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## Epidemiology and microbiological features of anaerobic bacteremia in two French University hospitals

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20 Abstract:

21 Bacteremia implicating anaerobic bacteria (BIAB) represents 2 to 6% of all episodes of  
22 bacteremia and is associated with high mortality. In this retrospective study from June 2015  
23 to December 2016, we compared BIAB frequency in two hospital centers in Montpellier  
24 (France): Montpellier university hospital (MUH) and a center specialized in cancer (ICM).  
25 Among the 2465 microbiologically relevant episodes of bacteremia, we identified 144 (5.8%)  
26 in which anaerobic bacteria were implicated. BIAB frequency was higher at ICM than MUH  
27 (10.4%, vs. 4.9%,  $p < 0.01$ ). Poly-microbial bacteremia was more frequent among the BIAB  
28 episodes (31.9% vs. 11.0% for aerobic-only bacteremia,  $p < 0.01$ ). *Bacteroides* and *Clostridium*  
29 were the most frequently identified genera of anaerobic bacteria (64 and 18 episodes,  
30 respectively), with the *B. fragilis* group (BFG) involved in 68/144 episodes. We could perform  
31 antibiotic susceptibility typing in 106 of the 144 anaerobic isolates, including 67 BFG isolates.  
32 All isolates but one were susceptible to metronidazole. In the BFG, sporadic resistant or  
33 intermediate results were found for amoxicillin-clavulanate (5/67), piperacillin-tazobactam  
34 (2/67) and imipenem (1/67). BFG isolates were susceptible also to cefoxitin (90.8%),  
35 rifampicin (97.0%) and tigecyclin (91.0%). Multidrug resistance in this group (7 isolates) was  
36 mostly due to acquired resistance to moxifloxacin, clindamycin and tigecyclin. This study  
37 shows that BIAB frequency can vary among hospitals and services. They should especially be  
38 taken into account in centers specialized in cancer treatment. However, the implicated  
39 bacteria remain frequently susceptible to the most used antibiotics used against anaerobic  
40 bacteria, although resistance does exist.

41

42

## 43 Introduction

44 Anaerobic bacteria are implicated in 2 to 6% of bacteremia episodes [1–4]. Conflicting data  
45 have been published on their incidence (increase, decrease or stability) during the last  
46 decades [2,5–7]. Mortality caused by bacteremia implicating anaerobic bacteria (BIAB) is  
47 high, from 13 to 25% [1,2,8–10], and even higher in patients who are inappropriately treated  
48 [3]. They should especially be taken into account in centers specialized in cancer treatment  
49 [1–4,9]. Antimicrobial resistance in BIAB remains rare: most of anaerobic bacteria are  
50 susceptible to metronidazole, to the association of amoxicillin and clavulanic acid, and to  
51 penems [1,4,10–12]. Resistance to clindamycin and fluoroquinolones has been more  
52 frequently reported, although about half of the isolates are still susceptible [1,4,11,12].  
53 Importantly, a clone of multi-resistant *Bacteroides fragilis* has been recently described in  
54 Europe [13]. The most frequent sources of BIAB are intra-abdominal and female genital tract  
55 infections [14]. Multiple conditions have been associated with higher risk of BIAB, such as  
56 solid and hematological malignancies and surgery of the gastro-intestinal tract or the  
57 urogenital system [14].

58 BIAB incidence in different centers has not been compared in recent studies. This could be a  
59 limit in epidemiology studies because the combination and frequency of local risk factors  
60 could influence their incidence and spread. Therefore, the aim of our study was to compare  
61 BIAB incidence, their microbial epidemiology, and the resistance to antibiotics of the  
62 involved anaerobic bacteria in two different French hospitals.

63

## 64 Material and methods

65 Blood cultures were received from two different hospital centers: Montpellier University  
66 Hospital (MUH), a training hospital of 2000 beds, and the Institute of Cancer in Montpellier  
67 (ICM), a center dedicated to cancer treatment with 210 beds.

68 For every positive blood culture identified in our bacteriology laboratory between 1 June  
69 2015 and 31 December 2016, the following data were retrieved: patients' demographic data  
70 (anonymized at the first step of data analysis except birth date), hospital service where the  
71 patient was hospitalized at sampling time, and results of the identification and antibacterial  
72 susceptibility testing (AST) assays of the isolated bacteria. AST data for anaerobic isolates  
73 (categorization in term of susceptibility and minimum inhibitory concentrations (MIC)) were  
74 retrieved from the SIRWEB software database.

75 From these data, all putative bacteremia episodes were determined for each patient and  
76 each bacterial species, using a bioinformatics pipeline. Briefly, a 5-day interval between two  
77 positive blood cultures was chosen to define two separate bacteremia episodes. For each  
78 episode, only the species with i) at least one positive blood culture for aerobic and anaerobic  
79 species that are known to be systematic pathogens in blood cultures (*e. g.*, *Staphylococcus*  
80 *aureus*, *Enterobacterales*, *Bacteroides* spp., etc.), ii) at least two positives blood cultures for  
81 an aerobic species known as possible contaminant and with comparable AST results (*i.e.*,  
82 coagulase-negative *Staphylococcus* or *Corynebacterium* spp.), or iii) the presence of more  
83 than one positive blood culture for an anaerobic species known as probable contaminant  
84 (*e.g.*, *Cutibacterium acnes*) were retained (see supplementary data to see which species are  
85 associated to which part of the algorithm). Fungi were excluded. Each bacteremia episode  
86 was associated with the service where the earliest positive blood culture was sampled.  
87 Episodes occurring in patients younger than 16 years old were automatically excluded.

