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Mycobacteriology

A new *Microbacterium* species isolated from the blood of a patient with fever: *Microbacterium pyrexiae* sp. nov.

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Abstract

A Gram-positive bacterium, SMC-A8265^T, which was isolated from the blood of a patient with fever but could not be identified by a conventional microbiologic method, was finally characterized by performing phenotypic and genotypic analyses. 16S rRNA gene sequence analysis revealed that the strain SMC-A8265^T belonged to the genus *Microbacterium*, but it did not correspond to any of the previously described *Microbacterium* spp. Biochemical tests and cellular fatty acid composition analysis also confirmed that this bacterium is distinct from other *Microbacterium* spp. Based on the phenotypic and genotypic characteristics, we propose that the strain SMC-A8265^T should be classified as a new species, namely, *Microbacterium pyrexiae* sp. nov.

Keywords: *Microbacterium*; Novel species; 16S rRNA gene

1. Introduction

The genus *Microbacterium* is generally classified as corynebacterium Centers for Disease Control and Prevention group A-5 or A-5 (Alonso-Echanove et al., 2001), and account for the majority of yellow-pigmented coryneform bacteria that have been isolated from diverse environments (Funke et al., 1995; Funke and Bernard, 2003). To date, about 40 *Microbacterium* spp. have been validated according to the "List of Prokaryotic Names with Standing in Nomenclature" by J.P. Euzéby (http://www.bacterio.cict.fr/), but only a few have been demonstrated to be of clinical importance. Only a small number of species proved to be the causative agent of the infection, not only for sporadic infections, but also for nosocomial outbreaks of bacteremia by the *Microbacterium* spp. (Alonso-Echanove et al., 2001). Outbreaks of *Microbacterium* sepsis among cancer patients have indicated its potential for causing morbidity and mortality in immunocompromised patients, and this suggests the potential for nosocomial dissemination (Alonso-Echanove et al., 2001). Catheter-related *Microbacterium* bacteremias have also been recently reported (Laffineur et al., 2003; Lau et al., 2002).

In this article, we report on a novel *Microbacterium* spp. that was isolated from the blood of a patient with a fever. This bacterium could not be identified by conventional methods. Comparative 16S rRNA gene sequence analysis showed that it belongs to the *Microbacterium* spp., but it did not correspond to any of the previously characterized species.

2. Materials and methods

2.1. Case

A 33-year-old woman was admitted to the hospital because of a fever she had experienced for the previous 3 weeks. The patient had been doing well until 3 weeks before admission, when she began to have a fever and chills. The results of the laboratory tests that had been performed in

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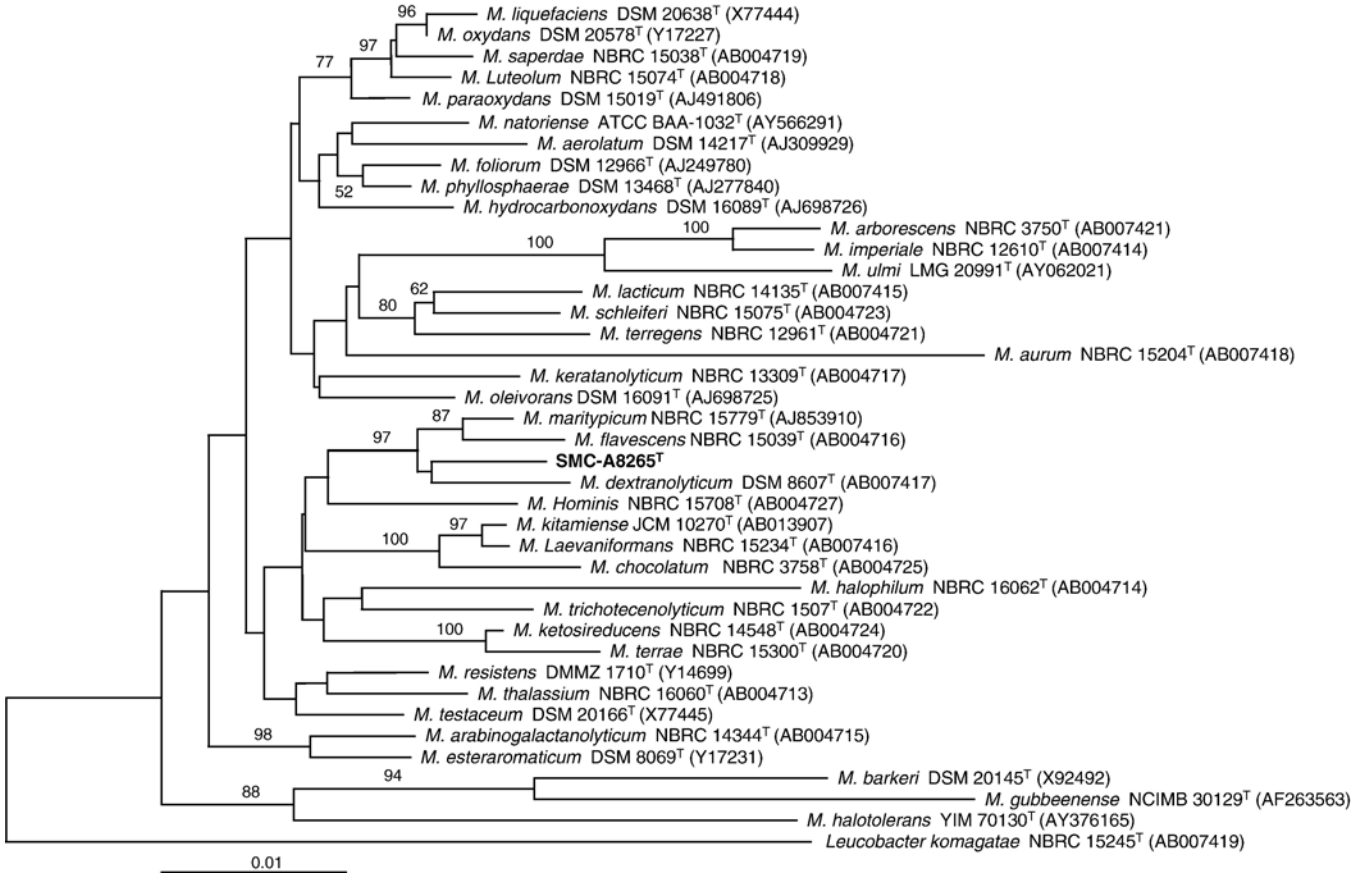

