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Bacteroides fragilis Associated with a
Totally Implantable Venous Port

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Four patients in an oncology ward developed *Bacteroides fragilis* bacteremia over a 12-day period. Cross-infection between two of them, due to an imipenem-resistant strain, was demonstrated by epidemiological investigation and genotypic typing methods (arbitrarily primed PCR fingerprinting and nucleotide sequencing of the *cflA* genes and upstream IS1168/IS1168 elements).

*Bacteroides fragilis* is often responsible for intra-abdominal sepsis and as such is an important cause of nosocomial infections (7–9, 12, 14, 17). However, very few studies have been conducted on the possible dissemination of this organism within hospitals, probably because it is typically an endogenous pathogen (6, 25). Earlier studies based on serotyping suggested that strains of *B. fragilis* might spread between hospitalized patients (4, 5). But more recently, by using molecular typing techniques, no clonal distribution could be detected within *B. fragilis* hospital isolates (13). We report here a case of cross-infection due to an imipenem-resistant *B. fragilis* strain, as demonstrated by epidemiological investigation and genotypic typing methods.

Over a 12-day period in September 2001, four patients hospitalized in the oncology ward of Saint-André Hospital in Bordeaux, France, presented *B. fragilis* bacteremia (Fig. 1) despite the low incidence of this organism among bloodstream isolates (ca. 3%) (14, 17). Of the four patients, only patients A (kidney carcinoma) and D (colic adenocarcinoma), both admitted for a subocclusive syndrome, were likely to develop *B. fragilis* bacteremia. Indeed, members of the *B. fragilis* group reside in the gut and, from this reservoir, can colonize the female genital tract but they are virtually absent in the upper respiratory tract (6, 12). Accordingly, *B. fragilis* bacteremia originates more frequently from abdominal (60 to 70%) rather than pelvic (3 to 5%) processes (patient B, cervical cancer) and almost never from respiratory disease (patient C, bronchial epidermoid carcinoma) (7–9, 14, 17). Nevertheless, all four patients had risk factors for *B. fragilis* bacteremia that included malignancy and use of immunosuppressive therapy (14, 17).

No epidemiological link could be found between the four patients, except for the insertion of a totally implantable venous port (IVP) in patients B and C on the same day, in the same operating room. The timetable for the event in this room on this day included a gastro-jejunal derivation with cholecystectomy performed in the morning by a surgical team in patient X (7:35 to 12:20 a.m.) which ended with compressive dressing of the wound with Mefix tape (Molnlycke Health Care, Waremere, Belgium). After a period during which the room was cleaned and thereafter not entered by anyone (12:20 a.m. to 3:00 p.m.), three Port-A-Cath systems (Sims, Orly, France) were implanted in patient B (3:00 to 3:45 p.m.), an unrelated patient Y (4 to 5 p.m.), and patient C (5:15 to 6:00 p.m.) by a second surgical team. In contrast to patient Y, patients B and C had an IVP outfit with a Huber needle secured by the sticking Mefix bandage instead of an ordinary dressing and they subsequently developed an IVP-related infection, as defined by bacteremia without another apparent infection focus and/or inflammation or discharge at the insertion site (15). Infection is a rare complication of IVPs, and the predominant pathogens are staphylococci (10, 15).

The nonsterile bandage used to fix the IVP and the Huber needle was suspected to be the source of the contamination. Actually, adhesive tapes that secure Huber needles are applied in close contact with the intravascular insertion site for extended periods of time and can contribute to local infections (23). A sampling campaign (12 sites), carried out in the same operating room 1 month after the initial episode showed that several articles of noncleanable, nonsterilizable equipment, including the Mefix tape, were contaminated by skin-commensal and environmental organisms. The roll of tape may have been contaminated by the digestive flora of the patient operated on in the morning (patient X). Anaerobes substantially outnumber aerobic organisms in the digestive flora, and *B. fragilis* appears to be one of the most virulent (6, 7–9, 25). Moreover, the *B. fragilis* strain Bf1149 was demonstrated to remain viable on the adhesive tape for at least 8 h when present at levels higher than 10⁶ CFU/ml (data not shown), in agreement with the fact that *B. fragilis* is only a moderate obligate anaerobe (26).