88 During this period, blood cultures were always concomitantly performed in BacT/Alert FA  
89 (aerobic) and FN Plus (anaerobic) bottles, containing antimicrobial-absorbing beads. Bottles  
90 were incubated and screened using the BacT/ALERT 3D system. Aerobic bottles were  
91 incubated for 5 days (standard conditions), or for 10 and 21 days when fungemia and  
92 endocarditis, respectively, were suspected. Anaerobic bottles were incubated in standard  
93 conditions for 7 days, or for 21 days when endocarditis was suspected. For each positive  
94 blood culture, the bacteria retrieved after subculture were identified Matrix Assisted Laser  
95 Desorption Ionization Time of Flight Mass Spectrometry (MALDI-TOF MS) using a Bruker  
96 Microflex system (Bruker Daltonics, Bremen, Germany) and the Bruker database. The  
97 European Network for the Rapid Identification of Anaerobes (ENRIA) database was also  
98 interrogated when needed [15]. AST was performed using the disk diffusion method  
99 according to the recommendations by the “Comité de l’Antibiogramme de la Société  
100 Française de Microbiologie” (Antibiogram Committee of the French Microbiology Society;  
101 CA-SFM) for aerobic bacteria (version 2015) and for anaerobic bacteria (version 2013). For  
102 anaerobes, AST was carried out only for species with known possible resistance (mostly  
103 *Bacteroides*) and in specific contexts. The MIC values were determined using strips for  
104 amoxicillin-clavulanic acid, cefoxitin, metronidazole and tigecyclin. Resistance for other  
105 antibiotics was tested using discs: piperacillin 75 µg, piperacillin 75 µg + tazobactam 10 µg,  
106 imipenem 10 µg, moxifloxacin 5 µg, rifampicin 30 µg and clindamycin 2 UI. For each genus  
107 and species, and for each antibiotic, the number of AST, the percentage of susceptible  
108 isolates, and when possible their MIC<sub>50</sub>, MIC<sub>90</sub> and MIC range were calculated. Multiple  
109 resistances (i.e., association of acquired resistance against at least three categories of  
110 antibiotics, adapted from the definitions for *Enterobacterales* (former *Enterobacteriaceae*)  
111 and *Pseudomonas aeruginosa* [16]) in the same isolate were verified manually. Categories of

112 molecules used were penicillins +  $\beta$ -lactams inhibitors (amoxicillin-clavulanic acid,  
113 piperacillin-tazobactam), cephamycins (cefoxitin), and carbapenems (imipenem),  
114 fluoroquinolones (moxifloxacin), ansamycins (rifampicin), lincosamides (clindamycin),  
115 nitroimidazole derivatives (metronidazole), and cyclins (tigecyclin). Statistical analyses were  
116 performed with the scipy package v1.3.0, in python 3.6.

117 The scripts used are published on GitHub (DOI 10.5281/zenodo.3601471). The different  
118 dataset can be requested to the corresponding, upon motivated request.

119

## 120 Results

121 Among the 82 463 records of blood cultures retrieved, 2 465 episodes of bacteremia were  
122 identified, including 144 BIAB episodes (5.8%). Bacteremia was poly-microbial in 301  
123 episodes (12.2%), including 46 episodes involving at least one anaerobe (31.5% of all BIAB),  
124 and 13 episodes involving only anaerobes (9.0% of all BIAB episodes). Poly-microbial  
125 bacteremia was significantly associated with the presence of anaerobes ( $p < 0.001$ ,  $\chi^2$  test).  
126 Overall, the mean number of bacteria species isolated in each episode was 2.29, and  
127 increased to 2.61 for BIAB episodes (range: 1 to 6 and 1 to 5, respectively).

128 The number of bacteremia episodes was 2040 at MUH and 425 at ICM among which 4.9%  
129 ( $n=100$ ) and 10.4% ( $n=44$ ) were BIAB, respectively ( $p < 0.001$ ;  $\chi^2$  test). In hospital services  
130 with more than 10 episodes of bacteremia, BIAB frequency ranged from 0 to 27.3% (mean:  
131 4.1%) at MUH and from 4.2 to 19.2% (mean: 10.8%) at ICM. At MUH, the highest BIAB  
132 frequency was detected in services specialized in abdominal surgery (including an intensive

133 care unit) and at the clinical hematology department. At ICM, the highest frequency was  
134 observed in the intensive care unit and in the two surgical departments.

135 Among the blood cultures, 26 different genera and 56 different species of anaerobic bacteria  
136 were identified (table 1). The most frequently detected genera were *Bacteroides* (n=64),  
137 *Clostridium* (n=18), *Lactobacillus* (n=13), and *Eggerthella* (n=13). The most frequently  
138 observed anaerobic species were *Bacteroides fragilis* (37 episodes), *Bacteroides*  
139 *thetaiotaomicron* (n=15), and *Eggerthella lenta* (n=13). The *B. fragilis* group (BFG) was  
140 detected in 68 episodes (46.6% of all BIAB episodes). All the identified *Bacteroides* species  
141 belonged to the BFG.

142 AST was performed in 106 isolates. Metronidazole was the most frequently tested antibiotic,  
143 and the only tested antibiotic in 20 isolates (18.9%). Only one isolate (*B. fragilis*) was  
144 resistant to metronidazole. The AST results for metronidazole are summarized in table 2.

145 Four isolates showed intermediate susceptibility to amoxicillin-clavulanic acid (n=1 *B. fragilis*,  
146 n=1 *Dysgonomonas capnocytophagoides*, and n=2 *B. thetaiotaomicron*), and two  
147 *Parabacteroides distasonis* isolates were resistant. One *B. thetaiotaomicron* was resistant to  
148 piperacillin-tazobactam and two isolates (n=1 *Bacteroides ovatus* and n=1 *Veillonella*  
149 *parvula*) showed intermediate susceptibility. Susceptibility to imipenem was intermediate in  
150 three isolates (n=1 *B. thetaiotaomicron* and n=2 *Lactobacillus rhamnosus*).

151 Sixty-seven isolates with AST belonged to the BFG (AST was not performed on 3 isolates).

152 The results of these isolates are summarized in table 3. AST was not realized in 3 cases.

153 Globally, isolates from the BFG were highly susceptible to piperacillin-tazobactam,  
154 imipenem, rifampicin and metronidazole (susceptibility rates of 97.0%, 98.5%, 97.0%, and  
155 98.5%, respectively). Results for amoxicillin-clavulanic acid, cefoxitin and tigecyclin were

156 slightly lower (92.5%, 90.8%, and 91.0%, respectively). Five of the six isolates non-susceptible  
157 to cefoxitin were identified as *B. thetaiotaomicron*. Isolates were inconstantly susceptible to  
158 piperacillin, moxifloxacin and clindamycin (50.7%, 58.2% and 50.8%, respectively).

