Clinical and microbiological features of bacteraemia with Gram-positive anaerobic cocci: a population-based retrospective study

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ABSTRACT

Objectives: Gram-positive, anaerobic cocci (GPAC) can cause infections in humans. Only a few cases of bacteraemia with GPAC have been reported. We describe the clinical and microbiological characteristics of GPAC bacteraemia.

Methods: A retrospective population-based study of GPAC bacteraemia 2012–2016 in southern Sweden was performed. GPAC were identified using matrix-associated laser desorption ionization time-of-flight mass spectrometry or 16S rRNA gene sequencing. Etests were used to determine antibiotic susceptibilities. Data on patient and infection characteristics, treatment, and outcome were collected from the medical records.

Results: A total of 226 episodes of GPAC bacteraemia in adults were studied; this corresponds to an annual incidence of 3.4 cases per 100,000 persons per year. The bacteria identified were Anaerococcus spp. (n = 43), Atopobium spp. (n = 7), Blautia spp. (n = 1), Finegoldia spp. (n = 15), Parvimonas spp. (n = 100), Peptostreptococcus spp. (n = 52), Peptostreptococcus spp. (n = 2), and Ruminococcus spp. (n = 9) of which 200 isolates were identified to the species level. Resistance to imipenem and piperacillin was not identified, whereas resistance among the 229 isolates to penicillin was detected in four, to metronidazole in six, and clindamycin in 16 isolates. The median age of patients was 73 years (55–83, IQR), 57% were male and comorbidities were common. Fifty-one per cent of infections were polymicrobial. In 60% of cases a focus of infection was identified. Forty per cent of patients had either organ dysfunction or shock. The 30-day mortality was 11%, and nosocomial infections were over-represented among the deceased.

Conclusions: GPAC bacteraemia is much more common than previously reported. GPAC-bacteraemia is a condition with significant mortality mainly affecting elderly persons with comorbidities. M. Badri, Clin Microbiol Infect 2019;25:760.e1–760.e6

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anerobic bloodstream infections [4–7]. In the only population-based epidemiological study on anaerobic bacteraemia, bacteremia with \textit{Peptostreptococcus} species was reported to have an incidence of around one case per 100,000 inhabitants per year [8], but further species determination was not performed in that study.

The largest report on clinical features of GPAC bacteraemia described 15 cases of bacteraemia with \textit{Peptoniphilus}, of which three had a fatal outcome. Bacteraemia was polymicrobial in seven cases and different foci such as pneumonia, septic abortion, urinary tract infection, and skin or soft tissue infection were described [9]. With regards to bacteraemia with other GPAC species, only sporadic case reports have been published including pneumonia, primary bacteremia, and intrapartum infections with \textit{Atopobium} [10–13], toxic shock syndrome and infective endocarditis (IE) caused by \textit{Finegoldia magna} [14–17], IE, meningitis, and primary bacteremia with \textit{Parvimonas micra} [18–20], bacteraemia and IE with \textit{Peptostreptococcus} [21,22], diverticulitis or gallbladder infection with \textit{Ruminococcus} [23,24], and bacteremia with \textit{Sarcina} [25].

To gain a better understanding of the clinical and microbiological features of GPAC bacteraemia, we performed a retrospective, population-based study in southern Sweden. We describe a large series of cases that allows for increased understanding of the features of GPAC bacteraemia.

