Bacteremia caused by *Paracoccus yeei* in patient with compensated cirrhosis of the liver

Bacteremia por Paracoccus yeei *en un paciente con cirrosis hepática compensada*

Dear Editor,

The patient was a 56-year-old man with a history of type 2 diabetes mellitus and partial hepatectomy and cholecystectomy due to a hepatocellular carcinoma diagnosed two years before. He presented at the emergency department with a three-day history of fever accompanied by chills, generalized joint pain and dyspnea. He had no diarrhea, expectoration, urinary symptoms, or skin lesions, so the working diagnosis was a bloodstream infection with a probable abdominal focus. The sediment was not abnormal, and abdominal ultrasonography ruled out cholelithiasis and bile duct obstruction. Two peripheral blood samples were started, and empirical antibiotic treatment with meropenem was initiated.

Two blood cultures, both aerobic bottles, were positive after 41 h of incubation (BacT/ALERT®, Biomérieux). Direct Gram staining of the blood culture revealed moderate-sized, gram-negative cocci with a characteristic vacuolated appearance (Fig. 1). Blood cultures were transferred to chocolate and blood agar plates and incubated at 37 °C in an atmosphere with 5% CO_2. Two days later, shiny brown, mucoid, non-hemolytic colonies were observed on the plates (Fig. 1). Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) identified the bacteria as *Paracoccus yeei* (*P. yeei*) with a score value of 2.212. Bacterial 16S rRNA gene was amplified and sequenced using universal primers 27 F (5′-AGAGTTTGATCMTGGCTCAG-3′) and 1492R (5′-TA CGGTTACCTTGTTACGACTT-3′). The obtained sequence was compared with data available from GenBank using BLAST (https://blast.ncbi.nlm.nih.gov/Blast.cgi) and a 99% identity with the *P. yeei* CCGU 32053 16S rRNA sequence was found.

Susceptibility testing was performed using the minimum inhibitory concentration (MIC) microdilution method (Microscan WalkAway, Beckman coulter). As no interpretative criteria have yet been published for *P. yeei*, we followed the *Pseudomonas* spp. EUCAST breakpoints for aminoglycosides, quinolones and piperacillin-tazobactam and PK-PD (Non-species related) EUCAST breakpoints for the rest.[1] The MIC values were as follow (all of them susceptible): piperacillin-tazobactam: ≤8 μg/mL, ceftazidime: ≤1 μg/mL, cefepime: ≤1 μg/mL, aztreonam: 4 μg/mL, meropenem: ≤1 μg/mL, amikacin ≤8 μg/mL and ciprofloxacin ≤0.5 μg/mL. Although others have reported strains resistant to ciprofloxacin[2] or to third-generation cephalosporins,[3] our strain was sensitive to these antibiotics.

In the days after the initiation of antibiotic treatment, the patient's condition improved and follow-up blood cultures were negative. At discharge, the patient was prescribed ciprofloxacin for two weeks.

P. yeei, which is classified within the family *Rhodobacteraceae*, are gram-negative, obligate aerobic, nonfermenting cocci or coccobacilli with a characteristic vacuolated or O-shaped appearance in Gram staining. Colonies grow after 24 h of incubation on blood and chocolate agar but not on MacConkey agar. Regarding the biochemical profile, it is catalase and oxidase positive and reduce nitrates.[4]

Since the natural habitat of this bacteria has not been fully defined, it is difficult to predict which patients are at risk of infection. In our patient, the diagnosis was oriented toward sepsis due to an abdominal source, although no abdominal focus of infection had been clearly established. Immunosuppression and certain environmental factors play a decisive role in the pathogenicity of this microorganism, although in our case, the patient's liver

