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 anthropophilic, 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 ticks in the 1 focus analyzed (*A. dubitatum*), 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* in an area with one of the highest fatal concentrations of BSF.

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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
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 infection disappeared, a polymorphonuclear cell count in ascitic fluid decreased to <250 cells/mL, and ascitic fluid cultures were negative for bacteria. 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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Collaboration on a Special Issue: Leishmaniasis and Related Diseases

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10. François B, Gissot V, Ploy MC, Vignon P. 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.

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 Hajjout hospital in Hajjout, 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.