Roseomonas mucosa Isolated from Bloodstream of Pediatric Patient

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We report a case of catheter-related bacteremia associated with Roseomonas mucosa isolated from an immunocompromised pediatric patient with a history of multiple episodes of urinary tract infection and bacteremia.

CASE REPORT

An 18-year-old male presented to the UCLA Emergency Department with a 2-day history of fever, malaise, and decreased activity level and was admitted to the UCLA Medical Center for suspected catheter-related sepsis. The patient had a past medical history that included pseudoobstruction, status post-colectomy, chronic total parenteral nutrition dependence, and G-tube placement. In addition to having multiple incidences of urinary tract infections with Morganella species and Enterococcus species, the patient also had multiple episodes of bacteremia in the past 2 years with Methylobacterium mesophilicum, Acinetobacter lwoffii, Delftia acidovorans, and another unidentified Gram-negative bacillus. The patient’s last admission to the UCLA Medical Center was 9 months ago for Broviac catheter-related bacteremia with Delftia acidovorans and the unidentified Gram-negative bacillus. For these past infections, the patient was treated with vancomycin and ceftriaxone. Blood samples were collected for culture, and the patient was empirically treated with vancomycin and ceftriaxone.

Two sets of Bact/T/Alert aerobic and anaerobic blood culture bottles were drawn from the Broviac catheter line within a 24-hour period. Bacterial growth was detected in one aerobic bottle on day 4 of incubation, using the Bact/Alert (bioMérieux, Marcy l’Étoile, France). Gram-negative cocccobacilli were detected on Gram stains, and the organism was subcultured to MacConkey agar, blood agar, and chocolate agar and incubated at 35°C in 5% CO₂. Growth on blood agar and chocolate agar revealed slightly pink, mucoid colonies; no growth was observed on MacConkey agar. The organism was further subcultured to Sabouraud dextrose (SAB) agar, which grew prominent pink mucoid colonies after 24 h incubation (Fig. 1). API NE (bioMérieux) identified the organism as Methylobacterium species, which was the same episodes of bacteremia that was previously identified 14 months prior. However, presumptive identification of Roseomonas species was obtained based on colonial morphology on chocolate agar and SAB agar, growth at 42°C, Gram stain morphology, and lack of UV light absorption.

To obtain a definitive identification of the organism, 16S rRNA gene sequencing was performed. The 16S rRNA gene fragments were amplified by standard methods. Two subregions of the 16S rRNA gene were amplified using two pairs of primers. The first part of the 16S rRNA gene was defined as an approximately 800-bp region between primers 8UA (5’-TACGGTTACCTTGTTACGAC-3’) and 907B (5’-CCGTCAATT CMTTTAGTIT-3’). The second part of the 16S rRNA gene, defined as approximately 700-bp sequences between primers 774A (5’-GTTTGATCCTGGCTCAG-3’) and 907B (5’-CCGTCAATT CMTTTAGTIT-3’), was amplified to obtain the complete 16S rRNA gene sequence. Sequencing data were analyzed by comparison of the consensus sequences in GenBank by using the Ribosomal Database Project (RDP-II) and the Basic Local Alignment Search Tool software (BLAST). Percentage of similarity to other sequences was determined, and Roseomonas mucosa was identified at 99%.

Antimicrobial susceptibility testing of the isolate was carried out using a Clinical and Laboratory Standards Institute (CLSI) reference broth microdilution method (1). MICs were read after 24 h of incubation by using the CLSI interpretative criteria for nonfermentative Gram-negative bacteria (1). The Roseomonas mucosa isolate was susceptible to the following antibiotics (at the MICs shown): amikacin (≤0.5 μg/ml), ciprofloxacin (0.5 μg/ml), gentamicin (≤0.5 μg/ml), imipenem (1 μg/ml), levofloxacin (≤0.5 μg/ml), meropenem (4 μg/ml), and tobramycin (≤0.5 μg/ml). It was intermediate or resistant to ampicillin (>32 μg/ml), cefazolin (>32 μg/ml), ceftazidime (>32 μg/ml), ceftriaxone (32 μg/ml), piperacillin-tazobactam (>512 μg/ml), and trimethoprim-sulfamethoxazole (>8/40 μg/ml).

