**Desulfovibrio fairfieldensis** Bacteremia Associated with Choledocholithiasis and Endoscopic Retrograde Cholangiopancreatography

Jason D. Pimentel* and Raymond C. Chan

Department of Microbiology and Infectious Diseases, Royal Prince Alfred Hospital, Camperdown, New South Wales, Australia

Received 9 May 2007/Accepted 4 June 2007

**CASE REPORT**

In January 2007, a 77-year-old man with a history of cholelithiasis was electively admitted to the day-procedure unit of the Royal Prince Alfred Hospital, Camperdown, NSW, Australia, for repeat endoscopic retrograde cholangiopancreatography (ERCP) with common bile duct stone extraction and lithotripsy. On admission to the unit, he was clinically stable and his laboratory values were as follows: white cell count, 11.8 × 10⁹/liter; hemoglobin, 154 g/liter; platelets, 203 × 10⁹/liter; red cell count, 5.31 × 10¹²/liter; neutrophils, 10.1 × 10⁹/liter; bilirubin (total), 37 μmol/liter; alkaline phosphatase, 440 U/liter; gamma-glutamyl transpeptidase, 562 U/liter; alanine transaminase, 243 U/liter; and aspartate transaminase, 384 U/liter.

Upon ERCP, there was extensive stone disease, including involvement of the hepatic ducts. The stones were trolled and cleared with a lithotripter, basket, and balloon, followed by stent insertion. After the procedure, the patient was admitted to the ward overnight for observation. That evening, the patient had nausea, or vomiting and remained hemodynamically stable.

The next day, the patient’s fever resolved the next day. After 4 days of i.v. ticarcillin-clavulanate intravenously (i.v.) at 3.1 g every 6 h. The blood cultures were taken, and the patient was commenced on oral ciprofloxacin at 500 mg twice a day (b.i.d.). At the time of discharge, blood cultures remained negative. The patient returned 1 month later for a further ERCP and remains well on follow-up.

**Microbiology.** Blood for culture was collected into BacT/ALERT FA and SN blood culture bottles (bioMérieux, Durham, NC) and incubated in a BacT/ALERT automated incubator (bioMérieux). Four days after the initial set of blood cultures were drawn, growth was detected in the anaerobic bottle. A strong sulfur smell was detected from the medium aspirated from the bottle. The aerobic bottle remained negative. The patient returned 1 month later for a further ERCP and remains well on follow-up.

Blood cultures were taken, and the patient was commenced on ticarcillin-clavulanate intravenously (i.v.) at 3.1 g every 6 h. The patient’s fever resolved the next day. After 4 days of i.v. ticarcillin-clavulanate, he was discharged home on oral ciprofloxacin at 500 mg twice a day (b.i.d.). At the time of discharge, blood cultures remained negative. The patient returned 1 month later for a further ERCP and remains well on follow-up.

The isolate was referred to the Identification Reference Laboratory at the Centre for Infectious Diseases and Microbiology, Institute of Clinical Pathology and Medical Research, Westmead, NSW, Australia, for further analysis. Additional phenotypic features reported were a negative reaction for glucose fermentation, positive reactions for nitrate reduction and H₂S production (in sulfur-indole-motility medium), and a positive desulfoxvinid test. Identification by long-chain-fatty-acid analysis was performed using a Hewlett-Packard 5890 series II gas chromatograph unit (Hewlett Packard Corporation, Palo Alto, CA), with analysis by the automated MIDI microbial identification system (MIDI, Newark, DE). The MIDI identification was consistent with *Desulfovibrio pigra* (*Desulfovibrio fairfieldensis* is not in the MIDI database). However, cluster analysis using MIS software clustered this isolate with previously identified *D. fairfieldensis* strains (M. Yuen, personal communication).

The first 500 bp of the 16S rRNA gene of this isolate were also sequenced after PCR amplification with both the blood culture medium and colonies from the anaerobic subculture plate. DNA extraction from colonies was performed using the QIAamp DNA Mini kit spin column method (QIAGEN, Hilden, Germany) according to the manufacturer’s instructions. Formal DNA extraction was not performed on the blood culture medium. Instead, 2 drops of the medium was added to 1 ml of H₂O. This mixture was vortexed and added directly to the master mix.
Amplification of the partial 16S rRNA gene was performed using a monochrome, real-time format. The reaction mixture consisted of SensiMix (Quintance, London, United Kingdom) (25 µl), SYBR green I (1 µl), the universal 16S rRNA gene primers Fd1 (5'-CAG AGT TTG ATC CTG GCT CAG-3') (2 µl; 10 pmol) and R2 (5'-GTA TTA CCG CGG CTG CTG-3') (2 µl; 10 pmol), (10), DNA template (10 µl), and H2O (10 µl). Thermocycling proceeded in a Corbett Rotor-Gene RG-3000 instrument (Corbett Research, Sydney, Australia). The parameters were 1 cycle at 95°C for 10 min, followed by 30 cycles at 95°C for 20 seconds, 58°C for 30 seconds, and 72°C for 30 seconds.

