Application of *rrs* Gene Sequencing To Elucidate the Clinical Significance of *Eggerthella lenta* Infection[▽]

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Eggerthella lenta, a bacterium of the intestinal human gut flora, has rarely been reported to cause significant infections. We report two cases of bacteremia and the first case of liver abscess due to *Eggerthella lenta* identified by *rrs* gene analysis.

CASE REPORTS

Case 1. An 82-year-old man was admitted with fecal peritonitis related to intestinal perforation. His past medical history was unremarkable except for senile dementia. He complained from an acute abdominal pain. At examination, abdominal contracture and high-grade fever were noted, but blood cultures remained sterile. A bowel colostomy was undertaken, and the patient was started on broad-spectrum antibiotic therapy (tazocillin at 12 g/day and ciprofloxacin at 500 mg/twice a day). After 10 days of such therapy, the fever relapsed. Urinary bacterial culture was sterile, but anaerobic gram-positive bacilli were isolated from one blood culture and identified by *rrs* sequencing as *Eggerthella lenta*. The isolate was susceptible to amoxicillin and clavulanic acid, imipenem, metronidazole, and vancomycin. A computed tomography scan did not show any deep abscess, and a transesophageal echocardiography was normal. The patient responded favorably to a 3-week course of imipenem (1.5g/day). He remains well at follow-up.

Case 2. A 33-year-old man was hospitalized with acute appendicitis. No underlying conditions were noted. After surgical removal of the appendix, the histopathologic analysis showed acute inflammation involving appendicular mucosa and submucosa but no suppurative inflammation. The surgical treatment was rapidly complicated by a febrile parietal abscess at the cecum, at the surgical insertion site. Two sets of blood cultures were collected, from which two anaerobic bacteria were identified. *Fusobacterium mortiferum* was identified by conventional methods by using the API 20NE system (bioMérieux, France), but the other gram-positive bacillus was identified as *E. lenta* by *rrs* gene sequencing. They were both susceptible to amoxicillin and clavulanic acid, imipenem, and vancomycin. The patient received amoxicillin and clavulanic acid (3 g/day), which had a quick and favorable outcome.

Case 3. A 42-year-old woman was admitted with fever and abdominal pain. Her medical history included an ovarian carcinoma with peritoneal metastatic involvement for which she received antimitotic chemotherapy. A gastrointestinal derivation had been placed for intestinal obstruction a few months before the admission for infection. At admission, an abdominal computed tomography scan confirmed the presence of a liver abscess that was treated by surgical drainage. Collected pus from the abscess grew two anaerobic bacilli, which were identified by *rrs* gene sequencing as *Clostridium paraputrificum* and *E. lenta*. They were only susceptible to metronidazole and vancomycin. Antibiotic therapy with metronidazole (1.5 g/day) was started. The patient responded favorably.

The bacterial strains in these cases were isolated in blood cultures from patients 1 and 2 and from a liver abscess from patient 3. After 2 to 4 days, gram-positive bacteria were isolated from anaerobic blood cultures with the BACTEC 9240 automated blood system (Becton Dickinson and Co., Sparks, MD). Then, blood and pus were cultured onto Columbia sheep blood agar (bioMérieux, Marcy l'Étoile, France) and incubated in an anaerobic atmosphere for 5 days. Small translucent colonies resulted. A test using API 20A strips (bioMérieux, France) was performed, allowing the identification of *E. lenta* to between 90% and 96% identity. In order to accurately identify these microorganisms, *rrs* gene comparisons were performed (Service of Bacteriology, Hospital Timone, Marseille, France), and the three bacteria were identified as *E. lenta* with 99% of homology upon a 1,499-nucleotide fragment (GenBank accession no. AF 292375) for all three strains (2).

The three clinical cases that we have reported thus far are described in Table 1 (patients 1, 2, and 3), as well as the other five cases cited by Lau et al. (6). The median age was 57 years (range, 33 to 82 years). Two of our patients had underlying severe diseases: notably one has an ovarian carcinoma. In the three cases, we reported, all patients had underlying intestinal diseases and only one had a monomicrobial infection. Antibiotic susceptibilities were different between the three strains. Two strains were susceptible to amoxicillin-clavulanic acid, imipenem, metronidazole, and vancomycin, but one was susceptible to metronidazole and vancomycin only.