Methods

GPAC isolates

GPAC genera were defined according to Table 1 in the review by Murphy and Frick [1]. The laboratory information management system (LIMS) database of Clinical Microbiology, Lund, Sweden, was searched regarding blood cultures positive for GPAC during a 5-year period (2012–2016). The laboratory is the only one in the administrative region of Skåne (1,322,193 inhabitants on December 31, 2016) serving all the ten hospitals in that area. From 2012 until late 2014, the BacT/Alert blood culture system (bioMérieux, Marcy l’Etoile, France) was used and was replaced by the BACTEC FX blood culture system (Becton Dickinson, Franklin Lakes, NJ, USA) in December 2014. Cultures were incubated for 120 hours before regarded as negative. Isolates were stored in a medium containing 10% glycerol and 20% horse serum at −70°C. Species identification was performed using Microflex MALDI-TOF MS (Bruker Daltronics, Bremen, Germany), and FlexControl and MBT Compass 4.1 software, with reference database MBT-BDAL-6903. A score value of ≥2 was regarded sufficient for species determination. A score value ≥1.8 but <2 was regarded sufficient for genus determination. In cases where MALDI-TOF MS had failed to identify an isolate to the species level, renewed species identification was performed. The isolate was then retrieved from the freezer and cultured on fastidious anaerobe agar (FAA) culture plates in an anaerobic chamber until visually satisfactory growth could be observed. MALDI-TOF MS analysis was performed again (as above), and if the score value was <2, 16S rRNA gene sequencing was performed [26]. Minimum inhibitory concentration (MIC) values had been determined using Etests (bioMérieux, Marcy l’Etoile, France) on Mueller–Hinton fastidious agar plates according to the instructions given by the manufacturer. The European committee on antimicrobial susceptibility testing (EUCAST) breakpoints for Gram-positive anaerobes were used to categorize isolates as sensitive, intermediate, or resistant.

Patients

Data on patients’ comorbidities, symptoms and signs of infection, vital parameters, laboratory results, antibiotic use, radiological examinations, and outcome were from the medical records. The Charlson Comorbidity Score (CCS) was used to assess comorbidities [27]. Sepsis was defined using the sepsis-2 criteria [28]. Severe sepsis was defined by infection-induced organ failure (P: creatinine increase of ≥50 μmol/L, \( \text{SaO}_2 < 86\% \), platelets <100 × 10^3/L, \( \text{PK-INR} > 1.5 \), APTT >60 seconds, \( \text{S-bilirubin} > 45 \mu\text{mol/L} \), \( \text{P-lactate} > 3.2 \mu\text{M} \), \( \text{aB-lactate} > 2.6 \mu\text{M} \), systolic blood pressure <90 mmHg or acute alteration of mental status). Septic shock was defined as severe sepsis with hypotension that either did not respond to adequate fluid resuscitation, or required inotropic support. Quick Sequential Organ Failure Assessment (qSOFA) was calculated giving 1 point each for systolic hypotension (≤100 mmHg), tachypnoea (≥22 per minute), or altered mentation [29]. A focus of infection was defined by the fulfilment of at least two of the following criteria: (1) isolation of bacteria from a focal culture, (2) radiologic or clinical signs of focal infection, (3) Symptoms of focal infection. Nosocomial infection was defined by a positive blood culture drawn after a hospitalization for 48 hours or more. The study was approved by the regional ethics committee at Lund University (2013/31).

Statistical analysis

IBM SPSS Statistics Version 23 was used for statistical analysis. The variables were not assumed to be normally distributed and Mann–Whitney U, Kruskal–Wallis H, Fisher’s exact, and chi-square tests were used. For comparisons between genera, only the three largest groups (\textit{Anaerococcus}, \textit{Peptoniphilus}, and \textit{Parvimonas}) were included. Logistic regression was used to identify independent risk factors for 30-day mortality. Known risk factors and factors that the authors deemed important were included. Age, sex, Charlson score, and nosocomial acquisition had no missing values while qSOFA was 93% complete (\( n = 213 \)), temperature was 96% complete (\( n = 220 \)).
white blood cell count was 99% complete \((n = 225)\), and C-reactive protein was 98% complete \((n = 224)\). In the multivariable model, a complete case \((n = 215, 94\%)\) analysis was performed. The multivariable model was produced by including each outcome with \(p < 0.25\) from the univariable model. A stepwise forward method was used where the limit for forward inclusion was \(p < 0.05\). The model was tested for goodness of fit with the Hosmer and Lemeshow where \(p < 0.05\) indicates a poor fit.