159 Multi-drug resistance was detected in seven *Bacteroides* isolates (6.6% of all anaerobic  
160 bacteria isolates with AST, and 10.4% of all *Bacteroides* with AST; table 4). Multi-drug  
161 resistance was mostly due to acquired resistance to moxifloxacin (n=7/7), clindamycin  
162 (n=6/7), and tigecyclin (n=4/7). Some isolates had paradoxical results: susceptible to  
163 amoxicillin-clavulanic acid and piperacillin-tazobactam and intermediate to imipenem, or  
164 susceptible to amoxicillin-clavulanic acid and resistant to piperacillin-tazobactam.

165

## 166 Discussion

167 This study found an important difference in BIAB frequency in two French hospital centers,  
168 and in the different services of each hospital (from 0% to 27.3%). Anaerobe presence in  
169 bacterial cultures related to bacteremia episodes was significantly associated with poly-  
170 microbial bacteremia. AST data analysis showed that resistance to the most frequently used  
171 anti-anaerobe antibiotics was rare, although a small fraction of multi-drug resistant isolates  
172 was detected.

173 The difference between hospital centers could easily be explained by the different patient  
174 populations treated. MUH is a multi-disciplinary teaching hospital in which some wards are  
175 specialized in cancer treatment, but others (such as rheumatology, neurology, and  
176 cardiology) display very few risk factors for BIAB. Conversely, ICM is a center specialized in  
177 cancer treatment. Therefore, the higher BIAB frequency at ICM could be explained by the

178 fact that malignancies are one of the prominent risk factors for BIAB [8,14]. Comparison of  
179 service-specific data shows higher frequency heterogeneity at MUH than ICM. This may be  
180 again explained by the difference in the incidence of risk factors among MUH services. This is  
181 also supported by the high BIAB frequency in some MUH services, sometimes higher than  
182 those observed at ICM.

183 In this study, BIAB occurrence was reported as the percentage of bacteremia episodes with  
184 anaerobic bacteria among all bacteremia episodes. Other approaches have been used in  
185 other studies, such as the number of BIAB cases per year, per patient-days, per inhabitant or  
186 per admission; or the number of positive anaerobic cultures per sampled blood cultures; or  
187 the percentage of anaerobic bacteria isolated from blood cultures per bacteria [2–6,8–10].

188 Our approach should be independent of the total number of patients, the length of hospital  
189 stay, and the frequency or indications of blood cultures because the number of BIAB  
190 episodes was normalized to the total number of bacteremia cases. The overall BIAB  
191 frequency at MUH was comparable to that reported by De Keukeleire et al. [2] in a Belgian  
192 university hospital. On the other hand, the overall frequency at ICM was much higher than  
193 that at those in other recent studies that were not performed in cancer-specific centers.

194 However, the main bias of our approach is the algorithm used to differentiate true  
195 bacteremia episodes from contaminations, and one episode from another. The number of  
196 bottles with the same bacteria and isolation of the same bacteria with the same antibiotic  
197 susceptibility pattern in multiple bottles are frequently used to detect false positives in  
198 blood cultures [17], but misinterpretation is always possible. In our study, antibiotic  
199 susceptibility patterns were used for aerobic bacteria because in our laboratory, AST of  
200 coagulase-negative staphylococci is systematically performed on two different isolates and  
201 the results are compared to conclude whether this is a true bacteremia or a contamination.

202 However, episodes with different antibiotic susceptibility patterns are sometimes considered  
203 as real episodes by the medical team in charge, since no other explanation for the sepsis can  
204 be found. Contamination of multiple blood culture samples by the same strain is also  
205 possible, and may be falsely interpreted as a real bacteremia. Hopefully, these two error  
206 types are rare, and may cancel each other out on a large scale. An alternative way to  
207 determine whether a positive blood culture is due to a true bacteremia or a contamination  
208 would have been to use the time-to-positivity of the blood culture, which relates to the  
209 biomass present in the blood culture. However, the time-to-positivity depends on several  
210 factors *e.g.* time of transportation, volume of blood in each blood culture, antimicrobial  
211 therapy administered before sampling. These factors are not standardly recorded in the  
212 participating hospitals and are therefore unknown. Another bias in the algorithm is the  
213 interval between two positive blood cultures in order to consider it as two separate  
214 bacteremia episodes. The 5-day interval was chosen because all bacteremia episodes must  
215 be evaluated and treated rapidly. When treatment is not appropriate, other blood cultures  
216 may be performed within this interval. A longer period, on the other hand, could falsely  
217 create multi-bacterial episodes in the case of episodes occurring close together.

218 The frequency of poly-microbial bacteremia in the BIAB group observed in our study (31.9%)  
219 is comparable to that of other studies (from 12.9% to 38%) [1–3,9,10].

220 In our study, BIAB microbial epidemiology was similar to that of previous works. *Bacteroides*  
221 spp. was the most frequently implicated genus, followed by *Clostridium* spp. [1–4,9]. The  
222 distribution of the different species included in the BFG was identical to what published  
223 previously: *B. fragilis* was the most frequent, followed by *B. thetaiotaomicron*, *P. distasonis*,  
224 and then *B. ovatus* and *B. vulgatus* [1–3,18]. This distribution is similar to that of the BFG

225 species in infections described by Nagy *et al.*, except for *P. distasonis*, but this was attributed  
226 by the authors to a taxonomic change [19]. *Cutibacterium* frequency was as low as in the  
227 study by Vena *et al.*, where this genus was only considered when more than two samples  
228 were positive, because it is considered to be a frequent blood culture contaminant [9]. On  
229 the other hand, *Lactobacillus* spp. was more frequently isolated compared to other studies.  
230 The ENRIA MALDI-TOF database allowed us to identify other genera unfrequently found in  
231 BIAB, such as *Tissierella praeacuta*. It should be noticed that the recovery of anaerobic  
232 bacteria differs between the different blood culture systems. With each system, some  
233 species are more easily retrieved, resulting in distribution differences [20,21]. This is  
234 particularly true for *Fingoldia magna*, rarely described in the literature, and *C. acnes* [21]. *E.*  
235 *lenta* detection has been reported by Bact/ALERT users [3,10,22] as in our study, but not by  
236 users of the BACTEC system.