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Discussion. The genus *Eggerthella* includes anaerobic, nonsporulating, gram-positive bacilli. These bacteria were named in honor of Arnold Eggerth, who made the first description in

TABLE 1. Characteristics of the patients with *E. lenta* bacteremia

Characteristic(s)	Result for patient ^a :							
	1	2	3	4	5	6	7	8
Age in yr (sex)	82 (male)	33 (male)	42 (female)	69 (female)	74 (male)	75 (female)	84 (female)	87 (female)
Diagnosis	Intestinal obstruction	Acute appendicitis	Liver abscess	Primary bacteremia	Primary bacteremia	Pelvic inflammatory disease	Infected sacral sore	Sore infected buttock
Complication(s)	Intestinal perforation, peritonitis	Parietal abscess	None	None	Septic shock, disseminated intravascular coagulation	None	Cerebrovascular accident	Diabetes mellitus, cerebrovascular accident
Underlying disease	Senile dementia	None	Ovary carcinoma, intestinal resection, immunodepression	Intestinal obstruction, carcinoma of lung	Alcoholic cirrhosis, gallstones, gastrointestinal bleeding	None	None	Multiorgan failure
No. of positive blood cultures	1	1	0	1	1	1	1	1
Type of bacteremia	Monomicrobial	Polymicrobial	Polymicrobial	Polymicrobial	Monomicrobial	Polymicrobial	Monomicrobial	Polymicrobial
Concomitant isolate(s)		<i>Fusobacterium mortiferum</i>	<i>Clostridium parvum</i>	<i>Prevotella intermedia</i>		<i>Morganella morganii</i>		<i>Bacteroides splanchinus</i> , <i>Arcanobacterium hemolyticum</i>
Antibiotic susceptibility	Amoxicillin-clavulanic acid, imipenem, metronidazole, vancomycin	Amoxicillin-clavulanic acid, imipenem, vancomycin	Metronidazole, vancomycin					
Treatment	Imipenem	Amoxicillin-clavulanic acid	Metronidazole	Metronidazole	Ticarcillin/clavulanate	Cefuroxime, metronidazole	Cefuroxime, metronidazole, netilmicin	Cefuroxime, cloxacillin
Outcome	Favorable	Favorable	Favorable	Cured	Died	Cured	Cured	Died

^a Patients 1 to 3 were from our unit. The characteristics of patients 4 to 8 are from reference 6.

1935 (3). *Eggerthella* gen. nov. was proposed to substitute for *Eubacterium lentum* in 1999 on the basis of the *rrs* sequence divergence from *Collinsella aerofaciens* and *Coriobacterium glomerans* and the presence of unique phenotypic characteristics (4, 12). *Eggerthella lenta* comb. nov. is one species of this new group.

E. lenta (formerly *Eubacterium lentum*) belongs to the intestinal microflora of humans. Few cases of infection due to *E. lenta* have been reported in humans. The following are examples of pathological cases due to *E. lenta*: postgynecological surgery, chorioamnionitis after cervical cerclage required for gravid patients, and infection of the female genital tract due to intrauterine devices (1). Specific and rare cases have been reported implying the same infectious agent, such as a case of frontal sinusitis with intracranial complications that occurred in a young man with sickle cell disease (10), a cutaneous abscess in an intravenous drug user (5), and the occurrence of bacteremia in two single cases—one after a subgingival irrigation (13) and another in association with a concomitant cytomegalovirus pneumonia (9).

E. lenta has also been isolated from appendix tissue samples obtained at surgery from children with suspected appendicitis (11) and isolated in polymicrobial infections with others anaerobic bacteria, notably in colonized aortic aneurysm wall (8). Pelvic inflammatory diseases and infected bed sores might be complicated by *E. lenta* bacteremia (6). Throughout the available literature, bacteremia associated with *Eggerthella* sp. was reported in 10 cases, including 5 due to *E. lenta* only. These five cases and the additional three cases encountered in our unit (Infectious and Tropical Diseases Department, Marseille, France) are described in Table 1.

E. lenta bacteremia has been associated with high risk of morbidity and mortality such as septic shock and disseminated intravascular coagulation (6, 7). Among patients with documented bacteremia, the major risk factors were advanced age and underlying diseases such as neoplasia, immunosuppression, and involvement of the gastrointestinal or genital tract (6, 12). In our three cases, patients had a past history of digestive disease.

To our knowledge, *E. lenta* has never been isolated in liver abscess, probably because the samples are currently polymicrobial and *E. lenta* is difficult to isolate by conventional methods.

Molecular techniques are very useful for the specific diagnosis of bacteremia associated with polymicrobial anaerobic nonsporulating gram-positive bacilli. Two novel species, *Egg-*

erthella hongkongensis and *Eggerthella sinensis*, have been identified by *rrs* gene sequencing (7). For the first time, we have been able to identify *E. lenta* in a hepatic abscess by molecular techniques.

The three cases that we report confirm that *E. lenta* is likely to be a more common pathogen than previously expected. Moreover, it is frequently associated with polymicrobial bacteremia, and a remarkable and consistent finding is that *E. lenta* is susceptible to different antibiotics, explaining the diversity of antibiotic treatment given to these patients.

Based on our findings, we assume that the application of *rrs* gene sequencing would thus enable us to widen the clinical spectrum of *E. lenta* infection.

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