



Eggerthella lenta Bacteremia in a 91-Year-Old Male

Hin Fung Tsang¹, Wai Ming Leung¹ and Sze Chuen Cesar Wong^{2*}

¹Department of Clinical Laboratory and Pathology, Hong Kong Special Administrative Region, China

²Department of Health Technology and Informatics, Hong Kong Special Administrative Region, China

Abstract

Eggerthella lenta, previously known as *Eubacterium lentum*, is a catalase positive, hydrogen sulfide positive, indole negative, non-motile, non-sporulating and slow-growing obligate anaerobic Gram-positive bacillus that belongs to the family *Coriobacteriaceae*. Infection by *E. lenta* is usually under-recognized. A 91-year-old male presented to the emergency department with a complaint of fever. The patient had no headache. Other symptoms noted at presentation included mild chills, poor appetite, and enlarged cervical lymph nodes. Multiple gallstones were identified in the gall bladder but there was no evidence of cholangitis. Urine culture and blood culture were performed, and the patient received meropenem therapy before the blood culture result was obtained. After 4 days of incubation, Gram-positive bacilli grew in an anaerobic blood culture bottle. The positive blood culture broth was inoculated onto Columbia sheep blood agar (bioMerieux, Marcy l'Etoile, France) and incubated anaerobically for 72 h. Small and translucent colonies grew on the Columbia sheep blood agar and Gram-positive bacillus was observed by Gram staining. Analysis of the colonies by two Matrix Assisted Light Desorption/Ionization Time of Flight Mass Spectrometry (MALDI-TOF MS) platforms (Bruker Daltonics, Bremen, Germany; bioMerieux, Marcy l'Etoile, France) identified the isolated organism as *E. lenta*. The patient was diagnosed with *E. lenta* bacteremia. In this case, we described a patient with a potentially fatal bacteremia caused by *E. lenta* and demonstrated that MALDI-TOF MS is a promising, fast, and accurate technology for the identification of clinically important anaerobic bacteria and its consistency in identifying bacteria by different platforms.

Keywords: *Eggerthella lenta*; Bacteremia; MALDI-TOF

Introduction

Eggerthella lenta, previously known as *Eubacterium lentum*, is a catalase positive, hydrogen sulfide positive, indole negative, non-motile, non-sporulating and slow-growing obligate anaerobic Gram-positive bacilli that belongs to the family *Coriobacteriaceae*. Infection by *E. lenta* is usually under-recognized and more frequent than reported due to prior antimicrobial treatments being used, difficulties in phenotypic identification as well as offering optimal culture conditions such as nutritional requirements. In this case, a 91-year-old male with *E. lenta* bacteremia was described.

Case Presentation

A 91 years old male presented to the emergency department with a complaint of fever. The patient had no headache. Other symptoms noted at presentation included mild chills, poor appetite, and enlarged cervical lymph nodes. Upon admission, the patient had a temperature of 39°C, blood pressure of 138/69 mmHg and a pulse of 99/min.

Laboratory investigations demonstrated Hemoglobin (Hb) concentration of 10.9 g/dL, leukocyte count of $7.7 \times 10^9/L$ (95% segmented neutrophils, 4% lymphocytes, 1% monocytes), platelet count of $138 \times 10^9/L$, Blood Urea Nitrogen (BUN)/creatinine level of 9.0/0.08 mmol/L, and total protein/albumin content of 62/33 g/L. C-Reactive Protein (CRP) and Procalcitonin (PCT) levels were 21.8 mg/L (normal reference range 0 to 4.9 mg/L), and 3.3 ug/L (normal reference range 0 to 0.04 ug/L) respectively. Multiple gallstones were identified in the gall bladder but there was no evidence of cholangitis. Urine culture and blood culture (aerobic and anaerobic) were performed and the patient received meropenem therapy empirically before the blood culture result was obtained.

After 4 days of incubation, Gram-positive bacilli grew in an anaerobic blood culture bottle that was incubated in a BacT/Alert three-dimensional (3D) automated microbial detection system (bioMerieux, Marcy l'Etoile, France). No microorganisms were detected in the urine culture. The positive culture broth was inoculated onto Columbia sheep blood agar (bioMerieux, Marcy l'Etoile,

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*Correspondence:

Sze Chuen Cesar Wong, Department of Health Technology and Informatics, The Hong Kong Polytechnic University, China,