**Results**

**Patients and isolates**

In total, 241 unique patients with GPAC bacteraemia were identified in the LIMS database. Thirteen patients were excluded due to inadequate or unavailable medical records. Three patients had growth of more than one GPAC species \((Parvimonas\) and *Peptoniphilus*, \(n = 2\) and *Finegoldia* and *Peptoniphilus* \(n = 1\)) in the blood culture. In 71 cases, the species determination did not fulfill our criteria and after renewed MALDI-TOF MS, 29 additional samples could be assigned to a species of which two were not GPAC and thus excluded. In the remaining 42 isolates the 16S rRNA gene was sequenced rendering a secure species determination in an additional ten isolates. The final number of patients included was 226 with 229 GPAC isolates. This corresponds to an incidence of 3.4 cases per 100,000 persons/year. The isolates were *Anaerococcus spp.* \((n = 43)\), *Atopobium spp.* \((n = 7)\), *Blautia spp.* \((n = 1)\), *Finegoldia spp.* \((n = 15)\), *Parvimonas spp.* \((n = 100)\), *Peptoniphilus spp.* \((n = 52)\), *Peptostreptococcus spp.* \((n = 2)\), and *Ruminococcus spp.* \((n = 9)\). The genus and species distribution of GPAC is given in Table 1. *Anaerococcus* was the genus where species determination proved most difficult.

Half of the patients had only the GPAC isolated from blood (monomicrobial bacteraemia), and of those with other bacteria isolated from blood cultures drawn at the same occasion (poly-microbial bacteraemia), 33 had two or more other species isolated. The most commonly co-isolated bacteria were coagulase-negative staphylococci \((n = 29)\), which were particularly often isolated together with *Anaerococcus*. Other common co-isolated bacteria were *Bacteroides spp.* \((n = 13)\), alpha haemolytic streptococci \((n = 13)\), and *Escherichia coli* \((n = 11)\). *Dermobacter* was co-isolated with *Finegoldia* in three cases whereas *Eggerthella* was found in five cases of *Parvimonas* bacteraemia. Growth of the GPAC occurred in two blood cultures in 70 cases whereas growth in a single culture was recorded in 156 patients of whom 139 had two or more blood cultures taken.

**Antibiotic susceptibility**

MICs for penicillin, piperacillin–tazobactam, imipenem, clindamycin, and metronidazole are presented in Fig. 1. All isolates were sensitive to imipenem and piperacillin-tazobactam. Resistance to penicillin was detected in four out of 220 isolates, to metronidazole in six out of 222 isolates, and to clindamycin in 16 out of 219 isolates. Resistance to clindamycin was most common in *Anaerococcus* comprising 11 of 43 isolates \((26\%)\).

**Characteristics of patients and infections**

The patients had a median age of 73 years \((IQR 55–82\) range\), 58% were male, and the median CCS was 2. There were no statistically significant differences in either the age or in gender distribution of patients infected with the three most common GPAC genera \((Table 2)\).

Details regarding the severity, focus, and type of infection are displayed in Table 3. Forty per cent presented with or developed severe sepsis or septic shock. A large proportion \((40\%)\) of patients had an unknown focus of infection. Most common focal infections were the abdominal tract, respiratory tract, skin, and soft tissue as well as the urogenital tract. There were no statistically significant differences between infection severity or the proportions of patients that had monomicrobial or nosocomial infection between the three most common GPAC genera.

**Treatment and outcome**

The median time for intravenous treatment was 6 days \((IQR 3–9\) days\) and the median per oral follow-up treatment time was 7 days \((IQR 0–10\) days\). The median length of stay in hospital was 8 days \((IQR 4–14\) days\) \((Table 4)\). In-hospital mortality was 10% whereas 11% and 14% of patients died within 30 and 90 days respectively. The differences in survival at 30 or 90 days between patients with the three most common GPAC genera were not significant \((Table 4)\).

Table 5 presents predictors of death. In univariable analysis, factors associated with 30-day mortality were age, Charlson comorbidity score, and nosocomial acquisition while higher body temperature was negatively associated with 30-day mortality. Nosocomial acquisition was an independent risk factors for 30-day mortality while higher body temperature predicted better 30-day survival.

**Discussion**

Given the scarcity of previous reports on GPAC bacteraemia it was surprising that the incidence was as high as 3.4 cases per 100,000 persons/year. The only previous population based study on bacteraemia with anaerobes reported much lower figures for GPAC-related species [8]. The most commonly isolated GPAC genera were *Parvimonas* followed by *Peptoniphilus* and *Anaerococcus*. Conclusions about the absolute incidence of bacteraemia with the different bacterial genera and species should be made with caution since the frequency of isolation from blood is affected by the propensity of the different organisms to grow under the conditions used. This was evident for *Finegoldia* isolates, which were only detected after the change from BacT/Alert to the BACTEC FX blood culture system. The differences in propensity of anaerobes to grow in different media has recently been systematically evaluated [30] demonstrating that BACTEC is superior in the detection of *Finegoldia*. Species determination was feasible for most isolates with the exception of *Anaerococcus* isolates, where a species could be determined for only a minority of isolates. This indicates that the taxonomy of most of the common GPAC species is relevant for clinical use.