237 AST was mostly performed on isolates identified as belonging to the BFG (63% of AST  
238 assays), due to its frequency of isolation in BIAB (46.6%). As this group is known for its high  
239 antibiotic resistance rates [23], this could have led to a distortion of the results toward  
240 higher resistance rates. Yet, these rates remained low for the most prevalent anti-anaerobic  
241 bacteria antibiotics (piperacillin-tazobactam, metronidazole, imipenem), and are comparable  
242 with those of other studies, even though they were performed in Asia [1,4,11,12]. The  
243 breakpoints used in our study are those of the CA-SFM version 2013 that have not been  
244 updated since the adoption of the European Committee on Antimicrobial Susceptibility  
245 Testing (EUCAST) methods. EUCAST (v8.1) only proposes breakpoints for anaerobic bacteria  
246 (the same as those used by CA-SFM 2013), but has none for ceftiofloxacin, tigecyclin,  
247 moxifloxacin and rifampicin. Therefore, our AST results should be interpreted with caution  
248 while waiting for new guidelines for anaerobic bacteria AST.

249 In the BFG, the frequency of susceptibility to clindamycin (50.8%) was equivalent to that of  
250 previous studies on anaerobic bacteria [1,4,11,12], but lower than that published for  
251 European collections in other contexts [19,24,25]. This could be due to the increasing  
252 prevalence of clindamycin resistance in anaerobic bacteria in Europe [25]. The BFG  
253 susceptibility to moxifloxacin was low (58.2%), as described in the literature [26]. A small  
254 percentage of isolates were non-susceptible to tigecyclin, as previously reported [25].

255 Seven multi-drug resistant BFG isolates were found in this study. None had a resistance  
256 profile compatible with the clone described by SÓki *et al.* (most were susceptible to  
257 piperacillin-tazobactam or imipenem, and all to metronidazole), thus *cfiA* and *nim* genes may  
258 not be present, or not expressed [13]. In our study, multi-drug resistance was mostly due to  
259 resistance to moxifloxacin and clindamycin, associated with resistance to at least another  
260 antibiotic. Major anti-anaerobic bacteria antibiotics were not affected in these isolates. The  
261 definition of multi-drug resistance for anaerobic bacteria used in our study was interpolated  
262 from that for aerobic bacteria proposed by Magiorakos *et al.*: “acquired non-susceptibility to  
263 at least one agent in three or more antimicrobial categories” [16]. This definition has a major  
264 pitfall, as resistance to moxifloxacin and clindamycin in the BFG is frequent (58.2% and  
265 50.8%, respectively), the cumulative probability of having at least one resistance within any  
266 of the six other categories of antibiotics is high (28.0% in our dataset, independently of the  
267 results for moxifloxacin and clindamycin), inflating the percentage of multi-drug resistant  
268 isolates, although these isolates remains susceptible to numerous antibiotics. Thus, criteria  
269 for multi-drug resistance in *Bacteroides* should be clearly established with differences  
270 between major (for example metronidazole, imipenem) and minor (moxifloxacin,  
271 clindamycin) molecules. Moreover, a new definition for extensively drug-resistant  
272 *Bacteroides* should be created.

273 To conclude, BIAB frequency was nearly two-fold higher at ICM, although some MUH  
274 services had higher frequencies. This underlines the need for clinicians to take into account  
275 the factors leading to an higher risk of BIAB, which can be a deadly condition [1,2,8–10]. *In*  
276 *vitro* susceptibility of the implicated anaerobic bacteria remains high, therefore empirical  
277 antimicrobial therapy against anaerobic bacteria should be effective. The development of  
278 multi-drug resistance is a concern because these molecules are mainly broad-spectrum  
279 antibiotics. Therefore, AST must be performed as frequently as possible, particularly for  
280 isolates belonging to the BFG, and new strategies should be developed to reduce the interval  
281 between blood culture positivity and AST results.

282

## 283 References

- 284 [1] T.Y. Tan, L.S.Y. Ng, L.L. Kwang, S. Rao, L.C. Eng, Clinical characteristics and antimicrobial  
285 susceptibilities of anaerobic bacteremia in an acute care hospital, *Anaerobe*. 43 (2017)  
286 69–74. <https://doi.org/10.1016/j.anaerobe.2016.11.009>.
- 287 [2] S. De Keukeleire, I. Wybo, A. Naessens, F. Echahidi, M. Van der Beken, K. Vandoorslaer,  
288 S. Vermeulen, D. Piérard, Anaerobic bacteraemia: a 10-year retrospective  
289 epidemiological survey, *Anaerobe*. 39 (2016) 54–59.  
290 <https://doi.org/10.1016/j.anaerobe.2016.02.009>.
- 291 [3] J. Kim, Y. Lee, Y. Park, M. Kim, J.Y. Choi, D. Yong, S.H. Jeong, K. Lee, Anaerobic  
292 bacteremia: impact of inappropriate therapy on mortality, *Infect. Chemother*. 48 (2016)  
293 91–98. <https://doi.org/10.3947/ic.2016.48.2.91>.
- 294 [4] L.S.Y. Ng, L.L. Kwang, S. Rao, T.Y. Tan, Anaerobic bacteraemia revisited: species and  
295 susceptibilities, *Ann. Acad. Med. Singapore*. 44 (2015) 13–18.

