Case report

Atopobium vaginae intrapartum bacteremia: A case report with a literature review

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ABSTRACT

Atopobium vaginae is an anaerobic Gram-positive bacterium recognized as a causative agent of bacterial vaginosis and associated with preterm delivery. Invasive infection and bacteremia have been rarely reported. We describe the case of a woman expecting her firstborn child who presented with a \(A.\) vaginae bacteremia during labor. Identification was performed using 16S rRNA gene sequencing. Both maternal and fetal outcomes were favorable due to the maternal treatment with amoxicillin-clavulanic acid. We identified three other cases in the literature with different fetal outcome. The genetic diversity of \(A.\) vaginae should be further explored in order to reveal potential strains with differential pathogenic potential.

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1. Introduction

Atopobium vaginae is a facultative anaerobic Gram-positive bacterium which is part of the human vaginal microbiota \([1,2]\). The genus Atopobium was established in 1992 for a group of bacteria formerly known as Lactobacillus minutum or \(L.\) rima and Streptococcus parvulus \([3]\). Recently, different studies have emphasized the role of \(A.\) vaginae in bacterial vaginosis (BV) \([2,4]\). Among the bacterial species associated with BV, \(A.\) vaginae has been independently associated with a higher risk of preterm birth \([5,6]\). However, invasive disease caused by \(A.\) vaginae, including bacteremia, has been rarely reported \([7–9]\).

We describe a case of \(A.\) vaginae bacteremia occurring during labor and present a short literature review of \(A.\) vaginae bacteremia during pregnancy.

2. Case presentation

A 29-years old caucasian woman was admitted to the delivery room for ongoing labor. She was primigravid and it was a singleton pregnancy. Gestational age was 39 weeks and 3 days. The pregnancy was uneventful. During labor, acceleration of fetal heart rate was detected indicating fetal distress. Delivery was assisted with vacuum and complicated by 0.5L blood loss. APGAR scores were 8, 9 and 10 at 1, 5 and 10 min respectively. Maternal temperature was elevated during labor and blood cultures were drawn. The empirical maternal treatment was initiated with intravenous amoxicillin-clavulanic acid immediately in the post-partum period. Two sets of blood cultures were collected and incubated in a Bactec system (Becton Dickinson, Erembodegem, Belgium) and anaerobic bottles were flagged as positive for gram-positive cocci in chain (Fig. 1). Matrix-Assisted Laser Desorption Ionization Time-of-Flight Mass Spectrometry (MALDI-TOF MS) identification was \(Atopobium\) sp. Treatment by amoxicillin-clavulanic acid was continued with favorable response. Both the mother and the newborn were discharged on the third day post-partum.

Antimicrobial susceptibility testing (AST) using EUCAST clinical breakpoints for Gram-positive anaerobic bacteria (http://www.eucast.org) and antibiotic gradient strip test indicated susceptibility to penicillin (0.03\(\mu\)g/mL), ampicillin (<0.016\(\mu\)g/mL), clindamycin (<0.016\(\mu\)g/mL), azithromycin (<0.016\(\mu\)g/mL), linezolid 0.125\(\mu\)g/mL, and resistance to metronidazole (>256\(\mu\)g/mL). Partial sequencing of the 16S rRNA gene was performed (GenBank accession no.: MH628052.1; 1436pb). The yielded sequence indicated 98.11% homology with \(A.\) vaginae strain DSM 15829(T) \([1]\) by using EZBiocloud (www.ezbiocloud.net). Nevertheless, 98%–99% similarity was also found with other partial 16S rRNA sequences of \(A.\) vaginae (GenBank accession no.: AF325325.1, AJ585206.2, JQ511973.1, JX942361.1).

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A. vaginae bacteremia has been rarely reported. We identified three other cases in the literature that are summarized in Table 1. All cases occurred during pregnancy; one case during labor, one case following chorionic villus sampling and one case probably due to an infected subchorionic hematoma. The mother outcome was favorable in all cases but pregnancy was terminated in two cases.

Identification of A. vaginae was performed using 16S rRNA gene sequencing in all 3 cases. In one study, MALDI TOF-MS successfully identified A. vaginae (Table 1) [6]. In our case, at the time of the diagnosis, the MALDI Biotyper IVD 4.2.80 database (Bruker, Germany) included 19 Atopobium main spectral profile (MSP) covering four species: A. parvulum (n=6), A. rimae (n=5), A. minutum (n=4), A. vaginae (n=3) and Atopobium sp. (n=1). As previously mentioned, our strain was only identified at the genus level, as “Atopobium sp.”, using MALDI-TOF MS. This identification was provided as the best match with a confident score value (>25). Interestingly, no matches with Atopobium MSP were encountered in the ten best matches listed. We assume that a high intra-species diversity could explain this phenomenon. This hypothesis is in agreement with the work of Mendes-Soares et al. who suggests that the genetic diversity among A. vaginae strains is underestimated [10]. The addition of Atopobium species MPS in the MALDI-TOF MS database, and of A. vaginae in particular, could therefore improve the microbiological diagnosis of such microorganisms in the future. The need to use 16S rRNA gene sequencing or MALDI-TOF MS techniques to identify Atopobium species might account for the few cases reports published and the low reported prevalence of peripartum infection due to different Atopobium spp.

