LETTERS

are a dominant species in the study area and usually parasitize a variety of wild and domestic animals. These ticks often feed on humans as alternative hosts. Because this *Roseomonas* sp. is not a common pathogen, its role in public health and veterinary medicine is unknown.

Phenotypic characterization of the isolates indicated similarities with previously reported *Roseomonas* spp. Phylogenetic analysis showed that the novel *Roseomonas* sp. is closely related to *R. cervicalis*, which was isolated from a cancer patient. Our isolates also differed from 2 reported strains isolated from freshwater lake sediment in Jiangsu Province, China (9) and from soil in Fujian Province, China (10). This result indicated the species diversity of the genus *Roseomonas*, which might be related to different bacterial origins. Because of the unique biochemical characteristics, antimicrobial drug susceptibilities, and novel isolation source of our isolates, the pathogenesis of this organism should be investigated.

Acknowledgment

We are grateful to Xiang Y. Han for critically reading the manuscript.

This study was supported by National Natural Science Foundation of China (grant 30600506), the National Science Fund for Distinguished Young Scholars (grant 30725032), and Beijing Technology New Star (grant 2007A066).

Wei Liu,1 Fang Zhang,1 Er-Chen Qiu, Jun Yang, Zhong-Tao Xin, Xiao-Ming Wu, Fang Tang, Hong Yang, and Wu-Chun Cao

Author affiliations: Beijing Institute of Microbiology and Epidemiology, Beijing, People’s Republic of China (W. Liu, F. Zhang, E.-C. Qiu, X.-M. Wu, H. Yang, W.-C. Cao); Chinese People’s Armed Police Force Center for Disease Control and Prevention, Beijing (J. Yang, F. Tang); and Chinese National Human Genome Center, Beijing (Z.-T. Xin)

DOI: 10.3201/eid1607.090166

References

1. Rihs JD, Brenner DJ, Weaver RE, Steigerwald AG, Hollis DG, Yu VL. *Roseomonas*, a new genus associated with bacteremia and other human infections. J Clin Microbiol. 1993;31:3275–83.

2. Christakis GB, Perlorenzou S, Alexaki P, Megalakaki A, Zarkadis IK. Central line–related bacteremia due to *Roseomonas mucosa* in a neutropenic patient with acute myeloid leukemia in Piraeus, Greece. J Med Microbiol. 2006;55:1153–6. DOI: 10.1099/jmm.0.46634-0

3. De I, Rolston KV, Han XY. Clinical significance of *Roseomonas* species isolated from catheter and blood samples: analysis of 36 cases in patients with cancer. Clin Infect Dis. 2004;38:1579–84. DOI: 10.1086/420824

4. McLean TW, Rooster-Stevens K, Woods CR, Shetty AK. Catheter-related bacteraemia due to *Roseomonas* species in pediatric hematology/oncology patients. Pediatr Blood Cancer. 2006;46:514–6. DOI: 10.1002/pbc.20339

5. Sipsas NV, Papaparaskevas J, Stefanou I, Kalatzis K, Vlachoyiannopoulos P, Avlamis A. Septic arthritis due to *Roseomonas mucosa* in a rheumatoid arthritis patient receiving infliximab therapy. Diagn Microbiol Infect Dis. 2006;55:343–5. DOI: 10.1016/j.diagmicrobio.2006.01.028

6. Shokar NK, Shokar GS, Islam J, Cass AR. *Roseomonas gilardi* infection: case report and review. J Clin Microbiol. 2002;40:4789–91. DOI: 10.1128/JCM.40.12.4789-4791.2002

7. Qiu EC, Zhang F, Liu W, Wu XM, Cao WC. Isolation and identification of *Roseomonas* spp. from ticks [in Chinese]. Wei Sheng Wu Xue Bao. 2000;38:456–7.

8. Bibashi E, Sofianou D, Kontopoulo K, Mitsopoulou E, Kokolina E. Peritonitis due to *Roseomonas fauriae* in a patient undergoing continuous ambulatory peritoneal dialysis. J Clin Microbiol. 2000;38:456–7.

