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Scientific letters

Tuboovarian abscess due to *Eikenella corrodens*☆

Absceso tubo-ovárico por Eikenella corrodens

Dear Editor,

Pelvic inflammatory disease (PID) is one of the most serious gynaecological infections in non-pregnant women of childbearing age,[1] and can lead to complications such as tubal infertility, ectopic pregnancy, abdominal pain and tubo-ovarian abscess.[1–3] *Neisseria gonorrhoeae* and *Chlamydia trachomatis* are the most common aetiological agents, with sexual contact being the principal route of transmission.[3] The insertion of an intrauterine device (IUD) and invasive gynaecological procedures are significant risk factors, and involve microorganisms from the normal microbiota of the genital tract, primarily species of *Streptococcus*, *Enterococcus*, *Peptostreptococcus* and *Bacteroides.*[2,3] *Eikenella corrodens* and *Finegoldia magna* form part of the oropharyngeal, gastrointestinal and genitourinary microbiota, and their involvement in intra-abdominal and gynaecological infections is rare.[3] We present the case of a tubo-ovarian abscess caused by *E. corrodens* and *F. magna* in a patient with no risk factors.

A 23-year-old woman without an IUD, and with no gynaecological history of interest, was seen for hypogastric pain and abundant vaginal secretions. The examination and transvaginal ultrasound revealed no signs of disease. The patient returned 10 days later due to intense pain and a fever of 38.3 °C. Transvaginal ultrasound was performed and revealed a mass compatible with tubo-ovarian abscess in the retrouterine area. Treatment was initiated with clindamycin, ampicillin and gentamycin, and laparoscopic surgery was performed. During the intervention, the abscess was ruptured, a sample was taken for microbiological cultures and left salpingectomy was performed. During the immediate post-operative period, the patient presented with fever, elevated procalcitonin (2 ng/l), leukocytosis (22.8×10^3/l) and signs compatible with sepsis, and was admitted to the intensive care unit. Blood cultures were taken, and the antibiotic therapy was switched to piperacillin/tazobactam and doxycycline. Following favourable evolution, the patient was transferred to the gynaecology ward.

With regard to the microbiological study of the abscess, the Gram stain revealed abundant polymorphonuclear leukocytes, gram-negative bacilli and gram-positive cocci. The aerobic culture isolated small greyish colonies that were catalase-negative and oxidase-positive, and produced a slight depression in chocolate agar. Additionally, small greyish colonies were observed in Schaedler agar and phenylethyl alcohol agar after anaerobic incubation. *E. corrodens* was identified using the Vitek® 2 (bioMérieux) system's NH card, and confirmed by mass spectrometry on the Vitek® MS system (bioMérieux). *F. magna* was identified from the API® rapid ID 32 A gallery (bioMérieux). The antibiogram for both microorganisms was performed using the E-test gradient diffusion assay (bioMérieux) and interpreted based on Clinical and Laboratory Standards Institute (CLSI) criteria. *E. corrodens* showed resistance to azithromycin and susceptibility to meropenem, ceftriaxone, ciprofloxacin, levofloxacin, tetracycline, ampicillin and amoxicillin/clavulanic acid. The MICs for gentamycin and piperacillin/tazobactam were 6 and <0.016/4 mg/l, respectively (without CLSI interpretation). *F. magna* showed resistance to metronidazole and susceptibility to meropenem, cefotaxime, clindamycin, penicillin, ampicillin, amoxicillin/clavulanic acid and piperacillin/tazobactam (MIC = 0.032 mg/l). Based on these results, antibiotic therapy with piperacillin/tazobactam was maintained for 10 days. The patient showed favourable evolution, and was asymptomatic at discharge.

The majority of *E. corrodens* infections are polymicrobial.[4,5] In our case, it was isolated together with *F. magna*, a combination which was not found in the literature reviewed.

Moreover, gynaecological infections caused by *E. corrodens* are rare, being associated primarily with PID in women with IUDs[4–6] and chorioamnionitis.[7] In the case presented, we highlight its role together with *F. magna* in causing a tubo-ovarian abscess in the absence of risk factors. Antibiotic therapy with clindamycin and gentamycin is one of the empirical treatments recommended by clinical guidelines.[2,8] In our case, ampicillin was added, as this combination has demonstrated good results in the treatment of tubo-ovarian abscesses.[9] Due to the rupture of the abscess during surgery and appearance of signs of sepsis, treatment was switched to piperacillin/tazobactam, following the recommendations for the management of intra-abdominal infection in high-risk patients.[10] Doxycycline was also added as antibiotic prophylaxis against *C. trachomatis*. After obtaining the microbiology results, the decision was made not to alter the treatment as the MICs for piperacillin/tazobactam were low for both microorganisms, and the patient showed favourable evolution. Due to the variety of serious infections that *E. corrodens* can cause and their possible complications, we believe it is important to correctly isolate and identify the microorganism, and to assess its role as a causal agent in obstetric and gynaecological infections.

