Five Clinical Cases of *Necropsobacter rosorum* Bacteremia

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Five cases of bacteremia with *Necropsobacter rosorum* are described, originating from intra-abdominal infections or localized soft tissue infections in the pelvic region. *N. rosorum* is consistently misidentified by commercial identification systems, which may delay recognition of this organism as a human pathogen.

**CASE REPORTS**

This case report presents five cases of bacteremia with *Necropsobacter rosorum*, together with a discussion of the microbiological characteristics of this clinically uncommon pathogen.

Case 1 was a 57-year-old male, admitted with a 1-week history of jaundice and abdominal pain. On admission, the patient was afibrile, with a normal peripheral white cell count and procalcitonin but abnormal liver function tests (aspartate transaminase, 338 U/liter; alanine transaminase, 448 U/liter; alkaline phosphatase, 256 U/liter; bilirubin, 190 μmol/liter). Abdominal computed tomography (CT) scan revealed a distal common bile duct calculus causing dilatation of the common bile duct (CBD) and cholangitis. Thickened gallbladder walls with enhancement were noted, which may have represented mild acute cholecystitis. Blood cultures on admission grew Gram-negative bacilli from aerobic and anaerobic vials. Clinical symptoms improved following duodenoscopy and removal of the CBD stone. The initial antibiotic therapy of ceftriaxone and metronidazole was subsequently changed to a 2-week course of oral ciprofloxacin.

Case 2 was a 61-year-old female presenting with colicky epigastric pain associated with mild epigastric tenderness. On admission, the patient was febrile (38.3°C) with leukocytosis (12.2 × 10⁹ cells/μl; 93.9% neutrophils; platelets, 263 × 10⁹ cells/μl) and abnormal liver function tests. Abdominal CT scan demonstrated intra- and extrahepatic biliary duct dilatation secondary to a 0.4-cm calculus in the distal CBD. There was stranding around the extrahepatic ducts, suggestive of cholangitis. Endoscopic retrograde cholangiopancreatography (ERCP) with papillotomy was performed 2 days after admission, with subsequent clinical improvement. Blood cultures collected on the day of admission were positive for Gram-negative bacilli from both aerobic and anaerobic vials. Magnetic resonance imaging (MRI) cholangiopancreatography performed 5 days post-admission showed interval thrombosis of the anterior segmental branch of the right and left portal veins. Subsequent blood cultures taken during the remainder of the admission episode were sterile. Initial antibiotic therapy consisted of ceftriaxone and metronidazole, with subsequent conversion to oral amoxicillin-clavulanate. The patient was discharged on an anti-coagulation regime.

Case 3 was a 21-year-old male who presented with right iliac fossa pain and tenderness, associated with systemic signs of infection. The patient was pyrexic at 39.2°C, had a full blood count demonstrating leukopenia at 3.7 × 10⁹ cells per μl (87.6% neutrophils; platelets, 207 × 10⁹ cells/μl), and had a raised C-reactive protein level (17.6 mg/liter). Initial antibiotic therapy consisted of ceftriaxone and metronidazole. Operative findings identified retrocecal appendicitis with the distal third of the appendix gangrenous and adherent to cecum. Aerobic blood cultures collected on the day of admission were positive for *Comamonas testosteroni*, and anaerobic blood cultures were positive for *Streptococcus milleri*, *Comamonas testosteroni*, and a Gram-negative bacillus. Post-operative recovery was uneventful, and the patient was discharged the next day on oral amoxicillin-clavulanate.

Case 4 was a 66-year-old diabetic male who was readmitted following recent excision of a gluteal abscess. MRI of the thigh on admission demonstrated a large intramuscular abscess within the left adductor magnus, with left ischial tuberosity osteomyelitis and myositis of the left obturator externus, adductor brevis, and adductor longus. Surgical debridement and wound inspection were performed over successive days, and initial tissue cultures grew mixed Gram-negative bacilli and *Streptococcus milleri* group organisms. Signs of clinical infection persisted, and a further CT scan of the pelvis 15 days following admission demonstrated an abscess overlying the osteomyelitis of the ischial tuberosity tracking along the intramuscular planes of the hamstring muscles. Blood cultures performed on the same day were positive for Gram-negative bacilli in the anaerobic vial. Superficial wound cultures from the debridement site were positive for *Pseudomonas aeruginosa*. Initial antibiotic therapy was piperacillin-tazobactam, and this was subsequently changed to imipenem. Following a 5-week course of antibiotics with repeated surgical episodes of wound debridement and inspection, the patient was discharged home.

