/L, an aspartate aminotransferase level of 70 U/, a serum albumin level of 2.66 g/dL, and an increase in prothrombin time to 22 s.

Spontaneous bacterial peritonitis was suspected. Abdominal paracentesis was performed and produced a turbid milky fluid, with a protein level of 1600 mg/dL; 1,340 cells/μL (90% neutrophils), a lactate dehydrogenase level of 221 U/L, and an amylase level of 34 U/L. Samples of blood and ascitic fluid were inoculated into aerobic and anaerobic blood culture bottles. Gram staining was performed and no organisms were observed.

Treatment with intravenous ceftriaxone (2g/day) was started after a diagnosis of spontaneous bacterial peritonitis associated with liver cirrhosis was made. After 48 h of incubation, cultures of blood and ascetic fluid were plated onto sheep blood agar and chocolate agar and incubated at 35°C in an atmosphere of 5% CO_2. After 24 h of incubation, cultures showed growth of α-hemolytic streptococci.

An API Strep Test (bioMérieux, Marcy l'Etoile, France) identified the isolate as *S. pneumoniae* (probability 58.7%) or *S. suis* (probability 20.7%). However, these 2 probability values are unacceptable identification confidence levels. Therefore, the species and serotype were identified by sequence analysis of a 16S rRNA gene and a coagglutination test as described (*4*,*5*). The isolate was identified as *S. suis* serotype 21.

The infection was considered resolved when all signs and symptoms of infection disappeared, a polymorphonuclear cell count in ascitic fluid decreased to <250 cells/mL, and ascitic fluid cultures were negative for bacteria. Antimicrobial drug therapy was given for 48 h after resolution of the infection. The patient denied any recent occupational or occasional contact with swine or other animals, and he had no history of eating raw or undercooked pork.

A biochemically and antigenically atypical strain was isolated from the patient with peritonitis. A reference strain of serotype 21 and most other strains of this serotype had been isolated from tonsils of healthy pigs (*6*). However, 16 strains had also been isolated from sick pigs during 2008–2011 in Canada (*7*). These findings indicate that this serotype is potentially virulent. Most strains, including the strain from the patient reported, are usually not identified as *S. suis* by rapid multitest identification systems (*6*).

There are only 2 reports of *S. suis* being isolated from humans in Latin America; these reports were also from Argentina (*8*,*9*). Because swine production in Argentina is a smaller industry than in other Latin American countries, the higher rate of *S. suis* isolation rate is probably the consequence of good surveillance systems and awareness of the pathogen by local diagnostic laboratories.

The patient did not have any contact with swine, pork-derived products, or raw/undercooked beef. A patient infected with *S. suis* might be unaware or have no recollection of exposure to animals. Latent infection, with reactivation many years later, has been reported (*10*). *S. suis* might become an opportunistic pathogen in persons who are stressed or immunodeficient. This pathogen has also been increasingly isolated from mammals other than pigs and from the environment. The patient in this study had a history of alcohol consumption, which is a reported risk factor for this infection (*3*).

This study was supported by Natural Sciences and Engineering Research Council of Canada grant 154280 to M.G.

Raquel Callejo, Monica Prieto, Francisco Salamone, Jean-Philippe Auger, Guillaume Goyette-Desjardins, and Marcelo Gottschalk

Author affiliations: Instituto Nacional de Enfermedades Infecciosas, Buenos Aires, Argentina (R. Callejo, M. Prieto); Hospital San Martín, Entre Ríos, Argentina (F. Salamone); and University of Montreal, St-Hyacinthe, Québec, Canada (J.-P. Auger, G. Goyette-Desjardins, M. Gottschalk)

