Case report

A 37-year-old male was transferred from a peripheral hospital to St Vincent’s Hospital, Sydney, Australia, for surgical management of an aortic root abscess and prosthetic valve endocarditis (PVE). The patient’s native aortic valve (AV) was replaced in November 2006 secondary to a meticillin-sensitive Staphylococcus aureus AV endocarditis following episodes of intravenous drug use. Following AV replacement, the patient returned to his normal activities. However, he denied any further intravenous drug use. A follow-up transthoracic echocardiogram in March 2007 revealed a normally functioning AV. Two months later (May 2007), the patient presented to a rural hospital with fevers, hypotension and congestive cardiac failure. A diagnosis of PVE was considered and intravenous gentamicin, ceftriaxone and vancomycin were commenced. However, the symptoms of sepsis and congestive cardiac failure failed to improve with medical therapy and the patient was transferred for surgical intervention. A repeat AV replacement and a homograft aortic root replacement were performed for PVE and multiple aortic root abscesses.

Blood cultures and tissue from the AV and root were sent for microbiological analysis. An oxidase-positive Gram-negative rod was isolated from both tissue and blood culture after 48 h of incubation. The Gram-negative rod from the blood culture was identified as Burkholderia cepacia by an API 20 NE (bioMérieux) with 99.5% probability and a ‘very good identification’ confidence level (biotype profile number 1047777), while the Gram-negative rod from the tissue cultures was identified as Achromobacter xylosoxidans by an API 20 NE (bioMérieux) with 94.5% probability (biotype profile number 1040477) and a ‘good identification’ confidence level. Identical phenotypic results were obtained on repeat API 20 NE testing on fresh subcultures from both the blood culture and the tissue isolates.

Due to identification discrepancies, further testing by analysis of whole-cell long-chain fatty acids and 16S rRNA were performed on both isolates. The Microbial Identification System (MIDI Corporation) confirmed both isolates to be A. xylosoxidans subsp. xylosoxidans (similarity index of 0.658; an index >0.5 is considered adequate for speciation). To exclude the possibility of the B. cepacia complex, a PCR was performed as previously described using primers targeting the recA gene (Mahenthiralingam et al., 2000). The PCR was negative for B. cepacia complex DNA.

Genomic DNA was extracted from both isolates using a QIAamp DNA Mini Kit (QIAGEN), and DNA amplification of the small-subunit rRNA gene was performed using universal primers as previously described by Fry et al. (2005). The PCR products were purified using the QIAquick PCR Purification kit (Qiagen) according to the manufacturer’s instructions. The PCR products were sequenced in both directions on an ABI Prism 3730 automated sequencer at the SUPAMAC facility (Royal Prince Alfred Hospital, Sydney). The sequences generated were compared to those available in the GenBank databases using the Blastn program run on the National Center for Biotechnology Information server (http://www.ncbi.nlm.nih.gov/BLAST/).

The sequence data generated from the 16S rRNA gene from both isolates were identical and demonstrated 100% similarity with the 16S rRNA gene sequence of numerous A. xylosoxidans subsp. xylosoxidans isolates (GenBank accession nos DQ466568, DQ361075, AF411021, AF411020, AF411019 and AB161691). The organism revealed the following susceptibilities by E-test: gentamicin MIC 0.094 µg ml⁻¹; ticarcillin–clavulanate MIC 12 µg ml⁻¹; cefepime MIC 0.016 µg ml⁻¹; cefotaxime MIC 12 µg ml⁻¹, ciprofloxacin MIC 0.75 µg ml⁻¹; and meropenem
Achromobacter on phenotypic and genotypic data, including the genus
Alcaligenaceae. The family Achromobacter comprises several genera, based
on phenotypic and genotypic data, including the genus Achromobacter (Yabuuchi et al., 1998). A. xylosoxidans is a ubiquitous environmental Gram-negative, oxidase-positive, non-glucose-fermenting rod. There are two subspecies, A. xylosoxidans subsp. xylosoxidans and A. xylosoxidans subsp. denitrificans.

Human infections are rare. Nosocomial infections predominate with an association between infection and immunosuppression, especially in patients with underlying malignancy, in HIV-infected patients and in premature infants (Aisenberg et al., 2004; Manfredi et al., 1997). Contaminated intravenous lines are the most common source of infection, with other potential sources including dialysis fluid, incubators and mechanical ventilators (Gómez-Cerezo et al., 2003; Reverdy et al., 1984). Community-acquired infections account for the minority of cases and are generally restricted to cystic fibrosis patients with temporary or persistent infections of the respiratory tract (Davies & Rubin, 2007).

The most common manifestation of infection with this organism is bacteraemia. Polymicrobial bacteraemia occurs in 28% of patients, with coagulase-negative Staphylococcus the most common accompanying organism (Gómez-Cerezo et al., 2003). Endocarditis has been described on four previous occasions only (Ahn et al., 2004; Duggan et al., 1996; Lofgren et al., 1981; Martino et al., 1990). Our patient is unique as infective endocarditis was secondary to a community-acquired bacteraemia as a consequence of intravenous injection of drugs. The previously reported cases required removal of the pacemaker leads and prosthetic valve. The virulence of this organism was confirmed in our patient, who required an AV and root replacement. The importance of an accurate medical history to ascertain the source of unusual organisms is highlighted.

Characteristic antimicrobial susceptibility patterns of A. xylosoxidans subsp. xylosoxidans include high levels of resistance to cephalosporin (>90%), aminoglycoside (>90%) and quinolone (>80%) antibiotics. Variable intrinsic resistance to broad-spectrum anti-psuedomonal penicillins is described. Although our isolate was sensitive to ticarcillin–clavulanic acid on MIC testing, a β-lactamase enzyme was detected by nitrocephin disc testing; therefore, meropenem was chosen as resistance to this antibiotic is rare (Gómez-Cerezo et al., 2003; Shie et al., 2005).

Identification of A. xylosoxidans subsp. xylosoxidans may be problematic. Traditional phenotypic and commercially available tests are often unreliable and may lead to misidentification as other non-fermenting organisms, in particular members of the B. cepacia complex (Wellinghausen et al., 2006). Tissue and blood isolates which were subsequently proven to be identical gave different profiles and hence a different identification using the API 20 NE system. Molecular methods such as sequencing of ribosomal genes allow for more accurate identification of non-fermenting Gram-negative rods than traditional phenotypic methods. However, care should be taken when interpreting the sequence data generated as public DNA databases such as GenBank may have faulty or incorrectly assigned sequences leading to the misidentification of isolates (Wellinghausen et al., 2006).

A. xylosoxidans bacteraemia has a mortality rate of between 15 and 48% (Duggan et al., 1996; Shie et al., 2005). Risk factors for higher mortality rates include age over 65 years, neutropenia, presence of polymicrobial infection and nosocomial infection (Gómez-Cerezo et al., 2003; Shie et al., 2005).

In conclusion, community-acquired A. xylosoxidans bacteraemia is uncommon while endocarditis is rare. An accurate intravenous drug use history should be sought, especially related to the paraphernalia and methods used in the injecting process. The most appropriate antimicrobial therapy has not been determined but our patient responded well to surgical intervention and meropenem.

Acknowledgements

We thank Marion Yeun and Maureen Lynch from the Identification Reference Laboratory, Centre for Infectious Diseases and Microbiology, Institute of Clinical Pathology and Medical Research, Westmead Hospital, NSW, Australia, for help with analysis of whole-cell long-chain fatty acid testing of the isolate.

References