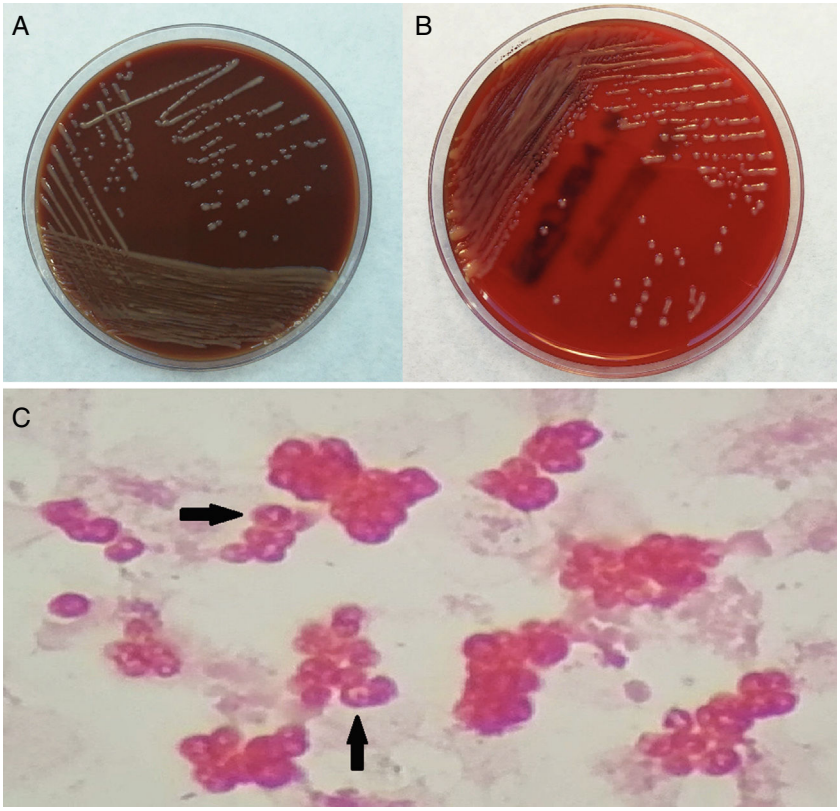

Fig. 1. Mucoid colonies of *Paracoccus yeei* isolated on Chocolate agar (A) and Blood agar (B) after 48 h of incubation. Direct Gram stain from the aerobic blood culture bottle revealed Gram negative cocci with characteristic "doughnut-shape" (arrows) (C).

function was adequate and there was no evidence of immunodepression.

Bacterial infections are much more common in patients with cirrhosis than in the general population due to the increased inflammatory response and dysregulation of the immune system.[5] *P. yeei* is unique within the genus because it has been associated with opportunistic human infections. Most reported cases are infections in immunosuppressed patients, most commonly peritonitis in patients undergoing peritoneal dialysis.[2,3,6,7] Other reported infections include myocarditis in a heart transplant recipient,[8] keratitis in patient who used contact lenses,[9] and septic arthritis.

To our knowledge, only two cases of bacteremia due to *P. yeei* have been reported. In one, the source was bullous lesions[4]; in the other, a patient with decompensated cirrhosis, the source was unidentified but presumably an abdominal focus.[10] Our patient had histologically confirmed cirrhosis, but no clinical, laboratory, or imaging signs of decompensation, despite a prior history of hepatocellular carcinoma. Like some other patients with *P. yeei* infections, he also had diabetes mellitus, a known risk factor for infections.

It is possible that infections caused by *P. yeei* are underdiagnosed due to low clinical suspicion, given the scant reports in the literature and the low a priori pathogenic potential for this microorganism. In addition, its macroscopic appearance with colonies initially resembling those of a coagulase-negative staphylococcus may lead to the misidentification of the strain if no further investigations are performed.

In recent years, the use of new molecular techniques such as MALDI-TOF MS has led to an increase in the identification of little known microorganisms as the cause of infections. The present case of bacteremia due to *P. yeei* confirms the role of this microorganism as a potential source of infection in humans.

Conflict of interest

The authors declare no conflict of interests.

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Aerococcus urinae infective endocarditis☆

Endocarditis infecciosa por Aerococcus urinae

Aerococcus spp. are gram-positive bacteria, facultative anaerobes and arranged in pairs and clusters. Since this genre was defined in 1938[1] new species have been identified —*Aerococcus viridans, A. sanguinicola, A. christensenii, A. urinaehominis, A. urinaeequi* and *A. suis*—, but it wasn't until 1992 that*Aerococcus urinae* was defined as a new species.[2] *Aerococcus* ssp. are found ubiquitously on the ground and in the air.[3] Their participation as part of the normal flora of the human urinary tract and of the human oral flora in patients undergoing treatment with cytostatics is relevant.[4] Despite this, *A. urinae* is a rare cause of urinary tract infection (UTI) and invasive disease or bacteraemia are unusual (0.5-3 cases/10^6 people-year). The overall incidence of infective endocarditis (IE) due to *A. urinae* is unknown, but to the best of our knowledge, no more than 50 cases.[5]

61-year-old male with a history of obesity, type 2 diabetes mellitus , arterial hypertension and dyslipidaemia under treatment with enalapril, metformin and gemfibrozil. He is admitted for community-acquired pneumonia and requires bladder catheterisation for acute urinary retention during admission without finding any previous structural or infectious urological history. He is taking levofloxacin when he presents with dyspnoea, poor general condition, and fever following 2 days of antibiotics treatment. On physical examination he has a fever of 39 °C and systolic murmur III/VI in the aortic area. The lab tests show 19,600 leukocytes/μl with 85% neutrophils and C-reactive protein (CRP) of 145 mg/l (normal value up to 5 mg/l). Blood cultures are taken and the growth of *A. urinae* is seen in two bottles. The microorganism was susceptible to the following antibiotics: penicillin (MIC = 0.008 mg/l), ampicillin (MIC = 0.015 mg/l), meropenem (MIC = 0.06 mg/l), vancomycin (MIC = 0,25 mg/l) and rifampicin (MIC = 0.015 mg/l). Ciprofloxacin was classified as resistant (MIC > 2 mg/l). Transthoracic and transesophageal echocardiograms are conducted, which reveal two

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