

Solobacterium moorei Bacteremia: Identification, Antimicrobial Susceptibility, and Clinical Characteristics[∇]

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Received 13 December 2010/Returned for modification 9 February 2011/Accepted 13 April 2011

We present five cases of *Solobacterium moorei* bacteremia. The isolates were identified with 16S rRNA gene sequencing and were susceptible to common antibiotics used for anaerobic infections. Bacteremia with *S. moorei* seems to be associated with debilitating conditions, but the prognosis of the infection appears to be good.

CASE REPORTS

Case 1. A 43-year-old man with a previous medical record of lymphoma and a kidney transplantation 11 years earlier was admitted to the department of nephrology. He had a fever, anemia, diarrhea, and general malaise and was complaining about a toothache. His temperature was 38.9°C. The total leukocyte count was 11.7×10^9 cells/liter (reference count is 3.0×10^9 to 10.0×10^9 cells/liter), and the C-reactive protein was 82 mg/liter (reference is ≤ 10 mg/liter). Two sets of blood cultures were performed. After 3 days of incubation in the Bactec 9240 blood culture system (Becton Dickinson Diagnostic Instrument Systems, Franklin Lakes, NJ), both anaerobic blood culture bottles were positive for a short, Gram-positive bacillus later identified as *Solobacterium moorei* with the use of 16S rRNA gene sequencing. Antibiotic treatment with intravenous benzylpenicillin and oral metronidazole was initiated. The same day, a dental examination was done and a tooth extraction was performed because of abscess formation. The patient's fever and symptoms responded to treatment. Six days after admission, the patient demanded himself discharged. Oral phenoxymethylpenicillin and metronidazole were continued for another week, and 13 days after admission the C-reactive protein had decreased to <10 mg/liter.

Case 2. A 66-year-old woman with a known non-small-cell lung carcinoma was admitted to the department of oncology because of fever and fatigue. Her temperature was 39.1°C. The total leukocyte count was 7.2×10^9 cells/liter, and the C-reactive protein was 208 mg/liter. Two sets of blood cultures were performed, and antibiotic treatment with intravenous cefuroxime and gentamicin was initiated. Three days later, both anaerobic blood culture bottles were positive for *S. moorei*. A chest X ray revealed progression of a previously known right-sided nodule. Magnetic resonance imaging of the brain showed meningeal carcinomatosis but no signs of cerebral infection. The fever and cerebral symptoms disappeared, and 1 week after admission the antibiotic treatment was stopped because the patient developed a rash. At this time, the C-reactive protein had decreased to 12 mg/liter.

Two weeks later, her fever relapsed and she became septic with low blood pressure. Treatment with meropenem and metronidazole was initiated, and 2 days later *Eikenella corrodens* was isolated from her blood cultures. A chest X ray revealed a pulmonary abscess for which she was treated with oral ciprofloxacin and metronidazole for 3 weeks.

Case 3. A 64-year-old man with a previous medical record of colon cancer and complicated abdominal surgery 3 years earlier was admitted to the department of abdominal surgery. He had a fever and signs of gastrointestinal atony. On the sixth day after admission, the patient became septic with low blood pressure. His temperature was 38.1°C. The total leukocyte count was 33.9×10^9 cells/liter, and the C-reactive protein was 284 mg/liter. Two sets of blood cultures were performed, and an acute exploratory laparotomy was done. The surgeons found intestinal obstruction and macroscopic relapse of the colon cancer. Four days later, one anaerobic blood culture bottle was positive for *S. moorei*. Antibiotic treatment was initiated with intravenous cefuroxime and metronidazole. The patient responded slowly with several episodes of fever and chills. Eventually, he was discharged after 4 weeks with no additional antibiotic treatment. At this point, the C-reactive protein had decreased to 90 mg/liter.

Case 4. A 33-year-old woman with a previous medical record of intravenous drug abuse and hepatitis B was admitted to the department of neurology. She had a fever, headache, and skin numbness in relation to an injection of heroin in her left groin 5 days earlier. Her temperature was 40.1°C. The total leukocyte count was 10.8×10^9 cells/liter, and the C-reactive protein was 189 mg/liter. Two sets of blood cultures were performed, and antibiotic treatment with intravenous cefuroxime was initiated. Magnetic resonance imaging of the brain and a spinal puncture showed no signs of infection in the central nervous system. The patient was transferred to the department of infectious diseases. Two days later, both anaerobic blood culture bottles were positive for two different types of Gram-positive bacilli. These were later identified as *S. moorei* and *Actinomyces meyeri* with the use of 16S rRNA gene sequencing. Antibiotic treatment was changed to intravenous benzylpenicillin and metronidazole. Three days after admission, the patient developed a swelling of the left lower extremity. Abdominal computer tomography revealed thrombosis of the left femoral vein and an abscess, 2.4 cm in diameter, around the vessel. The patient responded well to 5 weeks of antibiotic therapy, and

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[∇] Published ahead of print on 27 April 2011.

the C-reactive protein decreased to <5 mg/liter. On follow-up, an ultrasonography of the lower extremities showed complete remission of the abscess.