Fig. 1. Phylogenetic relationships of *M. pyrexiae* sp. nov. SMC-A8265^T and other *Microbacterium* spp. inferred from 16S rRNA gene sequences. *Leucobacter komagatae* NBRC 15245^T was used as an outgroup. Numbers on branches are percentages of 1000 bootstrap replications. Only values of > 50% are indicated. Scale bar represents 1 substitution per 100 nucleotides.

another hospital 2 weeks before admission were all within the normal ranges. She had undergone a discectomy at L5-S1 6 years ago because of a herniated intervertebral disc. On admission, the physical examination revealed a temperature of 38.2 °C without any obvious evidence of infection. The laboratory data, chest radiograph, and computed tomography of the abdomen were all within normal ranges. All 3 sets of blood cultures performed on admission were negative. On the 10th hospital day, she suddenly developed involuntary movements of the left-sided face and both lower legs, which were aggravated by the high fever, and this partially responded to benzodiazepine. However, the results of the neurologic examination, the cerebrospinal fluid study, the magnetic resonance imaging of the brain, and the electroencephalography were within the normal ranges. On the 55th hospital day, intermittent high-grade fever still persisted, and the patient's condition became worse than ever.

One set of blood cultures performed at that time grew a Gram-positive bacilli (SMC-A8265^T) that turned out later as *Microbacterium* sp. nov. On the 27th hospital day, 1 set of repeated blood cultures also grew Gram-negative bacilli (SMC-438-3), which were later identified as *Arcobacter butzleri*. She was treated empirically with vancomycin (2 g/day) and meropenem (3 g/day). Thereafter, the results of the subsequent blood cultures were negative and the patient became afebrile. On the 37th hospital day, when she again developed fever, all the sets of repeated blood cultures were negative. However, a subsequent course of antibiotic therapy was interrupted because of the possibility of drug fever. On the 45th hospital day, she left from the hospital against medical advice despite persistent fever. After discharge, defeverscence occurred spontaneously, and she has been doing well without fever for the next 3 months.

2.2. Bacterial isolates

Two bacterial isolates (SMC-A8265^T and SMC-438-3), which were from the blood of the patient, could not be identified by the conventional microbiologic methods such as VITEK (bioMérieux, Hazelwood, MO) and Microscan (Dade-Microscan, Sacramento, CA). To identify them, we performed phenotypic characterization, 16S rRNA gene sequencing, and cellular fatty acid (CFA) analysis.

2.3. 16S rRNA gene sequencing

For the 16S rRNA gene sequence analysis, genomic DNA was extracted from bacterial colonies by a simple