Case Report

Cellulosimicrobium cellulans isolated from a patient with acute renal failure

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Introduction: Cellulosimicrobium cellulans is a rare human pathogen that is associated with chronic immunosuppression, such as human immunodeficiency virus infection, post-transplantation or end-stage renal disease.

Case presentation: A 59-year-old man with a past medical history of significant cardiovascular, cerebrovascular and peripheral vascular disease was admitted to the intensive care unit (ICU) with intractable seizures. Physical examination, radiographic imaging and culture results suggested the patient had developed metabolic encephalopathy due to pneumonia caused by Staphylococcus aureus and Moraxella catarrhalis. The patient recovered neurologically with the use of broad-spectrum antibiotics but developed acute renal failure during his stay. Seven days later, he relapsed into seizure activity and two separate blood cultures grew Cellulosimicrobium cellulans. Despite maximal antibiotic therapy, the patient continued to deteriorate. After 16 days, the patient’s family withdrew care and he subsequently died.

Conclusion: We report the isolation of Cellulosimicrobium cellulans from a patient who developed acute renal failure following a prolonged stay in the ICU for sepsis encephalopathy.

Keywords: 16S rRNA sequencing; acute renal failure; antimicrobial therapy; Cellulosimicrobium cellulans.

Case report

A 59-year-old man was admitted to the intensive care unit (ICU) with intractable seizures. His past medical history was significant for ischaemic heart disease with two previous myocardial infarctions, peripheral vascular disease requiring a left femoral–femoral bypass and a right femoral–popliteal bypass surgery, chronic obstructive pulmonary disease, dyslipidemia, and a prior admission to the ICU for pneumonia and sepsis. Four months earlier, he had suffered a stroke in the left middle cerebral artery region, leaving him with word-finding difficulties and confusion.

On physical examination, the patient was confused, tachycardic (heart rate 120) and tachypneic (respiratory rate of 40). He had decreased air entry and crackles on auscultation of both lungs, and the rest of his physical examination was unremarkable. Laboratory tests showed a normal blood cell count, electrolytes, urea and creatinine. The patient’s venous blood gas analysis pH was 7.04, with a partial CO₂ pressure of 96 and an elevated anion gap of 16. He was intubated and underwent a computed tomography scan of his head, which showed old cerebral infarcts in both hemispheres, generalized atrophy of the brain, and no abscess or haemorrhage. A chest X-ray demonstrated diffuse pulmonary oedema with possible underlying pneumonia. Electroencephalogram recordings revealed moderate metabolic encephalopathy without a clear seizure focus. A lumbar puncture yielded normal results.

Empirical treatment with intravenous piperacillin-tazobactam (4.5 g every 6 h) and acyclovir (1500 mg initial...
dose and then 200 mg every 12 h) was started. One day after admission, Gram-positive and Gram-negative cocci grew in respiratory cultures and were subsequently identified as Moraxella catarrhalis and Staphylococcus aureus. Identification was initially made by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS; Bruker Daltonics), and was >2.0 on several repeats, including the formic acid extraction method, which yielded a score of >2.3. The S. aureus isolate was susceptible to vancomycin (MIC 1 µg ml⁻¹), cloxicillin (MIC 0.5 µg ml⁻¹), clindamycin (MIC <0.25 µg ml⁻¹), erythromycin (MIC <0.25 µg ml⁻¹) and sulfamethoxazole-trimethoprim (MIC <10 µg ml⁻¹).

At this time, the patient’s creatinine rose significantly to 160 µmol l⁻¹ (normal 62–120 µmol l⁻¹). Acyclovir was discontinued and the dosage of piperacillin-tazobactam [2.25 g intravenously (IV) every 12 h] was reduced because of the patient’s poor creatinine clearance. Vancomycin (1 g IV every 24 h) was also added based on the lack of response to treatment and suspicion of methicillin-resistant Staphylococcus aureus as a cause of the infection.

Seven days later, the patient developed fever, hypotension and tachycardia, and an increased frequency of seizures despite IV anti-epileptic treatment with phenytoin (100 mg every 6 h). Repeat lumbar puncture and respiratory cultures were negative. However, two sets of blood cultures drawn 6 h apart from a peripheral vein and the left internal jugular central venous catheter grew Gram-positive rods, which were identified as Cellulosimicrobium cellulans by MALDI-TOF MS. The catheter was replaced, and the patient remained on antimicrobial therapy with piperacillin-tazobactam and vancomycin. The patient did not recover his renal function and required daily haemodialysis. He could not be weaned off mechanical ventilation, and began requiring inotropic support to maintain his blood pressure. After 16 days in the ICU, the family elected to withdraw care, and the patient died.

