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* (PLIC937A) 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.

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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/S0070-427620070000007003
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/S0070-42761961000200001
4. Aljanabi SM, Martínez 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 amblyommi* 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/S0070-42762005000800004
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

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**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...
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 ascitic fluid were plated onto sheep blood agar and chocolate agar and incubated at 35°C in an atmosphere of 5% CO2. After 24 h of incubation, cultures showed growth of a-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).

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Cutaneous Leishmaniasis Caused by *Leishmania killicki*, Algeria

To the Editor: Cutaneous leishmaniasis (CL) is a widespread and resurfacing 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 a history of CL were included. A total of 146 patients (104 men and 42 women) were seen during this period. The average age of patients was 37.5 years. Of these patients, 96 were from the Tipaza area. The mean duration of symptoms before treatment was 8.5 months (range, 1–12 months). In 2 cases, the lesion 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

References

1. Gottschalk M. Streptococcus. 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, Roy D, Fittipaldi N, Grenier D. Characterization of *Streptococcus suis* serotypes characterized by analysis of chaperonin 60 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, Bonfait 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

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