Clin. Lab. 2017;63:XXX-XXX

CASE REPORT

Eubacterium moniliforme Bacteremia in a Woman with Fractures

Yuying Liang [*], Xiuyun Yin [*], Jianmin Xu, Shuiping Chen

[*] *These authors contributed equally to this study*
Department of Laboratory Medicine, Affiliated Hospital of Academy of Military Medical Sciences, Beijing China

SUMMARY

***E. moniliforme* infections in humans have not been reported previously. We firstly described blood-stream infections caused by *E. moniliforme* in an elder woman with fractures of her left thigh. This study highlights the strategies to detect this anaerobic pathogen and the importance of investigating its molecular epidemiology in humans. (Clin. Lab. 2017;63:xx-xx. DOI: 10.7754/Clin.Lab.2017.170424)**

Correspondence:
Shuiping Chen
Department of Laboratory Medicine
Affiliated Hospital of Academy of
Military Medical Sciences
100071 Beijing
China
Email: shpchen@hotmail.com

Case Report accepted April 26, 2017

KEY WORDS

E. moniliforme, bacteremia, sequencing

CASE REPORT

Eubacterium moniliforme is a strictly anaerobic, non-spore-forming, and gram-positive bacterium. *Eubacterium* infections are rarely reported, and most species are isolated from clinical samples like pleuropulmonary exudates, oral-dental exudates, and bloods [1-3]. However, there are no reports about *E. moniliforme* infections in humans yet. Here, we firstly described a case of *E. moniliforme* bacteremia in a woman in China.

In February 2017, a 67-year-old woman with fractures of her left thigh was admitted to the Department of Osteology in our hospital. She had a history of severe knee osteoarthritis for more than 10 years. At admission, she had an ache, tumescence, and limited mobility with her left thigh, but denied nausea, vomiting, coma, dizziness, and diarrhea. Soon after her admission, her body temperature increased up to 39ºC. Blood tests indicated elevated white cell counts (10.04 x 10^9 cells/L) and higher C-reactive protein level (40 mg/L). The PCT level was within the normal range. Serological antibody analysis performed for HBV, HIV, HCV, and Treponema Pallidum were all negative. Physical examinations and further diagnostic investigations (e.g., chest radiograph) revealed no focus of infection. Because she had elevated white cell counts and higher C-reactive protein level, empirical antimicrobial drug treatment with cefuroxime sodium was administered. On day 10 after admission,

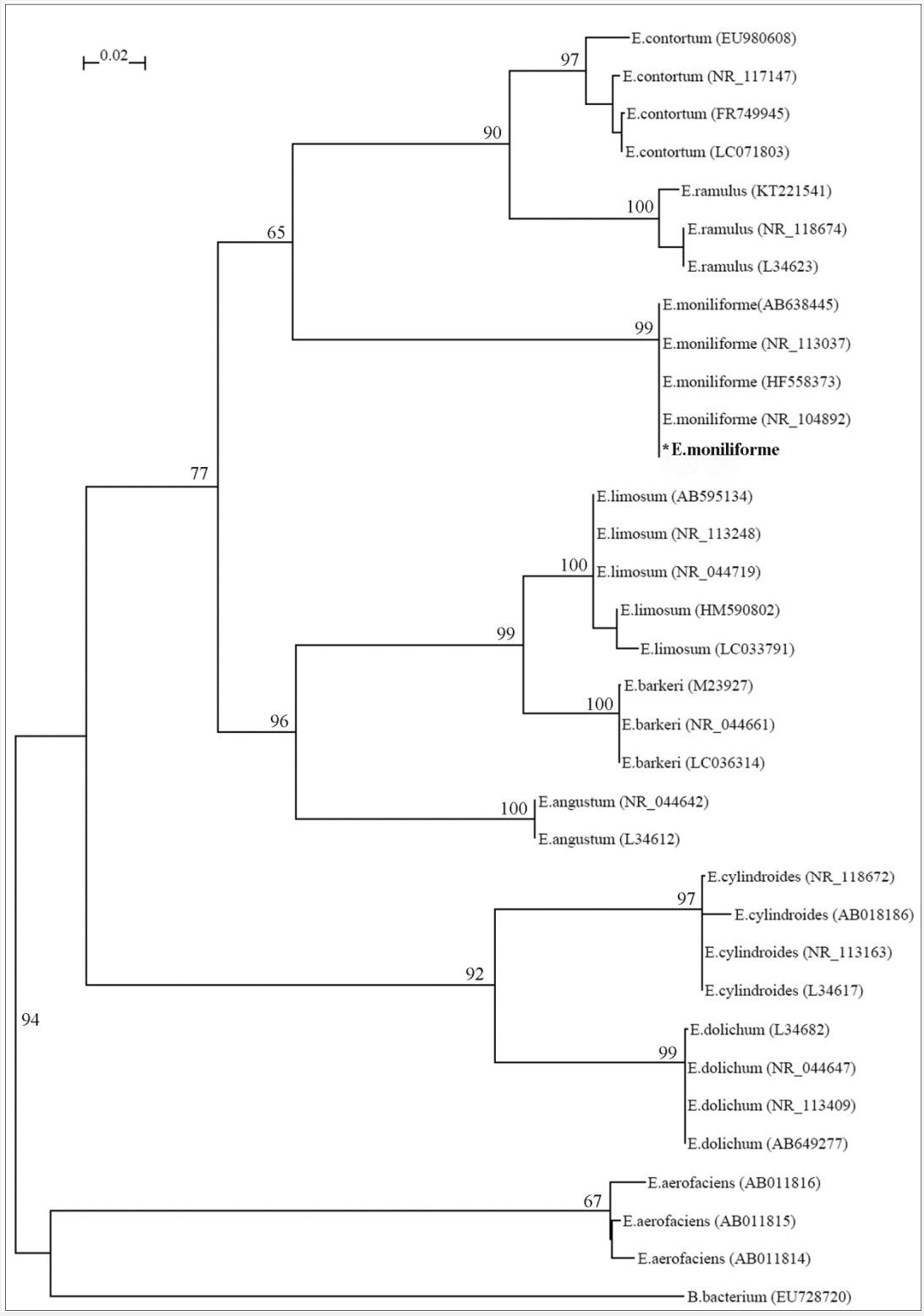

Figure 1. Phylogenetic tree of the *E. moniliforme* strain isolated in this study and the reference strains.

