

Borrelia, *Anaplasma*, filariae, *Treponema pallidum*, hepatitis viruses (A, B, and C), HIV, and dengue virus. Treatment for babesiosis was continued for another 14 days, after which PCR results were negative and the patient's general condition had clearly improved. One year later, PCRs indicated that she was still free of *Babesia* parasites.

We do not have solid evidence of the source of this patient's babesiosis. Every year since 2001, she spent a week in rural areas in Spain, where at least 1 case of human babesiosis caused by *B. microti* (also "Munich" type) has been recorded (7). However, initial symptoms occurred while the patient was in Equatorial Guinea, having arrived there several months earlier from Valencia, Spain, where the *B. microti* vectors in Europe, *Ixodes ricinus* ticks, are not known to occur. However, no data are available on the presence of *Ixodes* ticks or of vertebrate reservoirs infected with *B. microti* in Equatorial Guinea. This lack of information, together with the fact that the patient traveled to different locations inside and outside Africa, makes it difficult to determine whether the infection was acquired in Equatorial Guinea. In such regions, where infrastructure and resources are limited, molecular and serologic diagnostic methods are usually lacking, and diagnoses of febrile diseases are based on symptoms, physical findings at examination, and microscopy. These limitations, and the similarities between malaria and babesiosis, are sufficient to explain why this patient's babesiosis was initially misdiagnosed as malaria. Because of this misdiagnosis, the patient was treated for malaria 6 times over 8 months. An accurate diagnosis and appropriate treatment for babesiosis was necessary to end this sequence of mistakes. Increased awareness of the possibility of babesiosis, together with appropriate diagnosis, may result in the discovery of more cases of babesiosis in malaria-endemic areas.

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About the Author

Dr. Arsuaga is a medical doctor at the Hospital Universitario La Paz-Carlos III, Madrid, Spain. Her primary research interests include tropical infection diseases and bloodborne parasites.

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Address for correspondence: Estrella Montero, Centro Nacional de Microbiología, Instituto de Salud Carlos III, Carretera Majadahonda-Pozuelo, Km 2,2, Majadahonda, Madrid 28220, Spain; email: estrella.montero@isciii.es

***Paenibacillus assamensis* in Joint Fluid of Man with Suspected Tularemia, China**

Enmin Zhang,¹ Hongchao Lu,¹ Qihong Liu, Zhigang Tang, Duanjun Li, Lin Jiang, Qisheng He, Niu Pan, Yanhua Wang

Author affiliations: Chinese Center for Disease Control and Prevention, Beijing, China (E. Zhang, Y. Wang); Center for Disease Prevention and Control of Qianxinan Prefecture of Guizhou Province, Xingyi, China (H. Lu, Q. Liu, Z. Tang, L. Jiang, Q. He, N. Pan); Hospital of Traditional Chinese Medicine of Qianxinan Prefecture, Xingyi (D. Li)

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¹These authors contributed equally to this article.

Paenibacillus assamensis is a bacterium usually found in warm springs. We detected *P. assamensis* in a man with suspected tularemia. The strain isolated from the man's knee joint fluid was identified as *P. assamensis* after analysis of a homologous sequence of the 16S rRNA gene.

The genus *Paenibacillus* comprises >89 species. Some of these are pathogens in honeybees or other invertebrates; others are occasional opportunistic pathogens in humans (1,2). Bacteria belonging to the genus *Paenibacillus* have been isolated from various environments, such as soil, water, rhizospheres, vegetable matter, forage, and insect larvae, as well as from clinical samples (3). Tularemia, caused by the gram-negative intracellular pathogen *Francisella tularensis*, is highly virulent in humans and animals. An isolate from the joint fluid of a man in China in whom suspected tularemia was diagnosed recently was identified as *Paenibacillus assamensis*, a species usually found in warm springs.

A 44-year-old farmer was admitted to the surgical department of the Hospital of Traditional Chinese Medicine of Qianxinan Prefecture (Xingyi, China) on June 28, 2016. He had swelling and aching in his left knee that had appeared without an obvious cause and lasted for ≈6 months (Figure, panel A). He denied being bitten by a mosquito or other insect. Moreover, he had no contact with any animal before onset. In January 2016, he was admitted to the local county hospital for fever, cough, and pectoralgia. An antituberculosis regimen was started 3 days later. After he took the prescribed medicine for 15 days, his left knee began to swell and ache, accompanied by limitation of movement. However, no improvement was evident after drug withdrawal.

His body temperature fluctuated from 36.0°C to 36.8°C. A semisolid mass of 9.7 × 2.1 cm² was detected on ultrasound examination 0.4 cm from the left popliteal fossa to the subcutaneous surface. No acid-resistant bacilli

were detected in the articular puncture fluid, which was inoculated using blood plate media. Gray migratory colonies of gram-negative bacteria appeared after 2 days. The presumptive identification of the isolate using the gram-negative card on the VITEK 2 Compact System (bioMérieux, St. Louis, MO, USA) was *F. tularensis*. A Cystine heart agar enriched with chocolate erythrocyte medium was inoculated with the isolate, and gray opaque colonies ≈1 mm in diameter emerged after 2 days (Figure, panel B). The latex-agglutination test showed that the fresh strain and the patient's serum were negative for *F. tularensis*-specific antigens and antibodies.

