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Human Case of Atopobium rima Bacteremia

To the Editor: The genus Atopobium (1) accommodates species formerly designated Lactobacillus minutus, L. rima, and Streptococcus parvalus (2). Use of 16S rDNA sequence analysis showed these species to be closely related and to form a distinct line of descent within the lactic acid bacteria (3). Atopobium spp. usually have been recognized as part of the human gingival oral flora; some species, including A. rima and A. parvulum, have been identified as agents of chronic periodontitis (4,5). A. rima, formerly known as L. rima (1), forms short, gram-positive, strictly anaerobic, elliptical bacteria with low G+C content (4). A. rima produces large amounts of lactic acid and has been recovered previously from normal human gingival flora (4,5). Apart from periodontitis, it has not been implicated in other types of infection. We report an unusual case of A. rima bacteremia.

In May 2007, a 77-year-old woman with a history of right thoracotomy for pneumothorax 2 years earlier was hospitalized for inhalation pneumonia caused by paralysis of the right vocal cord. During hospitalization, septic shock and a fever of 38°C developed in the patient, complicated by acute respiratory failure and stroke. She was transferred to an intensive care unit with a PaO2/FiO2 >300 mm Hg, and the patient remained apyretic. The temperature was stopped after 7 days, and the patient remained apyretic.

In this case, phenotypic identification of gram-positive bacillus isolated from 2 blood cultures failed because the definite bacterial species A. rima was not included in the API database used for the phenotypic identification. Final identification was achieved within 2 days by comparison of the almost complete 16S rDNA sequence with homologous sequences deposited in Genbank. This comparison yielded a 99% sequence similarity, regarded but remained unidentified with use of API ANA strip (bioMérieux). Minimum inhibitory concentrations of antibiotics were determined for the gram-positive bacilli using E-test assay (AB BIODISK, Solna, Sweden) on Columbia agar supplemented with 5% sheep blood. Minimum inhibitory concentrations were 0.064 μg/mL for penicillin G, 0.023 μg/mL for ampicillin, 0.012 μg/mL for amoxicillin–clavulanic acid, 0.032 μg/mL for imipenem, <0.016 μg/mL for azithromycin, <0.016 μg/mL for erythromycin, 0.06 μg/mL for ciprofloxacin, and 1.25 μg/mL for vancomycin. DNA was extracted from 1 colony by using a QIAamp tissue kit (QIAGEN, Hilden, Germany) as described by the manufacturer. The 1,454-bp 16S rDNA sequence obtained using the fD1 5′-AGAGTTTGATCCTGGCTCAG-3′ and rP2 5′-ACGCTACCTGGTCAG-3′ primer pair (6,7) showed 99% sequence similarity with the 16S rDNA sequence of A. rima (GenBank accession no. AF292371) by use of BLAST version 2.2.9 software (National Center for Biotechnology Information). A phylogenetic neighbor-joining tree based on the Atopobium spp. 16S rDNA sequences made with the MEGA software confirmed that the isolate belonged to A. rima (Figure). Initial treatment by intravenous tazocillin–amikacin was changed to intravenous amoxicillin–clavulanic acid (2 g/200 mg). The fever resolved, and the patient’s condition improved. The treatment was stopped after 7 days, and the patient remained apyretic.
as criteria for accurate identification of bacterial organisms at the species level (8). In this patient, 2 *A. rimae* isolates were recovered from 2 different blood-culture bottles drawn 48 h apart, suggesting that *A. rimae* was not just a bypassing organism but indeed responsible for septicemia. In these specimens, *S. gordonii* was also isolated. Both species have been described as belonging to the oral flora, suggesting that these flora probably were the source for mixed septicemia in the patient. *A. rimae* was isolated as the patient was presenting with clinical features of septic shock, suggesting that *A. rimae* may have contributed to the shock. Antimicrobial drug treatment based on in vitro *A. rimae* susceptibility profile, along with reanimation measures, allowed for the patient’s recovery.

This case report illustrates the usefulness of 16S rDNA sequencing for accurate identification of anaerobic organisms and suggests that *A. rimae* should be added to the list of organisms responsible for bacteremia in patients.

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**References**


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**Systemic Infection with Enteric Adenovirus in Immunocompetent Child with Haemophilus influenzae Disease**

To the Editor: Recent articles have reported enteric human adenoviruses (HAdVs) types 40 and 41, previously thought to be restricted to the gastrointestinal tract (1), in multiple organ systems of a deceased immuno-deficient child (2) and in respiratory specimens of children with acute respiratory illnesses (3). Here we present a case in which enteric HAdV-40 was found in the cerebrospinal fluid (CSF) and blood of an apparently immunocompetent child with *Haemophilus influenzae* invasive disease.

The patient, a 10-month-old previously healthy Thai boy, met the criteria for a clinical case of encephalitis (4) and, after informed consent was obtained, was enrolled in the study of causes of encephalitis in Thailand (collaboration between the US Cen-