E-mail: cesar.wong@polyu.edu.hk

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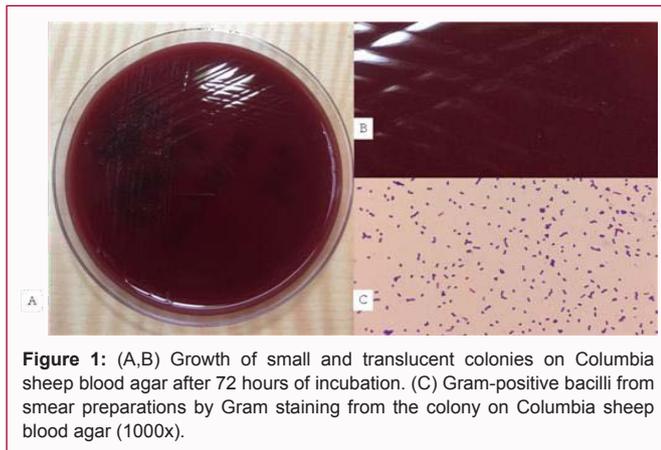


Figure 1: (A,B) Growth of small and translucent colonies on Columbia sheep blood agar after 72 hours of incubation. (C) Gram-positive bacilli from smear preparations by Gram staining from the colony on Columbia sheep blood agar (1000x).

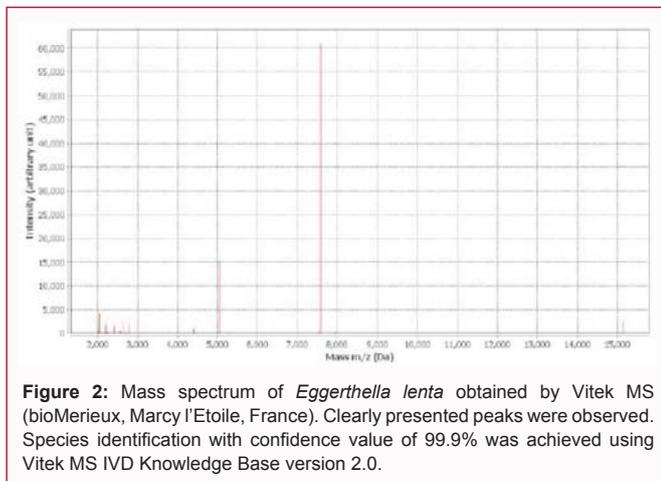


Figure 2: Mass spectrum of *Eggerthella lenta* obtained by Vitek MS (bioMérieux, Marcy l'Etoile, France). Clearly presented peaks were observed. Species identification with confidence value of 99.9% was achieved using Vitek MS IVD Knowledge Base version 2.0.

France) and incubated anaerobically for 72 h. Small and translucent colonies grew on the Columbia sheep blood agar and Gram-positive bacillus was observed by Gram staining (Figure 1). The aerobic blood culture was negative after 7 days of incubation.

Analysis of the colonies by two Matrix Assisted Light Desorption/Ionization Time of Flight Mass Spectrometry (MALDI-TOF MS) platforms (Bruker, Daltonics, Bremen, Germany; bioMérieux, Marcy l'Etoile, France) identified the isolated organism as *Eggerthella lenta* with high confidence value (Figure 2). *Escherichia coli* strains ATCC® 8739 and MB11464_1 were used as calibration standards in Vitek MS and Bruker MS respectively. The patient was diagnosed with *E. lenta* bacteremia. Antimicrobial Susceptibility Testing (AST) was performed by the E-test method (bioMérieux, Marcy l'Etoile, France) on supplemented *Brucella* blood agar (Thermo Fisher Scientific).

The Minimal Inhibitory Concentrations (MICs) were recorded after 48 h of incubation at 35°C under anaerobic conditions. The isolate was susceptible to amoxicillin-clavulanate, ertapenem, meropenem and metronidazole according to Clinical and Laboratory Standards Institute (CLSI) interpretative criteria.

Discussion

Eggerthella lenta, previously known as *Eubacterium lentum*, is a catalase positive, hydrogen sulfide positive, non-motile, non-sporulating and slow-growing obligate anaerobic Gram-positive bacillus that belongs to the family *Coriobacteriaceae*. To date, there are 2 species of *Eggerthella*, namely *Eggerthella lenta* and *Eggerthella*

