Elizabethkingia miricola bacteriemia in a young woman with acute alcoholic pancreatitis

Bactériémie par *Elizabethkingia miricola* chez une jeune femme avec pancréatite aiguë alcoolique

*Elizabethkingia miricola* is a Gram negative, non-motile, non-spor-forming rod (0,5 × 1,0-2,5 μm). It shows a good growth on MacConkey agar. On solid medium colonies are very sticky. It is characterized by indole production, urea hydrolysis and acid production from D-fructose, D-glucose, lactose, D-maltose, D-mannitol and trehalose, but not from D-arabinose, D-cellobiose, raffinose, sucrose, salicin or D-xylose [1]. It was first isolated in 2003 by Li from condensation water on the space station Mir [2].

The new genus *Elizabethkingia* was described using the technique Matrix Assisted Laser Desorption/Ionization Time Of Flight Mass Spectrometry (MALDI TOF MS) (BRUKER). The first patient reported with an infection caused by *E. miricola* was a hematologic patient with mantle cell lymphoma who had undergone stem cell transplantation and chemotherapy; the microorganism was isolated from blood and sputum [3].

*E. miricola*, initially named *Chryseobacterium miricola*, was reclassified along with *Chryseobacterium meningosepticum* into the new genus *Elizabethkingia*. The genus *Chryseobacterium* was first described during reclassification of members of the genus *Flavobacterium*. Recent genetic studies have revealed that the genus *Chryseobacterium* is genetically heterogeneous, and that *C. meningosepticum* and *C. miricola* can be readily differentiated from other *Chryseobacterium* species. We describe a bacteremia by *E. miricola* in a 34-year-old woman. The patient was hospitalized for acute alcoholic pancreatitis with evidence at the abdomen CT scan of haemorrhagic areas. The patient presented also respiratory distress, requiring non-invasive ventilation; CT of the lung showed atelectasic areas without inflammatory lung consolidation. She was treated with benzodiazepines to prevent abstinence syndrome. The Balthazar’s score was 10.

During antibiotic therapy with imipenem-cilastatin and fluconazole she developed fever. Blood cultures resulted positive for *E. miricola*, susceptible to levofloxacin, ciprofloxacin, trimethoprim/sulfamethoxazole and piperacillin.

Blood cultures (one bottle for aerobes and one for anaerobes) were processed with BACTEC (Becton Dickinson or BD) for 5 days. The positive sample underwent microscopical examination with GRAM stain and than spread on 3 plates: Chocolate Agar (BD), Blood Agar (BD) and Schaedler Agar (BD). After incubation in the thermostat at 37 °C for 24 hours the colonies growth was observed. A colony was taken and identified using the technique Matrix Assisted Laser Desorption/Ionization Time Of Flight Mass Spectrometry (MALDI TOF MS) (BRUKER). When the result of the blood culture showed the growth of *E. miricola*, ciprofloxacin 400 mg BID was started in association with imipenem-cilastatin. Successive blood cultures resulted negative. Reactive C Protein (RCP) decreased from 25 to 15 mg/dl but the patient remained febrile. Piperacillin/tazobactam was then added and imipenem-cilastatin was stopped. After this shift the fever reduced and after two weeks of therapy RCP had decreased to 3,99 mg/dl. The CT of the abdomen showed the reduction of haemorrhagic areas.

In contrast to *C. meningosepticum*, etiologic agent of pneumonic, septic shock in immunocompromized host [4], necrotizing fascitis [5], bacteriemia and meningitis in diabetics [6,7], burn infections [8], and meningitis, bacteriemia and pneumonia in pediatrics patients [9,10], *E. miricola* had been isolated only in one haematological patient from blood, likely after a pulmonary infection [3].

Although not strictly immunocompromized because not exposed to chemotherapy nor underwent invasive ventilation, the patient we describe was critically ill, with impaired general conditions as a result of chronic liver disease and alcohol abuse and she had been treated with broad spectrum antibiotic for a week. In all patients described in the literature review, the isolation of *Elizabethkingia meningoseptica* was always preceded by antibiotic therapies [11].

*E. meningoseptica* has been repeatedly isolated from environmental sources (soil, plants and water) and nosocomial transmission is the most common route of the infection and outbreak, while *E. miricola* has been rarely found.

The lack of interpretative standard for susceptibility to antibiotics and clinical break point, and the lack of other clinical report make it difficult to establish the most adequate therapy and if an antibiotic association is necessary to prevent the risk of antibiotic resistance development.

*E. meningoseptica* and *E. miricola* are multidrug-resistant organisms. *E. meningoseptica* possesses two different types of β-lactamases (class A extended-spectrum β-lactamases and class B metallo-β-lactamases), which makes it resistant to β-lactam antibiotics and carbapenems. Most of the *E. meningoseptica* isolates were sensitive to levofloxacin, ciprofloxacin, tigecycline, piperacillin/tazobactam and trimethoprim sulfamethoxazole and...
all were resistant to β-lactam antibiotics. In addition to β-lactam antibiotics, *E. meningoseptica* is usually resistant to aztreonam, aminoglycosides and vancomycin.

Some help in clinical practice could came from the reported antimicrobial experience in infection by *C. meningosepticum* (*E. meningoseptica*), which belongs to the same genus *Elizabethkingia*, but even this microorganism is relatively uncommon and there is no consensus for the empiric treatment regimen [4].

Also diagnostic tools raise some interpretation questions. MALDI TOF technique is able to distinguish between microorganisms very similar to each other through the comparison of the proteic spectra produced by the microorganism and those present in the Data Base. This technique is able to differentiate microorganisms belonging to the same species or able to produce toxins. For microorganisms belonging to uncommon genera such as *Elizabethkingia*, the identification can result more uncertain because bacterial proteic spectra are less represented in the Data Base. In this situation the association of different techniques such as molecular identification (sequencing) may be necessary for a reliable identification [12].

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**References**


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