surveillance. Second, health workers at all levels should be trained to recognize the disease. Third, a detailed assessment of the extent of Buruli ulcer in the 3 counties visited as well as in other counties should be prepared. Fourth, partner/donor support for Buruli ulcer activities should be enhanced. Fifth, capacity of the National Reference Laboratory to be able to perform PCR for confirmation of Buruli ulcer cases should be expanded. Last, Buruli ulcer should be incorporated into the national surveillance system to enable better data collection.

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Author affiliations: Neglected Tropical Diseases Control Program, Monrovia, Liberia (K. Kollie, T. Mulbah); Komfo Anokye Teaching Hospital, Kumasi, Ghana (Y.A. Amoako, F. Sarfo, R. Phillips); Medical Assistance Program International West Africa Region, Abidjan, Côte d’Ivoire (J. Ake, F. Zaizay); Agogo Presbyterian Hospital, Agogo, Ghana (M. Abass); American Leprosy Missions, Greenville, South Carolina, USA (L. Lehman); Korle Bu Teaching Hospital, Accra, Ghana (A. Paintsil); World Health Organization (WHO), Monrovia (C. Lugalaa); WHO, Brazzaville, Republic of Congo (A. Tiendrebeogo); and WHO, Geneva, Switzerland (K. Asiedu)

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Address for correspondence: Yaw Amoako, Department of Medicine, Komfo Anokye Teaching Hospital, Kumasi, Ghana; email: yamoako2002@yahoo.co.uk

Candidatus Neoehrlichia mikurensis and Anaplasma phagocytophilum in Urban Hedgehogs

To the Editor: Candidatus Neoehrlichia mikurensis is a member of the order Rickettsiales, family Anaplasmataceae (1). Manifestations of infection with these bacteria are atypical and severe and include cough, nausea, vomiting, anemia, headache, pulmonary infiltration, malaise, myalgia, arthralgia, fatigue, recurrent fever for ≤8 months, and/or death (2–5). Candidatus N. mikurensis has been detected in Ixodes ovatus, I. persulcatus, and Haemaphysalis concinna ticks in Asia (1,5).

Candidatus N. mikurensis has been identified as one of the most prevalent pathogenic agents in I. ricinus ticks throughout Europe (2,3,6). Rodents of diverse species and geographic origins have been shown to carry these bacteria, but transmission experiments have not been conducted to unambiguously identify natural vertebrate reservoirs (1–3,5–7). This emerging tickborne pathogen has been detected mainly in immunocompromised patients in Sweden (n = 1), Switzerland (n = 3), Germany (n = 2), and the Czech Republic (n = 2) and in immunocompetent patients in China (n = 7) (2–5).

Anaplasma phagocytophilum is an obligate, intracellular, tickborne bacterium of the family Anaplasmataceae and causes granulocytic anaplasmosis in humans and domestic animals. In Europe, I. ricinus ticks are its major vector, and red deer, roe deer, rodents, and European hedgehogs (Erinaceus europaeus) are suspected reservoir hosts (8).

Northern white-breasted hedgehogs (Erinaceus roumanicus) are urban-dwelling mammals (order Eulipotyphla, family Erinaceidae) that serve as major maintenance hosts for the 3 stages of
**Candidatus N. mikurensis** was detected in 2 (2.3%) of 88 hedgehog tissue samples. Formerly, rodents were the only wild mammals found to act as potential reservoirs for this pathogen. Results of studies that attempted to detect these bacteria in common shrews (*Sorex araneus*), greater white-toothed shrews (*Crocidura russula*) (2,3), or common moles (*Talpa europaea*) (2) were negative. However, our results indicate that northern white-breasted hedgehogs might be a non-rodent reservoir for *Candidatus N. mikurensis*.

The low pathogen prevalence observed in this urban hedgehog population compared with that in rodents in other locations (2,3) might be caused by use of skin samples. Skin samples from rodents showed only 1.1% positivity in a study in Germany; however, average prevalence of *Candidatus N. mikurensis* in transudate, spleen, kidney, and liver samples from the same animals was 37.8%–51.1% (2). Although we did not test other organs, we hypothesize that prevalence of *Candidatus N. mikurensis* infection in urban hedgehogs is probably >2.3%.

We detected *A. phagocytophilum* in 67 (76.1%) of 88 urban hedgehogs. This prevalence was similar to that found among European hedgehogs in Germany (8). *I. ricinus* ticks are more common than *I. hexagonus* ticks in this urban hedgehog population (9). Thus, *I. ricinus* ticks can acquire these bacteria when feeding on hedgehogs and the risk for human infection with *A. phagocytophilum* in this park in Budapest is relatively high.