The tree was constructed by using the complete 16S rDNA gene. Taxon names corresponded to "species name (GenBank accession number)". Bootstrap values were shown on the key nodes of the tree. The *E. moniliforme* strain isolated in this study was shown in bold and marked with the symbol (*). The tree was rooted by B. bacterium (EU728720).

she underwent internal fixation of distal thigh fractures. Two sets of blood cultures collected on day 2 after admission showed bacterial growth in the BacT/ALERT 3D system. One set was cultured in an anaerobic bottle, and the other set was cultured in an aerobic bottle. Only the anaerobic bottle grew gram-positive bacilli. The positive cultures were subcultured on blood agar plates at 37ºC in an anaerobic atmosphere. Small, smooth, and transparent colonies were formed after 2 days. The subcultured colonies were analyzed by Vitek 2 identification system using the ANC card, which gave no results. The complete 16S rDNA gene was amplified and sequenced [4], which showed 100% similarity with that of a known *E. moniliforme* strain (GenBank accession no. AB638445) by BLAST analysis (http://www.ncbi.nlm.nih.gov). The phylogenetic tree, based on the 16S rDNA gene, was generated by the maximum-likelihood method using the TREE-PUZZLE program [5], whose results showed that the strain was *E. moniliforme* (Figure 1).

Antimicrobial drug susceptibility tests, which were conducted by using E-test, showed that the strain was susceptible to ceftriaxone, ciprofloxacin, clindamycin, linezolid, imipenem, benzylpenicillin G, gentamycin, and vancomycin. After admission, the patient was empirically given a 5-day course of intravenous cefuroxime sodium (4.5 g, 3 x/d), which was replaced by a 5-day course of intravenous clindamycin (1.2 g, 3 x/d) after identification of the pathogen (*E. moniliforme*) and its antimicrobial drug susceptibility. On day 25 after admission, she requested to be discharged because of the perfect surgery, incision healing, and absence of fever.

DISCUSSION

Although *E. moniliforme* has been previously detected from human feces and polyherbal medicines [6,7], no human infections with this pathogen are reported yet. Here, we firstly report a human case of infection with *E. moniliforme*. To note, the following facts can rule out the possibility that our result is an introduced contaminant or false positivity: (a) *Eubacterium sp* is not a part of the common skin flora. (b) No invasive operations are performed before the venous blood is drawn for identification of pathogens. (c) We have never isolated or manipulated *E. moniliforme* in our laboratory previously. (d) There are no amplifications with the negative controls. Thus, in consideration of *Eubacterium*-associated infections reported previously [1-3], infections with *E. moniliforme*, although not reported before, should be carefully considered, especially for sterile body fluid samples.

Finally, *E. moniliforme* is not included in any database of conventional bacterial identification systems (such as API 20A and ANC ID cards from BIOMÉRIEUX, BBL CRYSTAL ANR ID system from BD, etc.), or MALDI-TOF mass spectrometers (Bruker Biotyper and VITEK MS), which would increase difficulties in clinical identification of this pathogen. Thus, 16S rDNA gene sequencing provides an effective and straightforward tool to identify *E. moniliforme*, and the routine use of this method would better define the epidemiology, clinical significance, and pathogenic potential of this pathogen.

Declaration of Interest:

All authors declare that they have no conflict of interest.

References:

1. Matsuki T, Watanabe K, Tanaka R, Oyaizu H. Rapid identification of human intestinal bifidobacteria by 16S rRNA-targeted species- and group-specific primers. FEMS Microbiol Lett 1998; 167:113-21 (PMID: 9809413).
2. McFarland LV, Elmer GW. Pharmaceutical probiotics for the treatment of anaerobic and other infections. Anaerobe 1997;3:73-8 (PMID: 16887565).
3. Lee MR, Huang YT, Liao CH, et al. Clinical and microbiological characteristics of bacteremia caused by *Eggerthella*, *Paraeggerthella*, and *Eubacterium* species at a university hospital in Taiwan from 2001 to 2010. J Clin Microbiol 2012;50:2053-5 (PMID: 22495556).
4. Yin X, Liang Y, Zeng L, Chen S. Bacteremia and bone marrow infection caused by moraxella atlantae in an elderly patient with pneumonia. Clin Lab 2016;62:2419-22 (PMID: 28164552).
5. Schmidt HA, Strimmer K, Vingron M, von Haeseler A. TREE-PUZZLE: maximum likelihood phylogenetic analysis using quartets and parallel computing. Bioinformatics 2002;18:502-4 (PMID: 11934758).
6. Schwiertz A, Le Blay G, Blaut M. Quantification of different *Eubacterium spp.* in human fecal samples with species-specific 16S rRNA-targeted oligonucleotide probes. Appl Environ Microbiol 2000;66:375-82 (PMID: 10618251).
7. Famewo EB, Clarke AM, Afolayan AJ. Identification of bacterial contaminants in polyherbal medicines used for the treatment of tuberculosis in Amatole District of the Eastern Cape Province, South Africa, using rapid 16S rRNA technique. J Health Popul Nutr 2016;35:27 (PMID: 27549141).