9. Jiang CY, Dai X, Wang BJ, Zhou YG, Liu SJ. *Roseomonas lacus* sp. nov., isolated from freshwater lake sediment. Int J Syst Evol Microbiol. 2006;56:25–8. DOI: 10.1099/ijs.0.63938-0

10. Jiang YJ, Deng YJ, Liu XR, Xie BG, Hu FP. Isolation and identification of a bacterial strain JS018 capable of degrading several kinds of organophosphate pesticides [in Chinese]. Wei Sheng Wu Xue Bao. 2006;46:463–6.

Address for correspondence: Wu-Chun Cao, Beijing Institute of Microbiology and Epidemiology, State Key Laboratory of Pathogen and Biosafety, 20 Dong-Da St, Fengtai District, Beijing 100071, People’s Republic of China; email: caowc@nic.bmi.ac.cn

Misidentifcation of *Mycobacterium kumamotonense* as *M. tuberculosis*

To the Editor: Because of slow growth of mycobacteria, use of rapid tests to identify them is strongly recommended; rapid tests are widely used as an advanced diagnostic tool in clinical laboratories (1,2). These tests are particularly useful for diagnosing extrapulmonary mycobacterioses and identifying unusual mycobacteria as etiologic agents (3). Commercial probes are frequently used for rapid and specific identification of mycobacteria, especially *Mycobacterium tuberculosis* complex. However, cross-reactivity of DNA probes between mycobacterial species could result in incorrect diagnosis and treatment of patients (4,5). Misidentification could be a problem if a newly described species, such as *M. kumamotonense* (6), were an etiologic agent of a disease.

In July 2006, we obtained a fine-needle, puncture aspiration biopsy specimen from a cervical lymph node of a 30-year-old man at Doce de Octubre Hospital (Madrid, Spain). The patient was a recent immigrant from Paraguay and was HIV positive (C2 stage of infection). A biopsy specimen from a cervical lymph node showed necrotizing granulomatous lymphadenopathy. A computed tomographic scan showed cervico-thoraco-abdominal, multiple cervical,
supravacular, axillary, paratracheal, and mediastinal lymphadenopathies. The patient had a CD4 cell count of 219 cells/mm² and an HIV viral load of 197,181 copies/mL.

The aspiration sample was positive for acid-fast bacilli by fluorescent staining. The clinical isolate (designated 1369) obtained from the aspiration sample was grown in liquid media (MGIT Diagnostic Kit; Becton Dickinson Diagnostics, Sparks, MD, USA) and identified as M. tuberculosis complex by using the AccuProbe System (bioMérieux, Marcy l’Étoile, France).

A diagnosis of lymphoid tuberculosis was made, and the patient was treated with isoniazid, rifampin, ethambutol, and pyrazinamide. After 1 month, rifampin was withdrawn because of a cutaneous exanthem. Three months later, the clinical status of the patient had improved, fever had disappeared, and sizes of cervical and axillary lymph nodes had decreased. Treatment with tenofovir, emtricitabine, and lopinavir/ritonavir was started. Two weeks later, an immune reconstitution syndrome and adenopathies developed, but these resolved in 1 month.

Five months after treatment was started, susceptibility testing in a reference laboratory showed that isolate 1369 was M. kumamonotense. The isolate showed 100% identity with the 16S rRNA gene sequence of M. kumamonotense (GenBank accession no. AB239925). Results of PCR restriction analysis of heat shock protein 65 gene (7) (http://app.chuv.ch/prasite/index.html) were consistent with those for M. kumamonotense. The isolate was susceptible to ethambutol, rifampin, cycloserine, and ethionamide and resistant to isoniazid, streptomycin, pyrazinamide, and kanamycin.

Because of the improvement in the clinical status of the patient, treatment continued without modification for 18 months. At this time, his CD4 cell count was 488 cells/mm² and his HIV viral load was ≤50 copies/mL. In July 2009, the patient was asymptomatic and had a CD4 cell count of 631 cells/mm² and an HIV viral load ≤50 copies/mL.