- 296 [5] L. Fenner, A.F. Widmer, C. Straub, R. Frei, Is the incidence of anaerobic bacteremia  
297 decreasing? Analysis of 114,000 blood cultures over a ten-year period, *J. Clin.*  
298 *Microbiol.* 46 (2008) 2432–2434. <https://doi.org/10.1128/JCM.00013-08>.
- 299 [6] B. Lassmann, D.R. Gustafson, C.M. Wood, J.E. Rosenblatt, Reemergence of anaerobic  
300 bacteremia, *Clin. Infect. Dis.* 44 (2007) 895–900. <https://doi.org/10.1086/512197>.
- 301 [7] T. Lazarovitch, S. Freimann, G. Shapira, H. Blank, Decrease in anaerobe-related  
302 bacteraemias and increase in *Bacteroides* species isolation rate from 1998 to 2007: A  
303 retrospective study, *Anaerobe.* 16 (2010) 201–205.  
304 <https://doi.org/10.1016/j.anaerobe.2009.09.003>.
- 305 [8] E. Urbán, Five-year retrospective epidemiological survey of anaerobic bacteraemia in a  
306 university hospital and review of the literature, *Eur. J. Microbiol. Immunol.* 2 (2012)  
307 140–147. <https://doi.org/10.1556/EuJMI.2.2012.2.7>.
- 308 [9] A. Vena, P. Muñoz, L. Alcalá, A. Fernandez-Cruz, C. Sanchez, M. Valerio, E. Bouza, Are  
309 incidence and epidemiology of anaerobic bacteremia really changing?, *Eur. J. Clin.*  
310 *Microbiol. Infect. Dis.* 34 (2015) 1621–1629. [https://doi.org/10.1007/s10096-015-2397-](https://doi.org/10.1007/s10096-015-2397-7)  
311 7.
- 312 [10] J.T. Ngo, M.D. Parkins, D.B. Gregson, J.D.D. Pitout, T. Ross, D.L. Church, K.B. Laupland,  
313 Population-based assessment of the incidence, risk factors, and outcomes of anaerobic  
314 bloodstream infections, *Infection.* 41 (2013) 41–48. [https://doi.org/10.1007/s15010-](https://doi.org/10.1007/s15010-012-0389-4)  
315 012-0389-4.
- 316 [11] Y. Lee, Y.-J. Park, M.-N. Kim, Y. Uh, M.S. Kim, K. Lee, Multicenter study of antimicrobial  
317 susceptibility of anaerobic bacteria in Korea in 2012, *Ann. Lab. Med.* 35 (2015) 479–  
318 486. <https://doi.org/10.3343/alm.2015.35.5.479>.

- 319 [12] F.D. Wang, C.H. Liao, Y.T. Lin, W.H. Sheng, P.R. Hsueh, Trends in the susceptibility of  
320 commonly encountered clinically significant anaerobes and susceptibilities of blood  
321 isolates of anaerobes to 16 antimicrobial agents, including fidaxomicin and rifaximin,  
322 2008–2012, northern Taiwan, *Eur. J. Clin. Microbiol. Infect. Dis.* 33 (2014) 2041–2052.  
323 <https://doi.org/10.1007/s10096-014-2175-y>.
- 324 [13] J. SÓki, M. Hedberg, S. Patrick, B. Bálint, R. Herczeg, I. Nagy, D.W. Hecht, E. Nagy, E.  
325 Urbán, Emergence and evolution of an international cluster of MDR *Bacteroides fragilis*  
326 isolates, *J. Antimicrob. Chemother.* 71 (2016) 2441–2448.  
327 <https://doi.org/10.1093/jac/dkw175>.
- 328 [14] I. Brook, The role of anaerobic bacteria in bacteremia, *Anaerobe.* 16 (2010) 183–189.  
329 <https://doi.org/10.1016/j.anaerobe.2009.12.001>.
- 330 [15] A.C.M. Veloo, H. Jean-Pierre, U.S. Justesen, T. Morris, E. Urban, I. Wybo, M. Kostrzewa,  
331 A.W. Friedrich, ENRIA workgroup, Validation of a for anaerobic bacteria optimized  
332 MALDI-TOF MS biotyper database: The ENRIA project, *Anaerobe.* (2018).  
333 <https://doi.org/10.1016/j.anaerobe.2018.03.007>.
- 334 [16] A.-P. Magiorakos, A. Srinivasan, R.B. Carey, Y. Carmeli, M.E. Falagas, C.G. Giske, S.  
335 Harbarth, J.F. Hindler, G. Kahlmeter, B. Olsson-Liljequist, D.L. Paterson, L.B. Rice, J.  
336 Stelling, M.J. Struelens, A. Vatsopoulos, J.T. Weber, D.L. Monnet, Multidrug-resistant,  
337 extensively drug-resistant and pandrug-resistant bacteria: an international expert  
338 proposal for interim standard definitions for acquired resistance, *Clin. Microbiol. Infect.*  
339 18 (2012) 268–281. <https://doi.org/10.1111/j.1469-0691.2011.03570.x>.
- 340 [17] B. Lamy, S. Dargère, M.C. Arendrup, J.-J. Parienti, P. Tattevin, How to optimize the use  
341 of blood cultures for the diagnosis of bloodstream infections? A state-of-the art, *Front.*  
342 *Microbiol.* 7 (2016). <https://doi.org/10.3389/fmicb.2016.00697>.

- 343 [18] T. Umemura, Y. Hamada, Y. Yamagishi, H. Suematsu, H. Mikamo, Clinical characteristics  
344 associated with mortality of patients with anaerobic bacteremia, *Anaerobe*. 39 (2016)  
345 45–50. <https://doi.org/10.1016/j.anaerobe.2016.02.007>.
- 346 [19] E. Nagy, E. Urbán, C.E. Nord, Antimicrobial susceptibility of *Bacteroides fragilis* group  
347 isolates in Europe: 20 years of experience, *Clin. Microbiol. Infect.* 17 (2011) 371–379.  
348 <https://doi.org/10.1111/j.1469-0691.2010.03256.x>.
- 349 [20] M. Almuhayawi, O. Altun, A.D. Abdulmajeed, M. Ullberg, V. Özenci, The performance of  
350 the four anaerobic blood culture bottles BacT/ALERT-FN, -FN Plus, BACTEC-Plus and -  
351 Lytic in detection of anaerobic bacteria and identification by direct MALDI-TOF MS, *PloS*  
352 *One*. 10 (2015) e0142398. <https://doi.org/10.1371/journal.pone.0142398>.
- 353 [21] M. Mueller-Premru, S. Jeverica, L. Papst, E. Nagy, Performance of two blood culture  
354 systems to detect anaerobic bacteria. Is there any difference?, *Anaerobe*. 45 (2017) 59–  
355 64. <https://doi.org/10.1016/j.anaerobe.2017.03.006>.
- 356 [22] K.E. Simmon, S. Mirrett, L.B. Reller, C.A. Petti, Genotypic diversity of anaerobic isolates  
357 from bloodstream infections, *J. Clin. Microbiol.* 46 (2008) 1596–1601.  
358 <https://doi.org/10.1128/JCM.02469-07>.
- 359 [23] A.N. Schuetz, Antimicrobial resistance and susceptibility testing of anaerobic bacteria,  
360 *Clin. Infect. Dis.* 59 (2014) 698–705. <https://doi.org/10.1093/cid/ciu395>.
- 361 [24] D. Mayne, M.J. Dowzicky, In vitro activity of tigecycline and comparators against  
362 organisms associated with intra-abdominal infections collected as part of TEST (2004–  
363 2009), *Diagn. Microbiol. Infect. Dis.* 74 (2012) 151–157.  
364 <https://doi.org/10.1016/j.diagmicrobio.2012.05.032>.
- 365 [25] A.C. Rodloff, M.J. Dowzicky, In vitro activity of tigecycline and comparators against a  
366 European collection of anaerobes collected as part of the Tigecycline Evaluation and

