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 unkown.

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.

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Misidentification 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,

supraclavicular, axillar, paratracheal, and mediastinal lymphadenopathies. The patient had a CD4 cell count of 219 cells/mm^3 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 aspirate 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'Etoile, 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. kumamotonense*. The isolate showed 100% identity with the 16S rRNA gene sequence of *M. kumamotonense* (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. kumamotonense*. 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/mm^3 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/mm^3 and an HIV viral load ≤50 copies/mL.

To confirm misidentification of *M. kumamotonense* 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. kumamotonense*. The clinical isolate was identified as *M. kumamotonense*, 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. kumamotonense* 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. kumamotonense* 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. kumamotonense*, may also cause pulmonary and extrapulmonary infections that are also caused by other members of this genus and could be misidentified as *M. tuberculosis*.

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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 cutaneomuscular 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 *rpo*B 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% CO_2 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, azythromycin, and amikacin for 3 weeks, followed by ciprofloxacin and azythromycin 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, azythromycin, 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		Reference
			Nature	Duration, mo	
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	*rpo*B§	Surgery and antimicrobial drug therapy: CIP and AZY; then CIP, AZY, and DOX; then DOX	18	This report

*AMC, amoxicillin/clavulanic acid; COT, cotrimoxazole; CLA, clarithromycin; DOX, doxycycline; LIN, linezolid; CIP, ciprofloxacin, AZY, azythromycin. 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.