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Blood culture time to positivity in oncology pediatric patients

Tiempo de positividad en hemocultivos de pacientes oncológicos pediátricos

Dear Editor:

Bloodstream infections (BSI) are common and severe in patients with oncologic and hematologic diseases, mainly accounting for chemotherapy-induced neutropenia alongside with invasive procedures.[1] In these patients, microorganisms of the saprophytic microbiota are frequently considered clinically significant, as they often colonize intravascular devices (IVD).[2] In our pediatric hospital, we inoculate blood from the IVD[3] only in one blood culture (BC) bottle and we do not usually obtain a peripheral BC, making it more complex to discriminate contamination from infection.[4] We aimed to assess the usefulness of time to blood culture positivity (TTP) to predict significant bacteriemia.

This is an observational prospective study in a cohort of oncology and hematology pediatric patients (<18 years at inclusion) that presented with fever during treatment, in most cases during neutropenia periods, at Hospital Sant Joan de Dèc)u (Barcelona, Spain) from January to December 2016. Blood samples were obtained from IVD, usually a one-lumen tunneled central venous catheter (Port-A-Cath), and inoculated into one pediatric aerobic BacT/Alert PF bottle, to be later processed using BacT/Alert (BioMèc)rieux, Durham, NC, USA) automatic incubation system. As per local protocols, BC were performed at onset of each febrile episode, and consecutively every 24•48 h if fever persisted despite antibiotics.

For isolates belonging to saprophytic microbiota to be considered clinically significant, at least one of the following criteria had to be fulfilled: (a) fever coincided with the use of the IVD; (b) the same strain was isolated in at least 2 consecutive BC; (c) the same strain was isolated from BC and the device exit site; and (d) the same strain was isolated from BC and the device culture after its removal. Clinical and microbiological data were collected and assessed together with the physician in charge of the patient.

During the study period, 1923 BC from pediatric hematology and oncology patients with fever were processed in the microbiology laboratory. Overall, bacterial growth was detected in 151 BC (7.9%, 95%CI: 6.7•9.1%) from 74 patients, of which 86 (4.5%), belonging to 47 episodes of bacteraemia from 37 patients, were considered clinically significant and 65 (3.4%), from 50 patients, were deemed contaminants.

Underlying diseases of patients with a clinically significant positive BC included solid tumors ($n = 39$), acute leukemia ($n = 30$), lymphoma ($n = 1$) and other hematologic diseases ($n = 4$). Primary pathogens included the following (number of isolates/episodes of bacteremia): 17/14 *Enterobacteriaceae*, 11/3 *Staphylococcus aureus*, 4/3 *Pseudomonas aeruginosa*, 2/2 *Streptococcus pneumoniae*, 1/1 *Haemophilus influenzae*, 1/1 *Enterococcus faecium*, 1/1 *Campylobacter jejuni* and 2/1 *Candida parapsilosis*. Microorganisms from the saprophytic microbiota that were considered clinically significant were: 35/14 *Staphylococcus epidermidis*, 5/2 *Staphylococcus hominis*, 3/2 *Micrococcus* spp., 3/2 *Bacillus cereus* and 1/1 *Streptococcus mitis*.

Finally, 42 coagulase-negative staphylococci, 9 *Micrococcus* spp., 2 *Bacillus* spp. and 12 isolates of other species were considered contaminants. Median (IQR) TTP of contaminants (25.2 h [18.0•34.3]) was significantly longer than that of all clinically significant BC (15.1 h [10.3•24.0]; $p < 0.0001$), but not enough to set up a useful TTP cut-off to discriminate both groups.

However, when only the first BC of each episode was considered, the TTP differences (13.2 h [8.9•18.0]) with contaminant BCs increased ($p < 0.0001$); 93.6% of clinically significant isolates (including all those from the saprophytic microbiota) were detected in less than 24 h, *versus* 43.1% of contaminants and 53.8% of significant isolates from non-first BCs ($p < 0.0001$). TTP exceeded 24 h in only 3 first clinically significant BCs (*C. parapsilosis*, *H .influenzae* and *C. jejuni*, which grew after 48, 57 and 91 h, respectively) that are known to usually show a slow growth.[5] Sensitivity, specificity, positive and negative predictive value for a clinically significant first BC to grow within 24 h after inoculation were 0.94, 0.57, 0.61 and 0.93, respectively.

In the oncologic child, the primary focus of bacteraemia is frequently the colonization of IVD,[6] and often the causative agent is part of the saprophytic microbiota. This fact would explain the differences among first and following BC TTP in clinically significant isolates. Despite adequate antibiotic therapy, some microorganisms remain in the inert structure of the IVD, out of reach of antibiotics, and are still detected in subsequent BC. In the latter, lower concentrations of the microorganism in the blood sample would lengthen the BC TTP. *S. epidermidis* was the most frequently isolated microorganism in our study, making it critical to discriminate between true infection and IVD contamination. At present, *S.*