There were no clear associations between species or genus on the one hand and focus of infection, severity of infection, and mortality on the other hand. The study was underpowered in regard of detecting such differences, especially between the less commonly isolated GPAC species. A tendency of *Atopobium* to cause intrapartum infections, including septic abortion, was however noted. Of particular interest was also a case of monomicrobial *P. micra* bacteraemia associated with a computerized tomography-verified infection of an aortic graft with fatal outcome. This study supports the notion that several types of infections can result in GPAC bacteraemia and that this is a severe condition. Severe underlying conditions were associated with a poor prognosis in the univariable analysis but only nosocomial acquisition was found to be an independent predictor of high 30-day mortality. In line with other reports, fever was...
identified as an independent factor associated with increased survival [31].

There are several limitations of this study, not least related to the retrospective design, which only allows for analysis of variables already included in the medical records. We chose to use the definitions of GPAC suggested by Murphy and Frick [1] but it is possible that additional species should be included in the GPAC group. Moreover, whereas Atopobium is regarded as a GPAC by Murphy and Frick [1] as well as in a very recent review [32]. The bacterium is described to appear as cocci, elliptical cocci, or even as rod shaped [33,34]. Moreover, the high number of polymicrobial infections also limits the possibility to determine the exact contribution of the GPAC to the infections studied. In addition, the change of blood culture system in the middle of the study period impedes the

Fig. 1. MICs of Gram-positive, anaerobic cocci isolates for penicillin G (a), piperacillin–tazobactam (b), imipenem (c), clindamycin (d), and metronidazole (e) where each isolate is represented by a filled circle. SIR breakpoints according to EUCAST are indicated. EUCAST, European committee on antimicrobial susceptibility testing; MIC, minimum inhibitory concentration; SIR, sensitive intermediate resistant.
Table 2
Demographic characteristics of patients with Gram-positive, anaerobic cocci bacteraemia

<table>
<thead>
<tr>
<th>Variable</th>
<th>Total (n = 229)</th>
<th>Anaerococcus spp. (n = 43)</th>
<th>Atopobium spp. (n = 7)</th>
<th>Blautia spp. (n = 1)</th>
<th>Finegoldia spp. (n = 15)</th>
<th>Parvimonas spp. (n = 100)</th>
<th>Peptostreptococcus spp. (n = 52)</th>
<th>Ruminococcus spp. (n = 9)</th>
<th>Peptostreptococcus spp. (n = 2)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Female sex, n (%)</td>
<td>97 (42)</td>
<td>25 (58)</td>
<td>3 (43)</td>
<td>0 (0)</td>
<td>3 (20)</td>
<td>37 (37)</td>
<td>22 (42)</td>
<td>6 (67)</td>
<td>1 (50)</td>
</tr>
<tr>
<td>Age, years (range)</td>
<td>73 (10–97)</td>
<td>78 (28–96)</td>
<td>52 (36–85)</td>
<td>76</td>
<td>69 (25–94)</td>
<td>72 (10–97)</td>
<td>75 (23–94)</td>
<td>79 (45–93)</td>
<td>83 (80–85)</td>
</tr>
<tr>
<td>CS (mean)</td>
<td>2</td>
<td>2</td>
<td>0</td>
<td>6</td>
<td>3</td>
<td>2</td>
<td>3</td>
<td>3</td>
<td>2</td>
</tr>
</tbody>
</table>