Cell morphology obtained from both sets of blood culture bottles showed Gram-positive rods. After overnight incubation at 37 °C in aerobic conditions on BBL Trypticase Soy Agar II plus 5 % sheep blood plates (Becton Dickinson and Co.), colonies were 1 mm in size, non-haemolytic, grey, smooth and convex (Fig. 1). A culture grown in aerobic tryptic soy broth (TSB; Becton Dickinson and Co.) demonstrated easily decolorized Gram-positive coccobacillary morphology during the stationary phase as seen in Fig. 2(a), and slender, long, Gram-positive rods in the exponential phase as demonstrated in Fig. 2(b). PCR of the 16S rRNA gene was performed on DNA isolated from cultures grown in TSB (forward primer: 5′-AGAGTTTTGATCTTGTGCTCA-3′; reverse primer: 5′-AAGGAGGTGATCCGCGCA-3′; Invitrogen). Sequencing of the purified PCR product (Robarts Research Institute Sequencing Facility, London, Ontario, Canada) and a BLAST search of related sequences in GenBank showed that the sequence matched the type strains of C. cellulans at 100 % nucleotide identity, Cellulosimicrobium funkei at 100 % nucleotide identity and Cellulomonas sp. at 100 % nucleotide identity.

The genus Cellulosimicrobium is composed of three species: C. cellulans, C. funkei and C. terreum. Cellulosimicrobium spp. are non-acid-fast, catalase-positive, Gram-positive bacilli belonging to the suborder Micrococcaeae, order Actinomycetales and class Actinobacteria (Brown et al., 2006; Rowlinson et al., 2006; Yoon et al., 2007). C. cellulans, formerly known as Cellulomonas cellulans or Oerskovia xanthineolytica, is an uncommon human pathogen that has been isolated from soil, grass cuttings, decaying plant materials and sewage facilities (Brown et al., 2006; Yoon et al., 2007).

Infections due to Cellulosimicrobium spp. have been reported in almost 30 cases, including bacteremia (Casanova-Roman et al., 2010), endocarditis (Urbina et al., 2003), intra-abdominal sepsis (Borra & Kleinfeld, 1996; Lujan-Zilbermann et al., 1999; Thomas et al., 2007), meningitis (Kailath et al., 1988; Vilmaz et al., 2006), keratitis (Shah et al., 1996), endophthalmitis (Jaru-Ampornpan et al., 2011) and septic arthritis (Magro-Checa et al., 2011) and in association with bone-marrow transplantation (Ellerbroek et al., 1998). In most of the cases, infection was secondary to a medical device or foreign body, and removal of the latter was required for resolution of the infection (Harrington et al., 1996; Kailath et al., 1988). Although two cases have been reported in previously healthy patients (Casanova-Roman et al., 2010; Tucker et al., 2008), infection with C. cellulans has typically been described in immunocompromised patients with human immunodeficiency virus infection (Heym et al., 2005), tumor-induced immunosuppression, post-transplant...
patients and patients with end-stage renal disease (Ellerbroek et al., 1998; Urbina et al., 2003). The latter was the most frequent underlying condition associated with C. cellulans infections (Rihs et al., 1990), although our patient developed an infection after sustaining acute renal failure, an occurrence that has not been reported elsewhere.

Similar to a previous study (Magro-Checa et al., 2011), our sequencing results demonstrated that 16S rRNA sequencing alone may not be able to distinguish between the three closely related species, although the differentiation may not necessarily affect treatment (Brown et al., 2006). C. cellulans has been reported as being resistant to erythromycin and other macrolides but is considered susceptible to vancomycin, which was the therapy of choice in most of the reported cases. Other treatment options such as linezolid or rifampin may be associated with a higher rate of cure (Magro-Checa et al., 2011; Tucker et al., 2008).

To our knowledge, this case represents the first documented case of C. cellulans infection following acute renal failure. While C. cellulans can cause infections in healthy patients (Casanova-Roman et al., 2010; Tucker et al., 2008), our case demonstrates its role as an opportunistic pathogen in the context of a patient who sustained renal injury and had a prolonged stay in the ICU.

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The authors do not have any actual or potential conflicts of interest to declare.

References


Fig. 2. Gram stain of C. cellulans from colony isolated on sheep blood agar demonstrated easily decolorized Gram-positive coccobacillary morphology during the stationary phase (a), and slender, long, Gram-positive rods in the exponential phase (b).