We amplified the 16S rRNA gene of the bacterial genomic DNA using 2 universal bacterial primers, 27f and 1492r (4). Next, a 1,379-nt continuous stretch (GenBank accession no. MG847149) was obtained by 2-way sequencing of high-quality amplicons, which we used as a query to search for homologous sequences in the GenBank database. The query coverage was 100%, and the highest consistent sequence was that of *P. assamensis* strain GPTSA 11 16S rRNA gene. We further amplified the 16S rRNA gene of the patient's DNA using another pair of primers, 8–27f and 1500r (5). The highest consistent sequence obtained this time was 1,429 nt (GenBank accession number MG847150), still in the 16S rRNA gene of *P. assamensis* strain GPTSA 11. The analysis of the sequences indicated that the 2 amplicons contained the consensus signature sequence stretches PAEN 515F (6) and PAEN 862F (7), which are mostly found among different species within the genus *Paenibacillus*.

The local hospital detected *F. tularensis* in the patient with suspected tularemia on the basis of PyrA-positive results using the VITEK 2 Compact System. No recent studies have reported the association between PyrA and *F. tularensis*. The biochemical tests also showed that the strain could

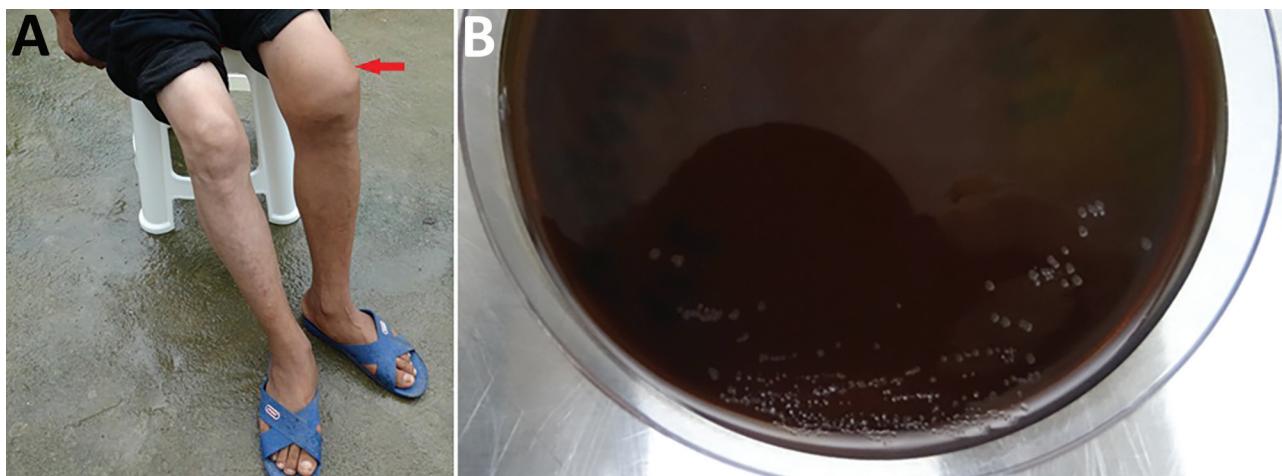


Figure. Patient from whom *Paenibacillus assamensis* was isolated from knee joint fluid, China, 2016. A) Left knee joint of the patient was obviously swollen (arrow). B) *P. assamensis* isolated from the patient's articular fluid appeared on chocolate erythrocytes. A color version of this figure is available online (<https://wwwnc.cdc.gov/EID/article/24/8/18-0260-F1.htm>).

not ferment glucose and maltose. However, *F. tularensis* type A and type B are capable of fermenting glucose and maltose (8). Moreover, *F. tularensis*-specific antigen and antibody tests did not confirm that this strain was *F. tularensis* (9).

Both amplicons of the patient's 16S rRNA gene contained PAEN 515F and PAEN 862F signature sequences. After searching the homologous sequence of the 2 amplicons, the 16S rRNA gene sequence of *P. assamensis* GPTSA 11 displayed higher homology. Therefore, we concluded that the bacterium isolated from the patient's joint fluid was not *F. tularensis* but *P. assamensis*.

In 2005, a new species of *Paenibacillus* named *P. assamensis* GPTSA 11 was isolated from a warm spring in Assam, India (10). Since then, *P. assamensis* had not been isolated from other environments or patients. Our findings emphasize the need to consider new approaches for preventing infection in the environments where *P. assamensis* exists.

This patient remained at home to recuperate because of his obscure symptoms and financial constraints, but his symptoms did not abate until the follow-up in July 2017. He was advised to return to the hospital for treatment with drugs targeting *P. assamensis*. Isolation of *P. assamensis* from the living and working environments of patients, including soil and water, can successfully reveal the source of infection.

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About the Author

Dr. Zhang is a microbiologist at the Chinese Centers for Disease Control and Prevention in Beijing. His research interests include the molecular epidemiology and control of bacterial zoonoses.

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Address for correspondence: Yanhua Wang, National Institute for Communicable Disease Control and Prevention, Chinese Center for Disease Control and Prevention, PO Box 5, Beijing 102206, China; email: wangyanhua@icdc.cn

Plasmodium falciparum Plasmepsin 2 Duplications, West Africa

Juliana Inoue,¹ Miguel Silva,¹ Bakary Fofana, Kassim Sanogo, Andreas Mårtensson, Issaka Sagara, Anders Björkman, Maria Isabel Veiga, Pedro Eduardo Ferreira, Abdoulaye Djimde, José Pedro Gil

Author affiliations: Uppsala University, Uppsala, Sweden (J. Inoue, A. Mårtensson, J.P. Gil); University of Minho, Braga, Portugal (M. Silva, M.I. Veiga, P.E. Ferreira); University of Science, Techniques, and Technologies of Bamako, Bamako, Mali (B. Fofana, K. Sanogo, I. Sagara, A. Djimde); Karolinska Institutet, Stockholm, Sweden (A. Björkman, J.P. Gil); Universidade de Lisboa, Lisbon, Portugal (J.P. Gil)

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¹These authors shared first authorship on this article.