367 Surveillance Trial (T.E.S.T.) 2010–2016, *Anaerobe*. 51 (2018) 78–88.  
368 <https://doi.org/10.1016/j.anaerobe.2018.04.009>.

369 [26] G.H. Genzel, W. Stubbings, C.S. Stîngu, H. Labischinski, R. Schaumann, Activity of the  
370 investigational fluoroquinolone finafloxacin and seven other antimicrobial agents  
371 against 114 obligately anaerobic bacteria, *Int. J. Antimicrob. Agents*. 44 (2014) 420–423.  
372 <https://doi.org/10.1016/j.ijantimicag.2014.07.006>.

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**Table 1: Anaerobic bacteria found in bacteriemia episodes involving anaerobic bacteria (n=144)**

Genus and species of anaerobic bacteria isolated in blood cultures <sup>a</sup>	occurrences <sup>b</sup> (% of all BIAB)	Genus and species of anaerobic bacteria isolated in blood cultures <sup>a</sup>	occurrences <sup>b</sup> (% of all BIAB)
<b>GRAM NEGATIVE</b>		<b>GRAM POSITIVE</b>	
<b>Bacilli</b>		<b>Spore forming bacilli</b>	
<b><i>Bacteroides</i></b>	<b>64</b> (44.4)	<b><i>Clostridium</i> and related genera</b>	<b>18</b> (12.5)
- <i>fragilis</i>	37 (25.7)	- <i>ramosum</i>	4 (2.8)
- <i>thetaiotaomicron</i>	15 (10.4)	- <i>tertium</i>	3 (2.1)
- <i>ovatus</i>	6 (4.2)	- <i>butyricum</i>	2 (1.4)
- <i>vulgatus</i>	5 (3.5)	- <i>cadaveris</i>	2 (1.4)
- <i>uniformis</i>	3 (2.1)	- <i>clostridioforme</i>	2 (1.4)
- <i>finnegoldii</i>	1 (0.7)	- <i>perfringens</i>	2 (1.4)
- <i>nordii</i>	1 (0.7)	- <i>glycolicum</i>	1 (0.7)
<b><i>Parabacteroides distasonis</i></b>	<b>6</b> (4.2)	- <i>Hungatella hathewayi</i>	1 (0.7)
<b><i>Fusobacterium</i></b>	<b>7</b> (4.9)	- <i>innocuum</i>	1 (0.7)
- <i>nucleatum</i>	5 (3.5)	- <i>septicum</i>	1 (0.7)
- <i>necrophorum</i>	2 (1.4)	<b><i>Flavonifractor plautii</i></b>	<b>1</b> (0.7)
<b><i>Prevotella</i></b>	<b>7</b> (4.9)	<b>Non-spore forming bacilli</b>	
- <i>buccae</i>	3 (2.1)	<b><i>Lactobacillus</i></b>	<b>13</b> (9.0)
- <i>melaninogenica</i>	1 (0.7)	- <i>plantarum</i>	4 (2.8)
- <i>nanceiensis</i>	1 (0.7)	- <i>rhamnosus</i>	4 (2.8)
- <i>nigrescens</i>	1 (0.7)	- <i>paracasei</i>	2 (1.4)
- <i>sp</i>	1 (0.7)	- <i>salivarius</i>	1 (0.7)
<b><i>Leptotrichia</i></b>	<b>3</b> (2.1)	- <i>sp</i>	2 (1.4)
- <i>trevisanii</i>	2 (1.4)	<b><i>Eggerthella lenta</i></b>	<b>13</b> (9.0)
- <i>sp</i>	1 (0.7)	<b><i>Actinotignum schaalii</i></b>	<b>5</b> (3.5)
<b><i>Dialister pneumosintes</i></b>	<b>3</b> (2.1)	<b><i>Bifidobacterium</i></b>	<b>4</b> (2.8)
<b><i>Porphyromonas asaccharolytica</i></b>	<b>2</b> (1.4)	- <i>breve</i>	2 (1.4)
<b><i>Capnocytophaga canimorsus</i></b>	<b>1</b> (0.7)	- <i>dentium</i>	1 (0.7)
<b><i>Desulfovibrio sp</i></b>	<b>1</b> (0.7)	- <i>longum</i>	1 (0.7)
<b><i>Dysgonomonas capnocytophagoides</i></b>	<b>1</b> (0.7)	<b><i>Cutibacterium acnes</i></b>	<b>3</b> (2.1)
<b><i>Sutterella wadsworthensis</i></b>	<b>1</b> (0.7)	<b><i>Actinomyces</i></b>	<b>2</b> (1.4)
<b><i>Tissierella praeacuta</i></b>	<b>1</b> (0.7)	- <i>oris</i>	1 (0.7)
<b>Cocci</b>		- <i>turicensis</i>	1 (0.7)
<b><i>Veillonella</i></b>	<b>4</b> (2.8)	<b><i>Slackia exigua</i></b>	<b>2</b> (1.4)
- <i>atypica</i>	2 (1.4)	<b><i>Alloscardovia omnicoles</i></b>	<b>1</b> (0.7)
- <i>parvula</i>	2 (1.4)	<b><i>Trueperella bernardiae</i></b>	<b>1</b> (0.7)
- <i>sp</i>	1 (0.7)	<b>Cocci</b>	
		<b><i>Parvimonas micra</i></b>	<b>3</b> (2.1)
		<b><i>Ruminococcus gnavus</i></b>	<b>1</b> (0.7)

AB anaerobic bacteria, BIAB bacteriemia involving anaerobic bacteria.