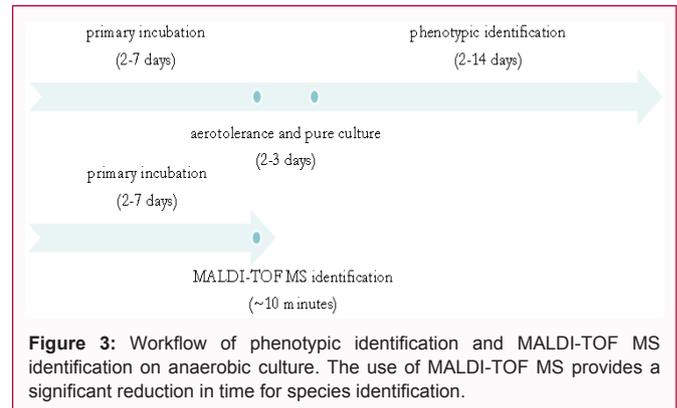


Figure 3: Workflow of phenotypic identification and MALDI-TOF MS identification on anaerobic culture. The use of MALDI-TOF MS provides a significant reduction in time for species identification.

sinensis. A 4-year study reveals that 63% (10 of 16) of clinically significant bacteremia caused by anaerobic, non-sporulating, Gram-positive bacilli in Hong Kong were caused by *Eggerthella* species with the aid of 16S rRNA gene sequencing [1]. However, infection by *E. lenta* is usually under-recognized and more frequent than reported due to prior antimicrobial treatments being used, difficulties in phenotypic identification as well as offering optimal culture conditions such as nutritional requirements [1,2].

The surface colonies of *E. lenta* were described as circular to slightly scalloped, convex, shiny, gray and translucent [3]. The optimal growth condition is 37°C under anaerobic condition and the growth is stimulated by arginine [3]. With the advent of new technologies such as MALDI-TOF MS in modern clinical microbiology laboratory, *E. lenta* is being increasingly identified from clinical specimens (Figure 3). In addition to MALDI-TOF MS, Vitek 2 ANC card (bioMérieux, Marcy l'Etoile, France) was also shown to be reliable to identify *E. lenta*. *E. lenta* is part of the normal gastrointestinal commensal of human [4]. Although diseases caused by *E. lenta* are uncommon, it is associated with a number of conditions such as appendicitis, cutaneous abscess, genitourinary tract infection, liver abscess, peritonitis, spondylodiscitis, wound infection and bacteremia [2]. The reports of *E. lenta* bacteremia are rare. Yet, *E. lenta* bacteremia is associated with significant mortality and morbidity [2]. Therefore, laboratory investigation is required to avoid clinical complications and to start optimal treatment as soon as possible. AST on *E. lenta* should be performed to guide the therapy, especially for serious infections. In most of the cases, *E. lenta* bacteremia occurs as a secondary translocation into the bloodstream from the colon of patients with malignancy, hepatobiliary disorders or Gastrointestinal (GI) disorders such as Inflammatory Bowel Disease (IBD) [5]. Bacterial translocation is the passage of viable bacteria from the GI tract to extraintestinal sites such as mesenteric lymph nodes. The translocation of indigenous bacteria from the GI tract is considered as the first step in the pathogenesis of opportunistic infections from the GI tract. Clinical presentation of *E. lenta* bacteremia includes fever, abdominal pain and emesis. Symptoms are consistent with those of systemic inflammatory immune response syndrome [6]. Blood culture followed by bacterial identification by MALDI-TOF MS remains the gold standard method for the diagnosis of *E. lenta* bacteremia.

The resistance mechanisms of *E. lenta* have not yet been studied systematically. Generally, *E. lenta* is susceptible to penicillins, ampicillin-sulbactam, metronidazole, carbapenems, tigecycline and daptomycin [2,7]. However, studies have shown a great variability

in the antimicrobial susceptibility profile of *E. lenta* [8,9]. In a recent study performed by Gardiner et al. [2], 33 patients with *E. lenta* bacteremia were retrospectively reviewed and 23 isolates have undergone AST [2]. In that study, all isolates were found to be susceptible to amoxicillin-clavulanate, cefoxitin, metronidazole, ertapenem, piperacillin-tazobactam and meropenem according to CLSI interpretative criteria [2]. Among the isolates, 91% isolates were found to be susceptible to clindamycin, 74% isolates were found to be susceptible to moxifloxacin and 39% isolates were found to be susceptible to penicillin [2]. All isolates were resistant to ceftriaxone and none of them were found to harbor vancomycin resistance genes *van A* or *van B* [2]. In our case, the patient was empirically started on meropenem treatment and returned to his normal state of health after the treatment.

Conclusion

In conclusion, we described a patient with a potentially fatal bacteremia caused by *E. lenta* that might have been under-recognized due to its fastidious and slow-growing nature, difficulties in culturing and phenotypic identification as well as the coexistence of non-fastidious aerobic bacteria in mixed infections. This case report also demonstrated that MALDI-TOF MS is a promising, fast, and accurate technology for the identification of clinically important anaerobic bacteria and its consistency in identifying those bacteria by different MALDI-TOF MS platforms.

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