DOI: http://dx.doi.org/10.3201/eid2003.131148

References

1. Gottschalk M. Streptococcocis. In: Straw BE, Zimmerman JJ, D'Allaire S, Taylor DJ, editors. Diseases of swine. 10th ed. Ames (IA): Blackwell Publishing; 2012. p. 841–55.
2. Wertheim HF, Nghia HD, Taylor W, Schultsz C. *Streptococcus suis*: an emerging human pathogen. Clin Infect Dis. 2009;48:617–25. http://dx.doi.org/10.1086/596763
3. Nghia HD, Tu le TP, Wolbers M, Thai CQ, Hoang NV, Nga TV, et al. Risk factors of *Streptococcus suis* infection in Vietnam. A case–control study. PLoS ONE. 2011;6:e17604. http://dx.doi.org/10.1371/journal.pone.0017604
4. Brousseau R, Hill JE, Prefontaine G, Goh SH, Harel J, Hemmingsen SM. *Streptococcus suis* serotypes characterized by analysis of chaperonin 60 gene sequences. Appl Environ Microbiol. 2001;67:4828–33. http://dx.doi.org/10.1128/AEM.67.10.4828-4833.2001
5. Gottschalk M, Higgins R, Boudreau M. Use of polyvalent coagglutination reagents for serotyping of *Streptococcus suis*. J Clin Microbiol. 1993;31:2192–4.
6. Gottschalk M, Higgins R, Jacques M, Mittal KR, Henrichsen J. Description of 14 new capsular types of *Streptococcus suis*. J Clin Microbiol. 1989;27:2633–6.
7. Gottschalk M, Lacouture S, Bonifait L, Roy D, Fittipaldi N, Grenier D. Characterization of *Streptococcus suis* isolates recovered between 2008 and 2011 from diseased pigs in Quebec, Canada. Vet Microbiol. 2013;162:819–25. http://dx.doi.org/10.1016/j.vetmic.2012.10.028
8. Lopreto C, Lopardo HA, Bardi MC, Gottschalk M. Primary *Streptococcus suis* meningitis: first case in humans described in Latin America [in Spanish]. Enferm Infecc Microbiol Clin. 2005;23:110. http://dx.doi.org/10.1157/13071618
9. Nagel A, Manias V, Busquets N, Sniadowsky S, Anzardi J, Mendez Ede L. *Streptococcus suis* meningitis in an immunocompetent patient [in Spanish]. Rev Argent Microbiol. 2008;40:158–60.
10. François B, Gissot V, Ploy MC, Vignon P. Recurrent septic shock due to *Streptococcus suis*. J Clin Microbiol. 1998;36:2395.

Address for correspondence: Marcelo Gottschalk, Department of Pathology and Microbiology, University of Montreal, 3200 Sicotte, St-Hyacinthe, Québec J2S 2M2, Canada; e-mail: marcelo.gottschalk@umontreal.ca

Cutaneous Leishmaniasis Caused by *Leishmania killicki*, Algeria

To the Editor: Cutaneous leishmaniasis (CL) is a widespread and resurging vector-borne disease caused by a protozoan parasite belonging to genus *Leishmania* (*1*). After Afghanistan, Algeria is the second largest focus of CL in the world. Although CL is a serious public health problem in Algeria, few data are available from this country.

During 2004–2008, an average of ≈44,050 CL cases were reported per year, and the estimated annual incidence ranged from 123,300 to 202,600 cases. Two main forms of CL have been described for more than a century in Algeria, the zoonotic, caused by *L. major* and the sporadic, caused by *L. infantum*. Since 2004, 11 strains belonging to the *L. tropica* complex, including *L. killicki* (*2*), were identified in 1 focus in the northern part of the Sahara (*3*) and in 2 foci in the northeastern Algeria (*4*,*5*). We report here a recent outbreak of CL, including infection with *L. killicki* strains, in the Tipaza area of northern Algeria.

Patients who sought treatment at Hajout hospital in Hajout, Algeria (a community of ≈51,000 persons), from January 2010 through April 2013 with cutaneous lesions consistent with leishmaniasis, underwent clinical examination. For each patient (146 total), we collected epidemiologic data (geographic origin, traveling history, especially to other leishmaniasis-endemic areas) and clinical data (number and size of lesions and clinical forms). Informed consent was obtained from all patients or their legal guardians. A particular characteristic of the infections was the unusual duration of some episodes, one of which persisted for >4 years, which is compatible with leishmaniasis recidivans (*6*).

Microbiological data were obtained as follows. Tissue samples, obtained by scraping the internal border of skin lesions from patients, were smeared onto a glass slide, fixed with methanol, stained with Giemsa, and examined by microscopy. Slides showing *Leishmania* amastigote forms were then processed further for molecular analyses. The immersion oil used to examine each slide was wiped off the smear with tissue paper, and then the dry smear was scraped from its slide by using a sterile scalpel. DNA extraction from smear scrapings was performed with the NucleoSpin Tissue kit (Macherey-Nagel, Düren, Germany). Species identification was performed by amplifying the topoisomerase II gene, followed by DNA sequencing (*7*).

In total, 60 patients exhibited *Leishmania*-positive cutaneous lesions as determined by microscopy. The topoisomerase II gene was successfully amplified and sequenced from samples from 38 patients. *Leishmania* species were identified by comparing sequences with those of the reference strains *L. infantum* MHOM/FR/78/LEM75, *L. killicki* MHOM/TN/80/LEM163, and *L. major* MHOM/MA/81/LEM265 (*7*). *L. infantum* was identified in 36 cases and *L. killicki* in 2 cases (Figure). No *L. major* isolates were found in this series.

The low proportion of *L. killicki* strains was similar to that found recently in the Annaba focus in northeastern Algeria (*5*). However, the observation of a new focus of CL and *L. killicki* as etiologic agent may indicate a modification of the epidemiology of CL in Algeria. This focus, located far from other previously described areas where the *L. tropica* complex is endemic, may reflect geographic spread of this complex in Algeria.

The results of this study can be placed in a larger framework as well. Since 2004, strains in the *L. tropica* complex have been increasingly reported as responsible for CL