Case 5. A 77-year-old man with a previous medical record of ischemic heart disease and cancer of the prostate was admitted to the department of internal medicine. He had a fever, dry cough, and general discomfort and had been complaining about a toothache. His temperature was 38.8°C. The total leukocyte count was 19.7×10^9 cells/liter, and the C-reactive protein was 94 mg/liter. Pneumonia was suspected, and a chest X ray revealed a left-sided lower lobe consolidation. Two sets of blood cultures were performed, and antibiotic treatment with intravenous benzylpenicillin was initiated. The patient had a brief episode of hypotension. The following day, he had no fever and was discharged with oral phenoxymethylpenicillin for a week. Three days later, both anaerobic blood culture bottles were positive for both a Gram-positive and a Gram-negative bacillus. With the use of 16S rRNA gene sequencing, the two isolates were later identified as *S. moorei* and *Porphyromonas uenonis*. Eleven days after admission, the C-reactive protein had decreased to 24 mg/liter.

Solobacterium moorei is a non-spore-forming strict anaerobic Gram-positive bacillus initially isolated from human feces and recognized with the use of 16S rRNA gene sequencing (15). *S. moorei* is the only species in the genus *Solobacterium* belonging to the *Clostridium* cluster XVI showing close phylogenetic association with *Bulleidia extracta*, *Holdemanian filiformis*, and *Erysipelothrix rhusiopathiae*. In the past, difficulties in characterizing *S. moorei* phenotypically has placed it among the *Eubacterium*-like strains. It is now recognized that DNA sequencing is necessary in the process of identifying this bacillus from clinical samples (25). In the last decade, *S. moorei* has been associated with halitosis (10, 11, 16) and has been isolated from endodontic infections (7, 22, 23), periradicular lesions (24), and subgingival plaques from patients with refractory periodontitis (4). There are only a few reports of infections outside the oral cavity. *S. moorei* has been reported in three single cases of bacteremia (5, 17, 18) and recently in patients with wound infections (25). Here, we present five cases of *S. moorei* bacteremia collected at Odense University Hospital from 2003 to 2009. The hospital is a tertiary referral hospital in the region of Southern Denmark with a bed count of 1,300. The associated department of clinical microbiology offers service to a surrounding area of approximately 500,000 inhabitants.

The microSeq 500 system (Perkin-Elmer, Applied Biosystems Division, Foster City, CA) was used for 16S rRNA gene sequencing. Consensus sequences (467 to 485 bp) were compared with the EzTaxon server (3). The highest sequence similarity for the five strains (99.57 to 99.79%) was obtained with the *Solobacterium moorei* strain JCM 10645(T) (GenBank accession no. AY044916) previously characterized by Kageyama and Benno (15). The three next best matches were with the *Bulleidia extracta* strain W1219(T) (89.71%) (GenBank accession no. ADFR01000011), the *Erysipelothrix inopinata* strain 1MF-EP02(T) (87.84%) (GenBank accession no. AJ550617), and the *Holdemanian filiformis* strain ATCC 51649(T) (86.81%) (GenBank accession no. Y11466). Conventional anaerobic

TABLE 1. Antimicrobial susceptibility of the five strains of *S. moorei* isolated from blood cultures

Antimicrobial agent	MIC (mg/liter)	
	Median	Range
Penicillin	0.006	0.002–0.008
Piperacillin-tazobactam	0.032	0.016–0.047
Clindamycin	0.047	0.016–0.094
Metronidazole	0.047	0.016–0.064
Meropenem	0.047	0.008–0.094
Moxifloxacin	0.19	0.125–0.38
Tigecycline	0.064	0.023–0.094
Vancomycin	0.5	0.38–0.5

characterization was performed according to the *Manual of Clinical Microbiology* (19) and was based on Gram stain, wet mount characteristics, and susceptibility to metronidazole, vancomycin, kanamycin, colistin, and bile. Fermentation of carbohydrates and enzyme tests were performed using commercially available substrates and diagnostic tablets/disks (Statens Serum Institut Diagnostica, Copenhagen, Denmark, and Rosco Diagnostica, Taastrup, Denmark). Antimicrobial susceptibility was determined by the Etest (bioMérieux, Solna, Sweden) gradient method on brucella blood agar supplemented with hemin and vitamin K (Becton Dickinson GmbH, BD Diagnostics, Heidelberg, Germany) according to the manufacturer's instructions (Table 1). Clindamycin results were confirmed after 48 h of incubation. *Bacteroides fragilis* ATCC 25285 was used as a quality control. As this is the first case series of *S. moorei* bacteremia, we have also described clinical characteristics of the patients and compared them to previous cases.