1 Charlson comorbidity score.

Table 3
Severity and focus of infection according to genus

<table>
<thead>
<tr>
<th>Diagnosis</th>
<th>Total (n = 229)</th>
<th>Anaerococcus spp. (n = 43)</th>
<th>Atopobium spp. (n = 7)</th>
<th>Blautia spp. (n = 1)</th>
<th>Finegoldia spp. (n = 15)</th>
<th>Parvimonas spp. (n = 100)</th>
<th>Peptostreptococcus spp. (n = 52)</th>
<th>Ruminococcus spp. (n = 9)</th>
<th>Peptostreptococcus spp. (n = 2)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sepsis</td>
<td>102 (45)</td>
<td>17 (40)</td>
<td>4 (57)</td>
<td>1</td>
<td>3 (20)</td>
<td>51 (51)</td>
<td>22 (42)</td>
<td>4 (44)</td>
<td>1 (50)</td>
</tr>
<tr>
<td>Severe sepsis</td>
<td>82 (36)</td>
<td>15 (35)</td>
<td>2 (29)</td>
<td>0</td>
<td>7 (47)</td>
<td>31 (31)</td>
<td>22 (42)</td>
<td>5 (56)</td>
<td>0 (0)</td>
</tr>
<tr>
<td>Septic shock</td>
<td>8 (3.5)</td>
<td>1 (2.3)</td>
<td>0 (0)</td>
<td>0</td>
<td>5 (50)</td>
<td>1.9 (1.9)</td>
<td>1 (0)</td>
<td>0 (0)</td>
<td>0 (0)</td>
</tr>
<tr>
<td>Focus</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Abdomen</td>
<td>24 (10)</td>
<td>3 (7.0)</td>
<td>2 (29)</td>
<td>1</td>
<td>1 (6.7)</td>
<td>16 (16)</td>
<td>1 (19)</td>
<td>1 (11)</td>
<td>0 (0)</td>
</tr>
<tr>
<td>Bones/joints</td>
<td>9 (3.9)</td>
<td>1 (2.3)</td>
<td>0 (0)</td>
<td>0</td>
<td>1 (6.7)</td>
<td>6 (6.0)</td>
<td>1 (19)</td>
<td>0 (0)</td>
<td>0 (0)</td>
</tr>
<tr>
<td>Skin/soft tissue</td>
<td>24 (10)</td>
<td>9 (21)</td>
<td>0 (0)</td>
<td>0</td>
<td>2 (13)</td>
<td>6 (6.0)</td>
<td>7 (13)</td>
<td>0 (0)</td>
<td>0 (0)</td>
</tr>
<tr>
<td>Genital tract</td>
<td>15 (6.6)</td>
<td>1 (2.3)</td>
<td>3 (43)</td>
<td>0</td>
<td>3 (3.0)</td>
<td>8 (6.0)</td>
<td>10 (10)</td>
<td>0 (0)</td>
<td>0 (0)</td>
</tr>
<tr>
<td>Urinary tract</td>
<td>21 (9.2)</td>
<td>3 (7.0)</td>
<td>0 (0)</td>
<td>0</td>
<td>1 (6.7)</td>
<td>8 (6.0)</td>
<td>9 (17)</td>
<td>0 (0)</td>
<td>0 (0)</td>
</tr>
<tr>
<td>Respiratory tract</td>
<td>33 (14)</td>
<td>11 (26)</td>
<td>0 (0)</td>
<td>0</td>
<td>2 (13)</td>
<td>11 (11)</td>
<td>7 (13)</td>
<td>1 (11)</td>
<td>1 (50)</td>
</tr>
<tr>
<td>Other</td>
<td>11 (4.8)</td>
<td>0 (0)</td>
<td>1 (14)</td>
<td>0</td>
<td>0 (0)</td>
<td>8 (8.0)</td>
<td>2 (13)</td>
<td>0 (0)</td>
<td>0 (0)</td>
</tr>
<tr>
<td>Unknown</td>
<td>92 (40)</td>
<td>15 (35)</td>
<td>1 (14)</td>
<td>0</td>
<td>8 (53)</td>
<td>42 (42)</td>
<td>17 (33)</td>
<td>7 (78)</td>
<td>1 (50)</td>
</tr>
<tr>
<td>Type of infection</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Monomicrobial</td>
<td>113 (49)</td>
<td>24 (56)</td>
<td>5 (71)</td>
<td>1</td>
<td>7 (47)</td>
<td>50 (50)</td>
<td>20 (38)</td>
<td>6 (67)</td>
<td>0 (0)</td>
</tr>
<tr>
<td>Nosocomial</td>
<td>38 (17)</td>
<td>8 (19)</td>
<td>1 (14)</td>
<td>0</td>
<td>1 (6.7)</td>
<td>15 (15)</td>
<td>11 (21)</td>
<td>2 (22)</td>
<td>0 (0)</td>
</tr>
</tbody>
</table>