<sup>a</sup> Genera are in bold. When only one species was isolated in a genus, lines were merged. Genus and species in a genus are ordered from the most to the least frequent. "sp" species were either not specified in the ENRIA database, or results were not sufficient to discriminate among species. <sup>b</sup> As multiple species of the genus could be found in a BIAB episode, the sum of the occurrences of all species from a genus can be higher than the occurrence of that genus.

**Table 2 : Results of antibiotic susceptibility testing of metronidazole**

Genus and species of anaerobic bacteria isolated in blood cultures	Metronidazole AST results (breakpoint > 4 mg/L)			
	n susceptible/n tested (%)	MIC50	MIC90	MIC range or value
<b><i>Bacteroides</i></b>	<b>61/62 (98.4)</b>	<b>.5</b>	<b>1.5</b>	<b>.064-6</b>
- <i>fragilis</i>	34/35 (97.1)	.38	1	.094-6
- <i>thetaiotaomicron</i>	13/13 (100)	.75	1.25	.25-2
- <i>vulgatus</i>	5/5 (100)	.38	1.5	.064-2
- <i>ovatus</i>	4/4 (100)	NA	1.5	.5-2
- <i>uniformis</i>	3/3 (100)	NA	NA	.19-.5
- <i>finnegoldii</i>	1/1 (NA)	NA	NA	1.5
- <i>nordii</i>	1/1 (NA)	NA	NA	.19
<b><i>Clostridium</i></b>	<b>11/11 (100)</b>	<b>.25</b>	<b>1.5</b>	<b>&lt;.016-2</b>
- <i>ramosum</i>	2/2 (100)	NA	NA	.125-.75
- <i>tertium</i>	2/2 (100)	NA	NA	.5-.75
- <i>cadaveris</i>	2/2 (100)	NA	NA	.047-.047
- <i>clostridioforme</i>	1/1 (NA)	NA	NA	<.016
- <i>perfringens</i>	2/2 (100)	NA	NA	1.5-2
- <i>glycolicum</i>	1/1 (NA)	NA	NA	.032
- <i>innocuum</i>	1/1 (NA)	NA	NA	1.5
<b><i>Fusobacterium nucleatum</i></b>	<b>1/1 (NA)</b>	<b>NA</b>	<b>NA</b>	<b>.016</b>
<b><i>Prevotella</i></b>	<b>3/3 (100)</b>	<b>NA</b>	<b>NA</b>	<b>.019-.75</b>
- <i>buccae</i>	2/2 (100)	NA	NA	.19-.75
- <i>melaninogenica</i>	2/2 (100)	NA	NA	.5-.5
<b><i>Parabacteroides distasonis</i></b>	<b>5/5 (100)</b>	<b>1.5</b>	<b>3</b>	<b>.75-4</b>
<b><i>Veillonella</i></b>	<b>2/2 (100)</b>	<b>NA</b>	<b>NA</b>	<b>.75-1</b>
- <i>parvula</i>	1/1 (NA)	NA	NA	.75
- <i>sp</i>	1/1 (NA)	NA	NA	1
<b><i>Dialister pneumosintes</i></b>	<b>1/1 (NA)</b>	<b>NA</b>	<b>NA</b>	<b>2</b>
<b><i>Porphyromonas asaccharolytica</i></b>	<b>1/1 (NA)</b>	<b>NA</b>	<b>NA</b>	<b>.032</b>
<b><i>Ruminococcus gnavus</i></b>	<b>1/1 (NA)</b>	<b>NA</b>	<b>NA</b>	<b>.064</b>
<b><i>Tissierella praeacuta</i></b>	<b>1/1 (NA)</b>	<b>NA</b>	<b>NA</b>	<b>.064</b>
<b>TOTAL</b>	<b>87/88 (98.9)</b>	<b>.5</b>	<b>1.5</b>	<b>&lt;.016-6</b>

NA: not applicable: the percentage of susceptible results was not calculated for n=1, and MIC50 and MIC90 were not calculated for n<5.

AST antibiotic susceptibility typing.

**Table 3 : Results of antibiotic susceptibility testing for *Bacteroides fragilis* group's isolates**

Genus and species of anaerobic bacteria isolated in blood cultures	Results of AST per antibiotic													
	Number of susceptible results/total number of results (percentage of susceptible results) ± MIC50, MIC90 and range for MIC/value													
	AMC (MIC)				PIP		PIT		CXI (MIC)				IMI	
Breakpoints (CASFM 2013)	S ≤ 4 mg/L ; R > 8 mg/L				R > 18 mm		S ≥ 21 mm R < 19 mm		R > 32 mg/L				S ≥ 24 mm R < 17 mm	
<b><i>Bacteroides</i></b>	<b>59/62 (95.2)</b>	<b>.75</b>	<b>4</b>	<b>.094-8</b>	<b>32/62 (51.6)</b>	<b>60/62 (96.8)</b>	<b>54/60 (90.0)</b>	<b>8</b>	<b>32</b>	<b>1.5-&gt;256</b>	<b>61/62 (98.4)</b>			
- <i>fragilis</i>	34/35 (97.1)	.5	3	.094-6	22/35 (62.9)	35/35 (100)	33/34 (97.1)	6	24	1.5->256	35/35 (100)			
- <i>thetaiotaomicron</i>	11/13 (84.6)	2	4	.25-8	4/13 (30.8)	12/13 (92.3)	8/13 (61.5)	32	64	12-64	12/13 (92.3)			
- <i>vulgatus</i>	5/5 (100)	1	3	.094-4	2/5 (40.0)	5/5 (100)	5/5 (100)	4	16	2-16	5/5 (100)			
- <i>ovatus</i>	4/4 (100)	NA	NA	.19-2	3/4 (75.0)	3/4 (75.0)	4/4 (100)	NA	NA	12-24	4/4 (100)			
- <i>uniformis</i>	3/3 (100)	NA	NA	.25-3	1/3 (33.3)	3/3 (100)	3/3 (100)	NA	NA	2-3	3/3 (100)			
- <i>finnegoldii</i>	1/1 (NA)	NA	NA	2	0/1 (NA)	1/1 (NA)	1/1 (NA)	NA	NA	6	1/1 (NA)			
- <i>nordii</i>	1/1 (NA)	NA	NA	1.5	0/1 (NA)	1/1 (NA)	1/1 (NA)	NA	NA	32	1/1 (NA)			
<b><i>Parabacteroides distasonis</i></b>	<b>3/5 (60.0)</b>	<b>2</b>	<b>16</b>	<b>1-24</b>	<b>2/5 (40.0)</b>	<b>5/5 (100)</b>	<b>5/5 (100)</b>	<b>24</b>	<b>24</b>	<b>16-24</b>	<b>5/5 (100)</b>			
<b>TOTAL</b>	<b>62/67 (92.5)</b>	<b>1</b>	<b>4</b>	<b>.094-24</b>	<b>34/67 (50.7)</b>	<b>65/67 (97.0)</b>	<b>59/65 (90.8)</b>	<b>8</b>	<b>32</b>	<b>1.5-&gt;256</b>	<b>66/67 (98.5)</b>			