To confirm misidentification of M. kumamonotense as a member of the M. tuberculosis complex, other commercial probes were tested. Isolate 1369 was also misidentified as M. tuberculosis complex by Inno-LIPA v2 (Innogenetics, Ghent, Belgium). The isolate was identified as Mycobacterium sp. by Geno-Type (Hain Lifescience, Nehren, Germany). The 3 commercial probes we used had different genome region specificities, all in the mycobacterial ribosomal operon. The AccuProbe System was specific for 16S rDNA, Inno-LIPA v2 was specific for internal transcribed spacer 1, and Geno-Type was specific for 23S rDNA. Only Geno-Type did not show cross-reactivity between M. tuberculosis complex and M. kumamonotense. The clinical isolate was identified as M. kumamonotense, a new, slow-growing mycobacterium that was first isolated from an immunocompetent patient in Japan (6). We showed that this species caused extrapulmonary disease in an HIV-positive patient.

Misidentification of M. kumamonotense as M. tuberculosis complex by commercial DNA probes has serious clinical implications. Once a patient is given a diagnosis of tuberculosis, he or she will be treated with specific drugs for a long period and be prone to adverse side effects. Furthermore, M. kumamonotense is resistant to many drugs used during typical treatment. After a diagnosis of tuberculosis, patient contacts need to be investigated to identify new cases. Emerging mycobacterial pathogens, such as M. kumamonotense, may also cause pulmonary and extrapulmonary infections that are also caused by other members of this genus and could be misidentified as M. tuberculosis.

This study was supported by the European Community Seventh Framework Programme (FP7-HEALTH-2007) under grant agreement no. 200999, and by the Spanish Network for Research in Infectious Diseases (RD06/008/0011).

Almudena Rodríguez-Aranda, María S. Jiménez, Jesús Yubero, Fernando Chaves, Rafael Rubio-García, Elia Palenque, María J. García, and M. Carmen Menéndez

Author affiliations: Hospital Universitario Doce de Octubre, Madrid, Spain (A. Rodríguez-Aranda, F. Chaves, R. Rubio Garcia, E. Palenque); Instituto de Salud Carlos III, Madrid (M.S. Jiménez); and Universidad Autónoma de Madrid, Madrid (J. Yubero, M.J. García, M.C. Menéndez)

DOI: 10.3201/eid1607.091913

References

1. Musial CE, Tice LS, Stockman L, Roberts GD. Identification of mycobacteria from culture by using the Gen-Probe Rapid Diagnostic System for Mycobacterium avium complex and Mycobacterium tuberculosis complex. J Clin Microbiol. 1988;26:2120–3.
2. Tortoli E, Nanetti A, Piersimoni C, Cicero P, Farina C, Mucignat G, et al. Performance assessment of new multiplex probe assay for identification of mycobacteria. J Clin Microbiol. 2001;39:1079–84. DOI: 10.1128/JCM.39.3.1079-1084.2001
3. Jarzembski JA, Young MB. Nontuberculous mycobacterial infections. Arch Pathol Lab Med. 2008;132:1333–41.
4. Butler WR, O’Connor SP, Yakrus MA, Gross WM. Cross-reactivity of genetic probe for detection of Mycobacterium tuberculosis with newly described species Mycobacterium celatum. J Clin Microbiol. 1994;32:536–8.
5. Lefmann M, Moter A, Schweickert B, Gobel UB. Misidentification of Mycobacterium leprae as Mycobacterium intracellulare by the COBAS AMPLI-COR M. intracellulare test. J Clin Microbiol. 2005;43:1928–9. DOI: 10.1128/JCM.43.4.1928-1929.2005
6. Masaki T, Ohkusu K, Hata H, Fujisawa N, Iihara H, Yamada-Noda M, et al. Mycobacterium kunamotoense sp. nov. recovered from clinical specimen and the first isolation report of Mycobacterium arupense in Japan: novel slowly growing, nonchromogenic clinical isolates related to Mycobacterium tave complex. Microbiol Immunol. 2006;50:889–97.

7. Telenti A, Marchesi F, Balz M, Bally F, Böttger EC, Bodmer T. Rapid identification of mycobacteria to the species level by polymerase chain reaction and restriction enzyme analysis. J Clin Microbiol. 1993;31:175–8.