Regarding the AST, A. vaginae is usually resistant to metronidazole [11] although MICs can be highly variable on the strains tested. Sensitivity to beta-lactams and clindamycin is generally conserved [12]. Amoxicillin-clavulanic acid was the treatment administered in most reported cases.

The association between A. vaginae and bacterial vaginosis has been found consistently in various studies: higher A. vaginae bacterial load is associated with higher risk of preterm birth [5,6]. However, it is noteworthy that substantial proportion of healthy women is also colonized by A. vaginae. Interestingly, a recent study performed in South Africa using quantitative PCR suggest a decrease of the vaginal concentration of A. vaginae during pregnancy [13]. Whether in our case, bacteremia was related to high vaginal concentration of A. vaginae could not be determined since the presence of A. vaginae was not specifically assessed.

Whether different species of Atopobium or different A. vaginae strains with distinct virulence co-exist in the vaginal microbiota remains to be established. Given the strong association between bacterial vaginosis, A. vaginae burden and unfavorable pregnancy outcome [5], trials to diagnose and treat BV associated with A. vaginae are ongoing [14]. This warrant more studies aiming at defining the genetic diversity and its relationship with virulence of A. vaginae isolates.

In conclusion, we report a case of A. vaginae bacteremia during labor. The fetal and maternal outcome was favorable. This case draws

Table 1

<table>
<thead>
<tr>
<th>Reference</th>
<th>Age</th>
<th>Clinical presentation</th>
<th>Gestational age (weeks, days)</th>
<th>Obstetric history</th>
<th>Identification</th>
<th>Antibiogram susceptibility testing (MICs mg/L)</th>
<th>Treatment received</th>
<th>Fetal Outcome</th>
<th>Maternal Outcome</th>
</tr>
</thead>
<tbody>
<tr>
<td>Knoester, 2010 [7]</td>
<td>40 y</td>
<td>Sepsis post-chorionic villus sampling</td>
<td>12</td>
<td></td>
<td>MALDI-TOF MS(A. parvulum sp) and 16S rRNA gene sequencing</td>
<td>PEN S (0.094) MTZ R (24) CLI S (&gt;0.016)</td>
<td>1/CXM 2/ AMX</td>
<td>Death</td>
<td>Favorable</td>
</tr>
<tr>
<td>Chan, 2012 [8]</td>
<td>33 y</td>
<td>Intrapartum sepsis with fetal distress</td>
<td>39.2</td>
<td></td>
<td>16S rRNA gene sequencing</td>
<td>PEN S (0.25) MTZ R (&gt;256)</td>
<td>AMC</td>
<td>Favorable</td>
<td></td>
</tr>
<tr>
<td>Jacqmin, 2017 [9]</td>
<td>38 y</td>
<td>Infected subchorionic hematoma</td>
<td>12</td>
<td></td>
<td>MALDI-TOF MS(A. rimae sp) and 16S rRNA gene sequencing</td>
<td>PEN S (0.016) MTZ S (1) AMC S (0.016) CLI S (&gt;0.016)</td>
<td>1/AMC/ 2/AMX</td>
<td>Termination of pregnancy at 20 weeks for preterm premature rupture of membranes</td>
<td>Favorable</td>
</tr>
<tr>
<td>Present case</td>
<td>29 y</td>
<td>Intrapartum sepsis with fetal distress</td>
<td>39.3</td>
<td></td>
<td>MALDI-TOF MS(A. vaginae sp) and 16S rRNA gene sequencing</td>
<td>PEN S (0.03) AMP S (&lt;0.0016) CLI S (0.016) MTZ R (&gt;256)</td>
<td>AMC</td>
<td>Favorable</td>
<td></td>
</tr>
</tbody>
</table>

AMC, amoxicillin-clavulanic acid; AMP, ampicillin; AMX, amoxicillin; CLI, clindamycin; CXM, cefuroxime; MIC, minimal inhibitory concentration; MTZ, metronidazole; PEN, penicillin; R, resistant; S, susceptible; y, years.

Fig. 1. Gram staining of A. vaginae: Gram staining of the blood culture isolate clearly shows Gram-positive cocci in chains.

NR_029349.1, NR_117757.1, Y17195.1) of the NCBI database (www.ncbi.nlm.nih.gov/).

3. Discussion
the attention that the genetic diversity *A. vaginae* isolates needs to be further explored, in order to assess if strains with different pathogenic potential exist within the species and whether this may be linked with unfavorable pregnancy outcome.

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**References**