The patient received a 10-day course of ciprofloxacin and was discharged home uneventfully. He did well for the following 3 months, until he was seen again in the Emergency Department with a fever. Blood cultures were obtained at the time, which yielded Pseudomonas oryzihabitans; the patient was treated with ciprofloxacin and gentamicin for this subsequent episode of bacteremia and recovered uneventfully.

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Roseomonas is a bacterial genus of pink-pigmented, oxidative, Gram-negative coccobacilli which have been cultured from blood and other clinical specimens for several decades. The genus and its species were first named in 1993 to include three named species (R. gilardii, R. cervicalis, and R. fauriae [genomospecies 1, 2, 3, respectively]) and three unnamed species (genomospecies 4, 5, 6) (10). R. mucosa and R. gilardii subspecies rosea were proposed in 2003 (5). Roseomonas spp. resemble Methylobacterium spp., phenotypically and genotypically and were commonly reported as Methylobacterium spp., as indicated by one study where 36 strains of Roseomonas spp. were misidentified as Methylobacterium mesophilicum (5). Interestingly, our patient previously had bacteremia associated with an organism that was likely misidentified as Methylobacterium mesophilicum. Roseomonas spp. differ by their inability to oxidize methanol and to assimilate acetamide and by lack of absorption of long-wave UV light (10). Roseomonas mucosa was initially grouped with R. gilardii but due to sufficient phylogenetic and phenotypic differences, it was reestablished as a distinct species (5). Han et al. described Roseomonas mucosa as slightly fastidious with the formation of very mucoid, runny colonies. On Gram stains, the organism appears as a Gram-negative coccobacillus measuring 0.9 by 1.0 to 0.9 by 1.9 μm. The organism has urease activity and assimilates arabinose, maltose, citrate, and glucose (5).

Roseomonas spp. appear to have low pathogenic potential for humans, but some species may cause clinically significant or even fatal disease in immunocompromised patients. Of the 36 adult patients with Roseomonas infection, six patients experienced persistent bacteremia due to central vein line-related infection (2). Although the natural reservoir of Roseomonas spp. is not known, it has been recovered from environmental sources, such as water and soil (4, 16). The organism has also been recovered from multiple clinical sources, including blood, wounds, peritoneal dialysis fluid, corneal scrapings, and bone (2, 3, 5, 8, 9, 11–15). The majority of Roseomonas infections involved R. gilardii and R. mucosa in adult patients with underlying conditions such as cancer (2). Twenty-two isolates of R. mucosa were characterized from 36 isolates of Roseomonas-like organisms collected over an 11-year period, indicating the prevalence of this particular species in bloodstream infections in adults (5). On the other hand, infections due to Roseomonas spp. are distinctly rare in the pediatric population, with a total of seven cases reported to date; R. gilardii was identified in three, R. fauriae was identified in one, and three were reported as species unknown (6, 7, 13). To our knowledge, R. mucosa has not been identified in any pediatric patients.

The R. mucosa strain isolated from our patient revealed an antimicrobial susceptibility pattern similar to that of other Roseomonas spp. previously reported (2, 5). This organism is typically susceptible to ciprofloxacin as well as to the aminoglycosides and carbapenems but frequently resistant to ampicillin, piperacillin-tazobactam, trimethoprim-sulfamethoxazole, and the extended-spectrum cephalosporins (5, 10). Therefore, extended-spectrum cephalosporins, including ceftazidime, ceftriaxone, and cefepime, should be avoided when choosing an effective drug for treatment of Roseomonas infections (2). When comparing the antimicrobial susceptibility patterns of different species of Roseomonas, R. mucosa has been found to be more resistant to antibiotics, whereas R. gilardii appears to be most susceptible (2, 5). Taking into account the resistant antibiogram pattern and the high prevalence of this species in bloodstream infections, R. mucosa may be indicated as the most clinically significant species (5).

The R. mucosa isolate was cleared from our patient’s bloodstream, and the patient was subsequently discharged. To our knowledge, our case represents the first reported case of R. mucosa isolated from the bloodstream in the pediatric population. It is suspected that the Methylobacte- rium mesophilicum bacterium previously identified in our patient was in fact a Roseomonas sp., leading us to speculate that this may be a recurrent infection. Since Roseomonas spp. appear to be resistant to broad-spectrum antibiotics (i.e., extended-spectrum cephalosporins) commonly utilized to empirically treat bloodstream infections, accurate identification of Roseomonas isolates from clinical sources may prove beneficial when selecting appropriate antibiotics for therapy.

REFERENCES