**Table 3 : Results of antibiotic susceptibility testing for Bacteroides fragilis group's isolates (continued)**

Genus and species of anaerobic bacteria isolated in blood cultures	Results of AST per antibiotic												
	Number of susceptible results/total number of results (percentage of susceptible results) ± MIC50, MIC90 and range for MIC/value												
	MOX	RIF		CLI		MET (MIC)			TIG (MIC)				
Breakpoints (CASFM 2013)	S ≥ 21 mm R < 18 mm	S ≥ 19 mm R < 14 mm	R < 15 mm		R > 4 mg/L			S ≤ 4 mg/L ; R > 8 mg/L					
<b>Bacteroides</b>	<b>34/62 (54.8)</b>	<b>60/61 (98.4)</b>	<b>31/62 (50.0)</b>	<b>61/62 (98.4)</b>	<b>.5</b>	<b>1.5</b>	<b>.064-6</b>	<b>56/61 (91.8)</b>	<b>.25</b>	<b>4</b>	<b>.032-8</b>		
- <i>fragilis</i>	20/35 (57.1)	35/35 (100)	21/35 (60.0)	34/35 (97.1)	.38	1	.094-6	31/34 (91.2)	.38	4	.047-8		
- <i>thetaiotaomicron</i>	8/13 (61.5)	12/13 (92.3)	4/13 (30.8)	13/13 (100)	.75	1	.25-2	11/13 (84.6)	.5	4	.032-6		
- <i>vulgatus</i>	2/5 (40.0)	5/5 (100)	2/5 (40.0)	5/5 (100)	.38	1.5	.064-2	5/5 (100)	.125	1	.032-2		
- <i>ovatus</i>	3/4 (75.0)	4/4 (100)	1/4 (25.0)	4/4 (100)	NA	NA	.5-2	4/4 (100)	NA	NA	.047-1.5		
- <i>uniformis</i>	1/3 (33.3)	3/3 (100)	2/3 (66.7)	3/3 (100)	NA	NA	.19-.5	3/3 (100)	NA	NA	.064-.094		
- <i>finnegoldii</i>	0/1 (NA)		0/1 (NA)	1/1 (NA)	NA	NA	1.5	1/1 (NA)	NA	NA	.047		
- <i>nordii</i>	1/1 (NA)	1/1 (NA)	1/1 (NA)	1/1 (NA)	NA	NA	.19	1/1 (NA)	NA	NA	1		
<b>Parabacteroides distasonis</b>	<b>5/5 (100)</b>	<b>5/5 (100)</b>	<b>3/5 (60.0)</b>	<b>5/5 (100)</b>	<b>1.5</b>	<b>3</b>	<b>.75-4</b>	<b>5/5 (100)</b>	<b>.5</b>	<b>1</b>	<b>.25-2</b>		
<b>TOTAL</b>	<b>39/67 (58.2)</b>	<b>65/66 (97.0)</b>	<b>34/67 (50.8)</b>	<b>66/67 (98.5)</b>	<b>.5</b>	<b>1.5</b>	<b>.064-6</b>	<b>61/66 (91.0)</b>	<b>.25</b>	<b>4</b>	<b>.032-8</b>		

NA: not applicable: the percentage of susceptible results was not calculated for n=1, and MIC50 and MIC90 were not calculated for n<5.

AMC, amoxicillin-clavulanic acid; AST, antibiotic susceptibility testing; CLI, clindamycin; CXI, ceftiofur; IMI imipenem; MIC, minimum inhibitory concentration; MOX, moxifloxacin; MET, metronidazole; PIP, piperacillin; PIT, piperacillin-tazobactam; RIF, rifampicin; TIG, tigecycline.

**Table 4: Antibiotic susceptibility testing of multi-drug resistant *Bacteroides fragilis* group's isolates**

<b>Species</b>	<b>AMC</b>	<b>PIT</b>	<b>CXI</b>	<b>IMI</b>	<b>MOX</b>	<b>RIF</b>	<b>CLI</b>	<b>MET</b>	<b>TIG</b>	<b>N. of families with resistance</b>
<i>B. thetaiotaomicron</i>	S	S	R	I	R	R	R	S	S	5
<i>B. fragilis</i>	I	S	S	S	R	S	R	S	I	4
<i>B. thetaiotaomicron</i>	I	S	R	S	R	S	S	S	I	4
<i>B. thetaiotaomicron</i>	I	S	R	S	R	S	R	S	S	4
<i>B. thetaiotaomicron</i>	S	R	S	S	I	S	R	S	S	3
<i>B. fragilis</i>	S	S	S	S	R	S	R	S	I	3
<i>B. thetaiotaomicron</i>	S	S	S	S	R	S	R	S	I	3

AMC, amoxicillin-clavulanic acid; PIT, piperacillin-tazobactam; CXI, ceftiofur; IMI, imipenem; MOX, moxifloxacin; RIF, rifampicin; CLI clindamycin; MET, metronidazole; TIG, tigecycline.