1 All figures are numbers with percentage given within parenthesis.

Table 4
Mortality and time spent in hospital, for each of the different Gram-positive, anaerobic cocci genera

<table>
<thead>
<tr>
<th>Mortality, n (%)</th>
<th>Total (n = 229)</th>
<th>Anaerococcus spp. (n = 43)</th>
<th>Atopobium spp. (n = 7)</th>
<th>Blautia spp. (n = 1)</th>
<th>Finegoldia spp. (n = 15)</th>
<th>Parvimonas spp. (n = 100)</th>
<th>Peptostreptococcus spp. (n = 52)</th>
<th>Ruminococcus spp. (n = 9)</th>
<th>Peptostreptococcus spp. (n = 2)</th>
</tr>
</thead>
<tbody>
<tr>
<td>In-hospital</td>
<td>22 (9.6)</td>
<td>5 (12)</td>
<td>1 (14)</td>
<td>0</td>
<td>1 (6.7)</td>
<td>10 (10)</td>
<td>3 (5.8)</td>
<td>1 (11)</td>
<td>1 (50)</td>
</tr>
<tr>
<td>30-day</td>
<td>26 (11)</td>
<td>7 (16)</td>
<td>1 (14)</td>
<td>0</td>
<td>1 (6.7)</td>
<td>12 (12)</td>
<td>3 (5.8)</td>
<td>1 (11)</td>
<td>1 (50)</td>
</tr>
<tr>
<td>90-day</td>
<td>32 (14)</td>
<td>8 (19)</td>
<td>1 (14)</td>
<td>1</td>
<td>2 (13)</td>
<td>15 (15)</td>
<td>4 (7.7)</td>
<td>1 (11)</td>
<td>1 (50)</td>
</tr>
<tr>
<td>Time in hospital</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Median (IQR)</td>
<td>8 (4–14)</td>
<td>9 (5–14)</td>
<td>3 (1–21)</td>
<td>13</td>
<td>9 (5–17)</td>
<td>7 (5–14)</td>
<td>6 (4–10)</td>
<td>9 (5–17)</td>
<td>18 (14–23)</td>
</tr>
</tbody>
</table>

1 In days.

Table 5
Predictors of death

<table>
<thead>
<tr>
<th>Variable</th>
<th>OR</th>
<th>Univariable 95%CI</th>
<th>p</th>
<th>OR</th>
<th>Multivariable 95%CI</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age, per 10-year increments</td>
<td>1.33</td>
<td>1.04–1.63</td>
<td>0.022</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Female sex</td>
<td>0.69</td>
<td>0.30–1.63</td>
<td>0.40</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Charlson score, 1-point increments</td>
<td>1.22</td>
<td>1.02–1.46</td>
<td>0.03</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>qSOFA score, 1-point increments</td>
<td>1.11</td>
<td>0.63–1.96</td>
<td>0.73</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Temperature, 1-point increments</td>
<td>0.68</td>
<td>0.47–0.98</td>
<td>0.04</td>
<td>0.68</td>
<td>0.46–0.99</td>
<td>0.045</td>
</tr>
<tr>
<td>Nosocomial acquisition</td>
<td>4.9</td>
<td>2.0–11.90</td>
<td>&lt;0.001</td>
<td>4.5</td>
<td>1.8–11.4</td>
<td>0.001</td>
</tr>
<tr>
<td>White blood cell count, per unit</td>
<td>1.003</td>
<td>0.98–1.02</td>
<td>0.74</td>
<td>1.03</td>
<td>0.99–1.06</td>
<td>0.11</td>
</tr>
</tbody>
</table>

* Hosmer Lemeshow test for goodness of fit: p = 0.51.
generalizability of the absolute figures. However, it also underlines that, especially with anaerobes, bacteraemia is not an absolute phenomenon but also a matter of detection limits using different blood culture systems and practices for sampling.

The results presented in this work allows for increased individualization of the care for patients with GPAC bacteraemia. Future research is needed to investigate the appropriate treatment for GPAC bacteraemia.

**Transparency declaration**

The authors have no conflicting interests to disclose.

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