Neoehrlichiosis and granulocytic anaplasmosis have not been diagnosed in humans in Hungary. This finding is probably caused by diagnostic difficulties rather than absence of these pathogens in the environment. Infection with *Candidatus N. mikurensis* and *A. phagocytophilum* cause predominantly noncharacteristic symptoms. Laboratory cultivation and serologic detection of *Candidatus N. mikurensis* has not been successful, and this pathogen has not been identified in blood smears. Thus, accurate diagnosis of suspected cases requires suitable molecular methods.

Parks can be considered points of contact for reservoir animals, pathogens, ticks, and humans. Our results indicate that *E. rossicus* hedgehogs play a role in urban ecorepidemiology of ≥2 emerging human pathogens. To better understand the urban cycle of these pathogens, potential reservoir hosts, ticks collected from these hosts, and vegetation in parks should be investigated.

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**Gábor Földvári,**
**Setareh Jahafari,** **Krisztina Rigó,**
**Mónika Jablonszky,**
**Sándor Szekeres,**
**Gábor Majoros,** **Mária Tóth,**
**Viktor Molnár,** **Elena C. Coipan, and Hein Sprong**

Author affiliations: Szent István University Faculty of Veterinary Science, Budapest, Hungary (G. Földvári, K. Rigó, M. Jablonszky, S. Szekeres, G. Majoros, V. Molnár); National Institute of Public Health and Environment, Bilthoven, the Netherlands (S. Jahafari, E.C. Coipan, H. Sprong); Hungarian Natural History Museum, Budapest (M. Tóth); and Budapest Zoo and Botanical Garden, Budapest (V. Molnár)

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References


Address for correspondence: Gábor Földvári, Faculty of Veterinary Science, Szent István University, 2 István St, Budapest H-1078, Hungary; email: foldvargar@gmx.de

Rickettsia and Vector Biodiversity of Spotted Fever Focus, Atlantic Rain Forest Biome, Brazil

To the Editor: Rickettsia rickettsii, R. felis, and R. parkeri, strain Atlantic rainforest, have been characterized after being found in areas to which Brazilian spotted fever (BSF) is endemic (1,2), which indicates the complexity of their epidemic and endo-zootic cycles. The Atlantic rain forest is one of the largest and richest biomes of Brazil, and antropic action has intensely influenced its transformation. Most BSF cases and all BSF-related deaths are recorded in this biome area.

Many BSF cases were recorded in Pará State of Brazil, one of the most urbanized and industrialized areas of Brazil. To better understand arthropod and Rickettsia diversity in this area, we analyzed 2,076 arthropods from Rio de Janeiro state, Atlantic rain forest biome.

During October 2008–November 2009, we collected ticks and fleas from hosts and environments in 7 cities where high numbers of BSF cases were recorded (Rio de Janeiro State Health Secretary, unpub. data) and where fi-siogeographic characteristics differed. After morphologic classification (3), the arthropods were individually separated or grouped by sex, developmental stage, and host for total DNA extraction (4).

We used 2 Rickettsia-specific primer sets (CS2–78/CS2–323 and CS4–239/CS4–1069) to amplify 401 bp and 834 bp, respectively, of the citrate synthase gene (gltA) (5,6). Presumptive Rickettsia-positive samples were tested for spotted fever group (SFG)–specific primer set Rr190.70p/Rr190.602n for 532 bp from the ompA gene (7). R. rickettsii DNA and bi-distilled water were used as positive and negative controls, respectively. PCR products were purified (NucleoSpin Extract II kit; Macherey-Nagel, Düren, Germany), cloned (pTZ57R/T; Fermentas-Thermo Fisher Scientific, Waltham, MA, USA), and sequenced by using specific vector primer sets (BigDye Reaction kit, Applied Biosystems, Foster City, CA, USA). Sequences were edited by using SeqMan program (Lasergene 10.1; DNASTAR Inc., Madison, WI, USA), and similarities were obtained by using BLAST analysis (http://blast.ncbi.nlm.nih.gov). The phylogenies were assessed by applying neighbor-joining and maximum parsimony methods, with the Kimura 2-parameter correction model. We used ClustalW 2.1 (www.clustal.org) to align sequences and produced phylogenetic trees by using 1,000 replicates bootstrap in MEGA 5.0 software (www.megasoftware.net).

We collected and analyzed ticks of the following species: Amblyomma cajennense (1,723 ticks), Rhic太平-ius sanguineus (109), Anocentor nitans (63), Boophilus microplus (33), Amblyomma aureolatum (2), and Amblyomma dubitatum (2). We collected and analyzed Ctenocephalides felis (143 fleas) and C. canis (1) fleas.

PCR analysis showed Rickettsia DNA in 11 individual or pooled samples. This finding indicated minimal infection rates of 0.2% (4/1,723) for A. cajennense ticks, 50% (2/4) for A. dubitatum ticks, 3.0% (1/33) for B. microplus ticks, 100% (1/1) for C. canis fleas, and 2.8% (4/143) for C. felis fleas. Expected amplicon size, determined by using the gltA 401-bp primer set, was observed for all positive samples. Two were also positive by PCR.