The entire 50-µl real-time reaction mixture containing the PCR products was purified using a Marligon Rapid DNA purification kit (Marligon Biosciences, Ljamsville, MD). Sequencing was carried out on-site at SUPAMAC, the Sydney University Prince Alfred Macromolecular Analysis Centre, using ABI Prism BigDye Terminator 3.1 chemistry (Applied Biosystems, Foster City, CA) and a GeneAmp 9700 thermocycler (Applied Biosystems). The sequence cycling products were analyzed by capillary electrophoresis and fluorescence detection in a 3730xl DNA analyzer (Applied Biosystems). The fluorescence data were analyzed with Applied Biosystems DNA sequencing analysis software (version 5.2; Applied Biosystems).

The sequence data derived from the isolates from the blood culture medium and the anaerobic subculture colonies were identical. A BLAST (1) search using the partial 16S rRNA gene sequence for this isolate showed it to be 100% similar (485 of 485 bases) to AJ251630 and AF192155, both of which were described as D. fairfieldensis by the citing publications (5, 9). The sequence was also 99% similar (483 of 485 bases) to D. fairfieldensis U42221, the first described isolate of this species (14).

**Discussion.** *Desulfovibrio fairfieldensis* is a gram-negative, curved, motile, non-spore-forming, asaccharolytic, anaerobic bacillus. It is catalase positive, oxidase negative, indole negative, and urease negative and produces H2S (4). Excellent photomicrographs and electron micrographs of this organism have been published previously (11, 14). While most *Desulfovibrio* species are found in the environment, *D. fairfieldensis* has been isolated only from human specimens and is thought to be a normal resident of the human intestinal tract (4). The first report of clinical infection with *Desulfovibrio fairfieldensis* was due to a liver abscess in Australia over 10 years ago (14). Since that time, however, this organism has not been reported frequently. We report the second case of *D. fairfieldensis* bacteremia reported from Australia; it is also the second case of *Desulfovibrio* infection associated with choledocholithiasis.

Our review of the literature identified four other cases of confirmed *D. fairfieldensis* bacteremia (Table 1). McDougall et al. identified the organism from the first case in a patient with a history of nonobstructive cholelithiasis and benign, bleeding adenomatous polyps (11). The second case, reported by Loubinoux et al., was a patient who presented with a perforated appendix (9). The same case report discusses a third patient with a history of rectorrhagia at the same center (9). The fourth case is mentioned by Warren et al. in a case series from California (15). No demographic details of this patient were provided. The investigators from the same center note that the very first case report of *Desulfovibrio* infection (13) may actually have been due to *D. fairfieldensis*. In this first report, also from California, a patient with cholelithiasis (similar to the present case) was found to be bacteremic with an organism identified at the time as *D. desulfuricans*. However, Warren et al. comment that this organism may have instead been *D. fairfieldensis*. This proposal was made on the basis that the isolate was reported to be catalase positive and urease negative, which are two key reactions that differentiate *D. fairfieldensis* from *D. desulfuricans*. We have included this case in our review.

Most patients (including the one from the present case) were >65 years of age and male. In three patients, compromise of the gastrointestinal tract, from bleeding polyps (11), a perforated appendix (9), and rectorrhagia (9), was the source of infection; in another two patients, the likely source was the biliary tree (13; the present case). Surgical or invasive intervention was reported in four of the cases, including colonoscopy (11), appendectomy (9), ERCP (present case), and cholecystectomy (13). The antimicrobial regimens employed were varied. The outcomes, where reported, indicated recovery in every case.

The organisms (Table 2) were relatively slow growing (4 to 6 days until positive), even in automated blood culture systems. The only biochemical variation was the presence or absence of

<table>
<thead>
<tr>
<th>Patient no.</th>
<th>Yr of report</th>
<th>Age (yr)</th>
<th>Sex</th>
<th>Past medical history</th>
<th>Source</th>
<th>Procedures</th>
<th>Antimicrobials</th>
<th>Recovery from other sites</th>
<th>Outcome</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1997</td>
<td>75</td>
<td>M</td>
<td>SGNP, COAD, HTN, DVT, NOCL</td>
<td>BBAP</td>
<td>CLNSC</td>
<td>i.v. CIP, p.o. CIP</td>
<td>No</td>
<td>Recovery</td>
<td>11</td>
</tr>
<tr>
<td>2</td>
<td>2000</td>
<td>23</td>
<td>M</td>
<td>GU</td>
<td>P. Apdx</td>
<td>Apdct</td>
<td>i.v. FAM, i.v. MTZ</td>
<td>No</td>
<td>Recovery</td>
<td>9</td>
</tr>
<tr>
<td>3</td>
<td>2000</td>
<td>85</td>
<td>M</td>
<td>CCF, RF</td>
<td>RCTRG</td>
<td>No</td>
<td>NR</td>
<td>No</td>
<td>Recovery</td>
<td>9</td>
</tr>
<tr>
<td>4</td>
<td>2005</td>
<td>NR</td>
<td>NR</td>
<td>NR</td>
<td>NR</td>
<td>NR</td>
<td>NR</td>
<td>NR</td>
<td>Recovery</td>
<td>15</td>
</tr>
<tr>
<td>5</td>
<td>2007</td>
<td>77</td>
<td>M</td>
<td>DM2, CVA, HTN, CAD, CDL</td>
<td>BT</td>
<td>ERCP</td>
<td>i.v. TIM, p.o. CIP</td>
<td>No</td>
<td>Recovery</td>
<td>This study</td>
</tr>
<tr>
<td>6</td>
<td>1997</td>
<td>67</td>
<td>M</td>
<td>CP, SYN</td>
<td>BT</td>
<td>CHCYST</td>
<td>Nil</td>
<td>No</td>
<td>Recovery</td>
<td>13</td>
</tr>
</tbody>
</table>
a nitrate reaction. Antimicrobial susceptibility varied for the beta-lactams, but there was consistent susceptibility to metronidazole. Methods used to determine antimicrobial susceptibility included disk diffusion (11), Etest (11), and CLSI agar dilution (9, 15) with results read at 96 h.