It is notable that we have been able to diagnose five cases of bacteremia with *S. moorei* in a 7-year period. One of the reasons could be, as recently published, that we use 16S rRNA gene sequencing as our primary diagnostic method for species identification of anaerobic bacteria from blood and other sterile body sites in our laboratory (14). Also, the primary use of an anaerobic agar, a chocolate agar containing hemin and supplemented with vitamin K and cysteine as the reducing agent (Statens Serum Institut Diagnostica, Hillerød, Denmark), proved to be an excellent agar for anaerobic culturing, as described by others (12, 13, 20). This agar is used as the primary subculture agar for anaerobic bacteria in most Danish clinical microbiology laboratories. The phenotypic identification of the isolates was not able to produce a uniform amount of positive and negative reactions, and the isolates also differed from the ones previously described (15, 17). The results of the phenotypic identification assay were as follows: fermentation of glucose, 5/5 positive; galactose, 5/5 positive; sucrose 7, 1/5 negative; maltose, 1/5 positive; mannitol, 5/5 negative; hydrolysis of esculin, 0/5 positive; arginine, 5/5 negative; gelatin, 5/5 negative; production of indole, 5/5 negative; H₂S 5/5 negative; reduction of nitrate, 5/5 negative; catalase, 5/5 negative; β-N-acetyl-glucosaminidase, 1/5 negative; α-galactosidase, 4/5 positive; α-glucosidase, 4/5 positive; and β-glucosidase, 1/5 negative. A newly published paper indicates that commercially available systems, such as Vitek 2 ANC, BBL Crystal Anaerobe, and RapID ANA II, cannot identify *S. moorei* and report results as “no identification” (2). Accordingly, we suggest that laboratories apply sequencing

technology of anaerobic non-spore-forming Gram-positive rods in relevant cases when phenotypic identification fails.

In accordance with other studies (5, 25), the antimicrobial susceptibility testing of the *S. moorei* isolates showed susceptibility to common antibiotics used for anaerobic infections (Table 1). None of the patients in the five cases had received antibiotics before blood cultures were taken. This indicates that common antibiotics administered before blood cultures are taken will probably reduce the sensitivity to detect *S. moorei*. Therefore, we speculate that *S. moorei* might be more prevalent in bacteremia than believed so far.

The patients were all admitted with fever, elevated biomarkers, and symptoms of infection, thus indicating the true nature of the bacteremia. The patients all improved clinically and had a decreasing C-reactive protein after initiation of antibiotic therapy, which we interpreted as response to treatment according to previous studies (21). All of the patients had comorbidity, and four of the patients had a malignant disease. This is in accordance with other cases. Lau et al. described bacteremia in a patient with carcinoma of the cervix (17), Detry et al. described bacteremia in a patient with multiple myeloma (5), while Martin et al. described bacteremia in an intravenous drug user (18). The patient in case 1 had a tooth abscess as the most likely source of infection. The same is reported by Detry et al. (5), and *S. moorei* has been isolated from different types of dental infections (7, 22, 23, 24). The patient in case 2 had a lung abscess. Others have indicated that *S. moorei* could be related to a lung abscess (9), but we are the first to describe this in association with bacteremia. The patient in case 3 probably had an abdominal source of infection. *S. moorei* was originally isolated from feces (15), and Lau et al. have described a case of bacteremia from a presumed abdominal source (17). The patient in case 4 was an intravenous drug user with a groin abscess. The same clinical picture is described by Martin et al. (18). The patient had a mixed infection with commensals of the oral flora. We hypothesize that the patient practices a needle-licking behavior before injections and by this introduced oral flora into the injection area. Indeed, others have described this behavior in up to one-third of intravenous drug users (1, 6). The patient in case 5 had a complex clinical presentation. He had a mixed bacteremia with *S. moorei* but also *Porphyromonas uenonis*, which is a rare pathogen primarily isolated from abdominal infections (8). The most likely sources of infection are his teeth, because of his previous complaints, or his abdominal cavity, because of his predisposition and the nature of the bacteremia. The types of antibiotics and the durations of treatment were different among the five cases. However, no one relapsed with *S. moorei* bacteremia, and none of the patients died within 30 days.

In summary, our case reports demonstrate the value of 16S rRNA gene sequencing for identification of *S. moorei*. We found that *S. moorei* is susceptible to common antibiotics used for anaerobic infections, and we speculate that the prevalence of *S. moorei* bacteremia is underestimated. The clinical characteristics of the patients with *S. moorei* bacteremia are associated with debilitating conditions, such as malignant disease

and intravenous drug use across gender and age. The prognosis of the infection appears to be good if the source of infection is identified and appropriate drainage and/or surgery and antibiotics are administered.

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