

based on the consideration that *R. aeschlimannii* is usually found in ticks of the genus *Hyalomma*, primarily in *H. marginatum* (1). Therefore, 1 of the PCRs amplified a fragment of the *Hyalomma* tick mitochondrial cytochrome oxidase I gene and the other a fragment of the internal transcribed spacer 2 (7).

The ITS2 fragment displayed the highest (99%) similarity with the respective fragment of *H. marginatum*, *H. dromedarii*, *H. truncatum*, and *H. lusitanicum*. Cytochrome oxidase subunit I fragment was 99% identical to *H. marginatum*, *H. dromedarii*, and *H. truncatum*. The 16S RNA fragment was 98% identical to *H. marginatum*; its identity to the second closest sequence belonging to *H. lusitanicum* was 96%.

Earlier, *R. aeschlimannii* had been detected in sub-Saharan and North Africa, southern Europe, and southwestern Russia (8). Therefore, the area of Zerbst, the middle of Germany, marks the northernmost point of *R. aeschlimannii* detection.

Hyalomma spp. ticks are distributed in Africa, the Mediterranean climatic zone of southern Europe, and in Asia. The only documented *Hyalomma* spp. tick in Germany was found on a human in the southern part of the country (Lake Constance area) in May 2006, but the possibility of tick transportation from Spain was not ruled out (9).

Acrocephalus scirpaceus birds are migratory birds and live in central Europe from April to October and winter in sub-Saharan Africa in the region inhabited by *Hyalomma* spp. ticks. Therefore, it is reasonable to suggest that the *Hyalomma* spp. ticks that we examined had been transported by the birds from Africa. The fact that a randomly caught bird was infested with *R. aeschlimannii*-infected ticks is suggestive of the intensive stream of new pathogens transported through Europe by migrating birds. The first possible implication of a bird as a vector of infected ticks was proposed for *Hyalomma* spp. ticks infected by *R. sibirica*

mongolitimonae (10). Until now, the role of migrating birds in distribution of tick-borne pathogens has been poorly understood (9). The changing climate and environment in central Europe may facilitate the establishment of pathogen-carrying tick species transported by birds. These new pathogens can be directly transmitted from infected birds to the species of the local fauna.

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**Leonid Rumer, Elmara Graser,
Timo Hillebrand,
Thomas Talaska, Hans Dautel,
Oleg Mediannikov,
Panchali Roy-Chowdhury,
Olga Sheshukova,
Oliver Donoso Mantke,
and Matthias Niedrig**

Author affiliations: Robert Koch Institut, Berlin, Germany (L. Rumer, P. Roy-Chowdhury, O. Sheshukova, O. Donoso Mantke, M. Niedrig); AJInnuscree GmbH, Berlin (E. Graser, T. Hillebrand); Practice for Microbiology and Epidemiology of Infectious Diseases, Lindow, Germany (T. Talaska); IS Insect Services GmbH, Berlin (H. Dautel); and Université de la Méditerranée, Marseille, France (O. Mediannikov)

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Address for correspondence: Thomas Talaska, Facharzt für Mikrobiologie und Infektionsepidemiologie, Georg-Schacht Str 23, 15295 Brieskow-Finkenheerd, Germany; email: thomas.talaska@t-online.de

Dogs as Reservoirs for *Leishmania braziliensis*

To the Editor: I have read the review by Sousa and Pearson (1), which provides a fascinating historical account of the Great Drought and the smallpox epidemic of the 1870s and their association with the emergence of cutaneous leishmaniasis in Ceará, Brazil. In their review, the authors went back to the 19th century, remembering the hard years experienced by those who faced the Great Drought,

which prompted the immigration of thousands of persons from Ceará to the Amazon region, and a devastating smallpox epidemic, which resulted in the death of >100,000 persons. Later, they returned to the present situation of cutaneous leishmaniasis in Brazil.

I would like to address the role of dogs as reservoirs of *Leishmania (Viannia) braziliensis*. Sousa and Pearson stated that “no animal reservoir other than dogs has been identified in Ceará” and that “a sylvatic reservoir has not been identified for *L. (V.) braziliensis* in Ceará and other areas,” concluding that “dogs appear to be the most important reservoir in domestic and peridomestic transmission.”

Conversely, recent studies have indicated that rodents and other small mammals are the primary reservoirs for *L. (V.) braziliensis* (2) and that, so far, no strong evidence indicates that dogs could act as reservoirs for this parasite (3,4). The finding of dogs infected by *L. (V.) braziliensis* in leishmaniasis-endemic areas is expected because they are susceptible to this parasite and are often exposed to phlebotomine sandflies. However, this finding does not imply that dogs are important reservoirs. Indeed, they represent a poor source of *L. (V.) braziliensis* (3). For these reasons, dogs cannot be incriminated as the most important reservoirs in the domestic and peridomestic transmission cycles of *L. (V.) braziliensis*.

Filipe Dantas-Torres

Author affiliation: Università degli Studi di Bari, Bari, Italy

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Address for correspondence: Filipe Dantas-Torres, Dipartimento di Sanità Pubblica e Zootecnia, Facoltà di Medicina Veterinaria, Università degli Studi di Bari, Strada Provinciale per Casamassima km 3, 70010 Valenzano, Bari, Italy; email: f.dantastorres@veterinaria.uniba.it

In Response: We agree with most points raised by Dantas-Torres (1). However, so far our statement related to the reservoir(s) of *Leishmania (Viannia) braziliensis* (2) is correct for Ceará. Oliveira-Lima (3) conducted a case-control study that definitively incriminated dogs as a reservoir host of *L. (V.) braziliensis* in Baturite, Ceará. He showed that infected dogs in households increased the risk for infection with *L. (V.) braziliensis* by 3.2-fold among resident children. The risk increased to 6-fold when infected dogs had leishmaniasis-like skin lesions. Additionally, his observations suggested that animals other than dogs might be involved. In another study, Santana (4) examined 272 small mammals (213 rodents and 59 marsupials) in the same area; tissue culture and hamster inoculation showed none to be infected with *L. (V.) braziliensis*, although some cultures were contaminated by fungi and bacteria. On the basis of these findings, a sylvatic reservoir for *L. (V.) braziliensis* has not been identified in Baturite, Ceará. However, Brandão-Filho et al. found that rodents in Pernambuco

State, Brazil, were infected with *L. (V.) braziliensis* and stated that they were the primary reservoir (5). We concur with Lainson and Shaw (6) and conclude that information about mammalian reservoirs of *L. (V.) braziliensis* is incomplete.

Anastácio de Queiroz Sousa and Richard D. Pearson

Author affiliations: Federal University of Ceará School of Medicine, Fortaleza, Brazil (A.Q. Sousa); and University of Virginia School of Medicine, Charlottesville, Virginia, USA (R.D. Pearson)

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Address for correspondence: Anastácio de Queiroz Sousa, Departamento de Medicina Clínica, Federal University of Ceará School of Medicine, Rua Professor Costa Mendes, 1608-4º Andar, Rodolfo Teófilo, CEP 60430-140, Fortaleza, Ceará, Brazil; email: aqsousa@gmail.com