In addition to blood, *D. fairfieldensis* has been isolated from various other sites of infection. The most frequent sites of isolation have been peritoneal fluid (n = 8) (8, 15), periodontal pockets (n = 6) (5, 7), and abdominal collections (n = 5) (8, 9, 15). This organism has also been isolated from a pelvic and a colorectal collection (15), a liver abscess (14), and urine (6). The majority of the 26 clinical isolates have been isolated in France (n = 10) (6, 7, 9), the United States (n = 10) (15), and Australia (n = 5) (8, 11, 14). The true incidence of disease is likely to be underestimated because of the difficulties associated with the identification of anaerobic organisms (2, 9). Still, it appears that *D. fairfieldensis* is found most frequently by those who seek it. Indeed, the majority of the reported isolates are from the following three groups: J. Loubinoux and coworkers in France (7, 8, 9), Y. Warren and coworkers in the United States (15), and W. Tee and coworkers in Australia (8, 11, 14).

We noted that molecular identification has played a major role in the identification of this organism, as all of the isolates reported were definitively identified by either 16S rRNA gene sequencing (n = 17) (5, 6, 9, 11, 14, 15) or amplification with specific PCR primers (n = 9) (7, 8).

Due to the association with infections involving the gastrointestinal tract, it has been suggested that *D. fairfieldensis* possesses more invasive pathogenic potential than other Desulfovibrio species (9). In addition, *D. fairfieldensis* also possesses the most antimicrobial resistance of the genus (15). In spite of these two features, there have been no deaths directly attributed to *D. fairfieldensis* infection. We also note that our review found that at least half of the bacteremic patients had gallstone disease, which may signify that this organism may be associated with the biliary tree as well. Consequently, manipulation of the biliary tree may predispose patients to *D. fairfieldensis* bacteremia.

We found the use of 16S rRNA gene sequencing to be a very useful method to identify this organism and provide a faster turnaround time than conventional methods. The time required to obtain a sequence-based identification directly from the positive blood culture medium was about 30 h. The anaerobic subculture alone took 4 days until colonies were visible with a loupe. Further investigations then required additional subcultures. However, we note that phenotypic characters still remained important, as they assisted in correlating the sequence-based data.

The use of DNA sequencing for bacterial identification has become more practical with the advent of automated genetic analyzers and alignment software, and sequence-based identification is now beginning to play a larger role in the identification of infectious organisms (3). The role of 16S rRNA gene sequencing for bacterial identification has been demonstrated for various organisms, including mycobacteria, *Nocardia* species, and noncultured bacteria (3). Since anaerobes may often be regarded as difficult to identify, there appears to be a role for sequenced-based identification of these organisms as well (4, 12). Indeed, wider use of this utility can assist in the accurate and consistent identification of *D. fairfieldensis* and other
anaerobes, thereby further delineating their true epidemiology and importance in human infection. However, we acknowledge that culture methods, even if carried out by a reference laboratory, remain necessary in order to determine antimicrobial susceptibility.

In conclusion, 30 years on, we would like to reiterate the admonition of Porschen and Chan that the clinical microbiologist be aware of and able to identify this uncommon anaerobe (13). Suspicion should be raised when curved, motile, anaerobic bacilli are isolated after 4 to 6 days from blood cultures from patients who are known to have gastrointestinal compromise or recent biliary manipulation. If the resources for anaerobic culture and identification are not readily available, identification by 16S rRNA gene sequencing may offer a relatively rapid method of identification. When the diagnosis is suspected or confirmed, effective treatment appears to be metronidazole accompanied by surgical intervention, where appropriate, to remove the focus of infection.

Nucleotide sequence accession number. The partial 16S rRNA gene sequence of the case isolate was deposited in GenBank under accession number EF532788.

We are grateful for the assistance of Khanh Pham and George Stathopoulos of the Royal Prince Alfred Hospital Department of Microbiology Laboratory, Camperdown, Australia. We also acknowledge Marion Yuen and Maureen Lynch of the Identification Reference Laboratory at the Centre for Infectious Diseases and Microbiology at Westmead, Laboratory at the Centre for Infectious Diseases and Microbiology at Camperdown, Australia. We also acknowledge Stathopoulos of the Royal Prince Alfred Hospital Department ofMicrobiology.

REFERENCES