Case 5 was a 51-year-old diabetic male who was admitted with a two-day history of diarrhea and vomiting associated with fever and poor oral intake. On admission, there was evidence of sepsis with pyrexia (40.0°C), leukocytosis (13.3 × 10⁹ cells/μl; 90.6% leukocytes; platelets, 90 × 10⁹ cells/μl), abnormal liver function tests, and persistent hypotension despite inotropes. A CT scan showed moderately dilated intrahepatic biliary ducts with evidence of cholangitic abscesses. There was also the presence of a previously inserted biliary stent, displaced inferiorly. Two sets of blood cultures taken on admission were positive with a mixture of organisms in all vials, including *Klebsiella pneumoniae*, *Enterococ-
Table 1: Results obtained from commercial identification systems

<table>
<thead>
<tr>
<th>Isolate</th>
<th>API 20E Identification</th>
<th>API 20E ID confidence</th>
<th>BioCode</th>
<th>Vitek ID-GN Identification</th>
<th>Vitek ID-GN ID confidence</th>
<th>Bruker FLEX identification (BD test score)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. Klebsiella pneumoniae subsp. aerobius</td>
<td>Poor profile</td>
<td>0000272</td>
<td></td>
<td>Sphingomonas pascinobilis</td>
<td>Excellent (96%)</td>
<td>Aggregatibacter actinomycetemcomitans</td>
</tr>
<tr>
<td>2. Pasteurella pneumotropica/Mannheimia haemolytica</td>
<td>Poor profile</td>
<td>0004266</td>
<td></td>
<td>Shigella boydii</td>
<td>Good (90%)</td>
<td>Pasteurella canis</td>
</tr>
<tr>
<td>3. Pasteurella pneumotropica/Mannheimia haemolytica</td>
<td>Poor profile</td>
<td>0001236</td>
<td></td>
<td>Sphingomonas pascinobilis</td>
<td>Excellent (96%)</td>
<td>Pasteurella canis</td>
</tr>
<tr>
<td>4. Pasteurella pneumotropica/Mannheimia haemolytica</td>
<td>Poor profile</td>
<td>0001236</td>
<td></td>
<td>Pasteurella sp., Shigella sp., Sphingomonas pascinobilis</td>
<td>Good (90%), acceptable (86%)</td>
<td>Aggregatibacter actinomycetemcomitans</td>
</tr>
<tr>
<td>5. Pasteurella pneumotropica/Mannheimia haemolytica</td>
<td>Poor profile</td>
<td>0001236</td>
<td></td>
<td>Sphingomonas pascinobilis</td>
<td>Excellent (96%)</td>
<td>Pasteurella canis</td>
</tr>
</tbody>
</table>

*Results are with respect to each of the organisms in the V2 ID-GN column, immediately to the left.
with DNA sequencing performed using the ABI PRISM BigDye Terminator Cycle Sequencing Kit v3.0/3.1 (Applied Biosystems, CA). Sequencing electropherograms were viewed, and low-quality sequences (with >1% probability of error) from the 5’ and 3’ ends were excluded. Partial 16S rRNA sequences were compared with known sequences in the GenBank database (http://www.ncbi.nlm.nih.gov/GenBank/) using standard search parameters, with results interpreted following recommendations by the Clinical and Laboratory Standards Institute (3). All five isolates were identified as *Necropsobacter rosorum* with sequence identity similarity indexes of >99%.

*N. rosorum* is a recently proposed reclassification of the SP group of organisms, which was previously classified in the family *Pasteurellaceae*. The organism was first reported by Mannheim and colleagues from the pneumatic tissue of a guinea pig (4). Subsequent reports noted the occasional recovery of SP group organisms from human sources (5), including one report of cellulitis following a guinea pig bite (6). The type species of *N. rosorum* was first proposed by Christensen et al., who performed phenotypic and genotypic characterization of this species using a collection of 30 veterinary and 5 human strains (7).

The five isolates in our case report showed phenotypic characteristics similar to those described by Christensen et al., except for one strain that was persistently oxidase negative. However, two of the four oxidase-positive isolates displayed delayed positivity when tested by a commercial oxidase reagent, which may delay accurate species identification. Key phenotypic tests for the presumptive identification of this organism include colony growth resembling *Enterobacteriaceae* on BAP and MAC, oxidase positivity, and slow glucose fermentation on OF medium. These characteristics may also be seen in *Vibrio* species and the *Pasteurellae*. Vibrios may be differentiated by larger colony sizes of >4 mm on both BAP and MAC after 18 h of incubation, indole positivity, and growth on thiosulfate-citrate-bile salts-sucrose agar. *N. rosorum* shares similar phenotypic characteristics with *Pasteurella* species of clinical importance, but differential characteristics that can be used to aid identification of this organism include its ability to grow on MAC and negative tests for indole production and ornithine decarboxylase.

Antibiotic susceptibility testing for the five isolates was performed by broth microdilution (Sensititre; Trek Diagnostic Systems, United Kingdom), with susceptibilities interpreted using Clinical and Laboratory Standards Institute (CLSI) breakpoints for non-*Enterobacteriaceae* (8). Isolates were susceptible to ampicillin-sulbactam, ciprofloxacin, imipenem, meropenem, doripenem, aztreonam, piperacillin-tazobactam, polymyxin B, cephalosporins, and cefepime (Table 2). All isolates were also susceptible to aminoglycosides but with raised MICs for gentamicin (1 to 2 mg/liter) and amikacin (4 to 8 mg/liter), which is a common feature of *Pasteurella* species (9).

This case series is the first to describe the clinical features of patients with *N. rosorum* bacteremia. All cases were associated either with intra-abdominal infections (cholangitis and appendicitis) or localized soft tissue infection in the pelvic region. The organism is consistently misidentified by current commercial identification systems, which compounds the difficulty of accurate characterization of disease by this organism. At present, se-
sequencing of the 16S rRNA gene remains the only definitive means to accurately identify \textit{N. rosorum}.

**REFERENCES**