The four strains of *B. fragilis* isolated from patients A to D gave identical or similar biochemical reactions (12) (Table 1). Antibiotyping by the disk diffusion method (23 tested antibiotics) showed that Bf1149 and Bf1150 were resistant to all β-lactams including imipenem, in contrast with the two other
strains (MICs of 128 mg/liter and 0.5 mg/liter, respectively) (Table 1). Imipenem resistance is an exceptional trait among B. fragilis strains (0 to 3%) (6, 16, 21). This resistance is due to the production of a group 3a class B metallo-/H9252-lactamase encoded by the silent cfIA chromosomal gene, the expression of which is promoted by the insertion of an insertion element (IS) immediately upstream (1, 18, 19, 21).

In order to type the four strains of B. fragilis by a molecular method, arbitrarily primed PCR fingerprinting with four primers was undertaken (2, 18). Bf1149 and Bf1150 gave strictly identical patterns, whereas Bf1148 and Bf1151 yielded different and distinct profiles (Fig. 2). Previous PCR fingerprinting experiments have demonstrated that the cfIA-positive B. fragilis strains yield a homogeneous DNA fragment pattern (2, 18). The same data were obtained with reference genotypic typing methods (18). Thus, conventional genotypic methods are inadequate for typing the genetically homogenous cfIA-positive B. fragilis.

The presence of the cfIA gene and an upstream IS in Bf1149 and Bf1150 was confirmed by PCR (27). Sequence analysis of the 2,250-bp amplified DNA fragment (GenBank sequence database accession number AF429432) showed that the 747-bp cfIA genes of Bf1149 and Bf1150 were identical and differed from the most closely related cfIA sequence available in GenBank by eight mismatches, including two missense mutations (Met-79→Thr and Arg-113→Lys) (22). In addition, both Bf1149 and Bf1150 strains harbored an identical 1,320-bp IS 8 bp upstream of the cfIA gene which differed from IS1186 and IS1168 by three and seven mismatches, respectively, including one (Glu-200→Lys) and two (Ala-178→Glu and Arg-46→Cys) missense mutations, respectively. IS1186 is one of the five elements reported at present to promote the expression of cfIA.

### TABLE 1. Characteristics of the B. fragilis strains used in this study

<table>
<thead>
<tr>
<th>Strain</th>
<th>Patient</th>
<th>Hospital unit</th>
<th>Clinical specimen</th>
<th>Date (day/mo/yr)</th>
<th>Methoda</th>
<th>Drug resistance byb antibiotyping</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bf1148</td>
<td>A</td>
<td>1</td>
<td>Blood</td>
<td>11/09/00</td>
<td>API 20 A code: 46546240</td>
<td>TIC, TET</td>
</tr>
<tr>
<td>Bf1149</td>
<td>B</td>
<td>1</td>
<td>Blood</td>
<td>14/09/00</td>
<td>Rapid ID32A code: 4517453332</td>
<td>TIC, TIM, IPM, TET</td>
</tr>
<tr>
<td>Bf1150</td>
<td>C</td>
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<td>Blood</td>
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<td>46544240</td>
<td>4517453332</td>
</tr>
<tr>
<td>Bf1151</td>
<td>D</td>
<td>2</td>
<td>Blood</td>
<td>23/09/00</td>
<td>46544240</td>
<td>4517453332</td>
</tr>
<tr>
<td>ATCC 25285</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>wt</td>
<td></td>
</tr>
</tbody>
</table>

a bioMérieux, Marcy l’Etoile, France.
b TIC: ticarcillin; TET: tetracyclines; TIM: ticarcillin-clavulanic acid; IPM: imipenem.
c wt, wild-type susceptibility.