Address for correspondence: M. Carmen Menéndez, Department of Preventive Medicine, Public Health and Microbiology, School of Medicine, Autonoma University of Madrid, St/ Arzobispo Morcillo s/n 28029, Madrid, Spain; email: carmen.menendez@uam.es

**Mycobacterium conceptionense Infection after Breast Implant Surgery, France**

To the Editor: Mycobacterium fortuitum complex members are rapidly growing mycobacteria found in water and soil (1). These opportunistic pathogens are responsible for posttraumatic skin and soft tissue infections. They also account for 60%–80% of postsurgical wound infections caused by rapidly growing mycobacteria (2), particularly after breast surgery (with or without prosthetic implants) (3). *M. conceptionense*, an emerging member of the *M. fortuitum* complex, was initially described in a case of osteomyelitis that occurred after an open fracture of the tibia (4). We report a case of *M. conceptionense* infection that occurred after breast surgery.

A woman 58 years of age had a left mastectomy with lymph node dissection and chemotherapy for breast carcinoma in March 2004. Three years later, she underwent breast reconstruction that used a cutaneousomuscular latissimus dorsi flap with a prosthetic implant. Immediately after surgery, a fever (39°C) developed, but 3 blood cultures remained sterile. No treatment was administered, and she became afebrile within 3 days.

At day 15 after surgery, a serous discharge appeared in the tip of the skin flap. By day 21, the patient was again febrile, and the wound discharge was swabbed for analysis. On day 27, she underwent surgical revision with ablation of the breast implant, drainage, and sample collection. The leukocyte count was normal. However, the C-reactive protein level was 99 mg/L, and the erythrocyte sedimentation rate was 111 mm (first hour). Treatment with intravenous amoxicillin/clavulanic acid was started. Although the biologic parameters normalized, the serous discharge continued. Microscopic examination of specimens from days 21 and 27 yielded no bacteria in Gram- and Ziehl-Nielsen–stained pus specimens, and standard bacteriologic cultures remained sterile. *M. conceptionense*, identified by partial *rpoB* gene sequencing (100% identity with GenBank accession no. AY859695.1) (4), grew in both specimens after 8 days of incubation at 37°C under a 5% CO₂ atmosphere in Coletsos medium (bioMérieux, La Balme-les-Grottes, France). By the Etest method (4), both isolates were susceptible to several antimicrobial drugs, including clarithromycin, amikacin, ciprofloxacin, and doxycycline. The patient was treated with ciprofloxacin, azithromycin, and amikacin for 3 weeks, followed by ciprofloxacin and azithromycin for 4 weeks.

At patient’s relapse 3 months later, *M. conceptionense* exhibiting identical antimicrobial drug susceptibility pattern was again isolated from the wound fluid. The patient was then treated with ciprofloxacin, azithromycin, and doxycycline for 6 months; subsequently, doxycycline alone was given for a total of 18 months. Results from the 2-month follow-up examination were unremarkable.

*M. conceptionense* was unambiguously identified by partial *rpoB* gene sequencing, a first-line tool for accurate identification of nontuberculous mycobacteria (5). A pathogenic role for *M. conceptionense* was supported by 1) its repetitive isolation from the wound;

---

**Table. Three cases of *Mycobacterium conceptionense* infection in female patients**

| Patient age, y | Clinical situation                   | Identification          | Treatment                                                                 | Nature | Duration, mo | Reference |
|----------------|-------------------------------------|-------------------------|---------------------------------------------------------------------------|--------|--------------|----------|
| 31             | Posttraumatic osteitis              | 16S rRNA, sodA, hsp65, recA, rpoB† | Antimicrobial drug therapy: AMC                                           |        | 3            | (4)      |
| 43             | Subcutaneous abscess without trauma | partial 1,464-bp 16S rRNA gene† | Surgery and antimicrobial drug therapy: COT and CLA; then DOX and CLA; then LIN and CLA |        | 5            | (10)     |
| 58             | Breast implant infection           | rpoB§                    | Surgery and antimicrobial drug therapy: CIP and AZY; then CIP, AZY, and DOX |        | 18           | This report |

*AMC, amoxicillin/clavulanic acid; COT, cotrimoxazole; CLA, clarithromycin; DOX, doxycycline; LIN, linezolid; CIP, ciprofloxacin, AZY, azithromycin. The outcome for all 3 patients was favorable.*

†GenBank accession nos.: 16S rRNA, AY859684; rpoB, AY859695; hsp65, AY859678; sodA, AY859708; recA, AY859690.

‡GenBank accession no. AM884289.1.

§GenBank accession no. AY859695.1.