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First Case of Bacteremia Caused by *Coprobacillus catenaformis*

Won Young Heo ⓘ, M.D.[1], Jong Kwon Lee ⓘ, M.D.[1], Yoo Na Chung ⓘ, M.D.[1], In Young Yoo ⓘ, M.D., Ph.D.[1], On-Kyun Kang ⓘ, M.T.[1], Duk Hyun Sung ⓘ, M.D., Ph.D.[2], Sun Young Cho ⓘ, M.D., Ph.D.[3,4], Hee Jae Huh ⓘ, M.D., Ph.D.[1], and Nam Yong Lee ⓘ, M.D., Ph.D.[1]

Departments of [1]Laboratory Medicine and Genetics, [2]Physical and Rehabilitation Medicine, [3]Division of Infectious Diseases, Department of Internal Medicine, [4]Center for Infection Prevention and Control, Samsung Medical Center, Sungkyunkwan University School of Medicine, Seoul, Korea

Dear Editor,

Coprobacillus catenaformis is a gram-positive, obligatorily anaerobic, non-spore-forming rod bacteria. In 2000, *Coprobacillus* gen. nov. (*Copro*, feces; *bacillus*, a small rod) *catenaformis* spp. nov. (*catena*, chain; *formis*, shaped) was proposed as a member of the *Clostridium* subphylum of gram-positive bacteria that is phylogenetically closely associated with *Clostridium ramosum* and *C. spiroforme* [1]. *C. catenaformis*, the only known species in the genus *Coprobacillus*, is a member of the intestinal microbiota of humans and mice, as shown by metagenomics studies [2, 3]. To the best of our knowledge, this species has not been isolated from clinical specimens, including blood cultures. We report the first case of bacteremia caused by *C. catenaformis*. The Institutional Review Board of Samsung Medical Center, Seoul, Korea, approved this study (approval number: 2020-03-085) and waived the need for informed consent.

A patient in her 60s, who received several cycles of chemotherapy and radiotherapy for non-small cell lung cancer with pleural and bone metastases since August 2014, was admitted to Samsung Medical Center in August 2019 for a decompressive laminectomy with pedicle screw fixation and tumor removal. On post-operative day 8, a bisacodyl enema was administered for >10 days without defecation. A few hours after the enema, the patient complained of chilling sensation and had a body temperature of 38.6°C. Her blood pressure was 108/55 mm Hg, pulse rate was 142 bpm, and respiratory rate was 18 breaths per minute. Her C-reactive protein was 56.3 (reference interval, 0–5.0) mg/L and leukocyte count was 10.44×10^9/L (neutrophils, 98.0%). After preparing two sets of aerobic and anaerobic blood culture bottles (bioMérieux, Marcy l'Etoile, France), empirical antibiotic therapy with intravenous piperacillin/tazobactam 4.5 g at eight hours interval was administered. On day 2 of incubation in a BacT/ALERT 3D blood culture instrument (bioMérieux), growth was observed in both anaerobic bottles of the two sets of blood cultures. Signal-positive bottles were subcultured and the following bacteria were isolated: *Eubacterium callanderi* and unidentified gram-positive bacilli from both sets of blood culture bottles and *Granulicatella elegans* from the blood culture bottle of the first set.

Microscopic examination revealed that the unidentified species was a gram-positive, non-spore-forming bacillus, which grew as small, grayish colonies on a Brucella agar plate (Fig. 1). The microorganism could not be identified by matrix assisted laser desorption ionization-time of flights mass spectrometry using the VITEK-MS (bioMérieux) or the GP card of the VITEK 2 System (bioMérieux). To accurately identify the isolate, we performed

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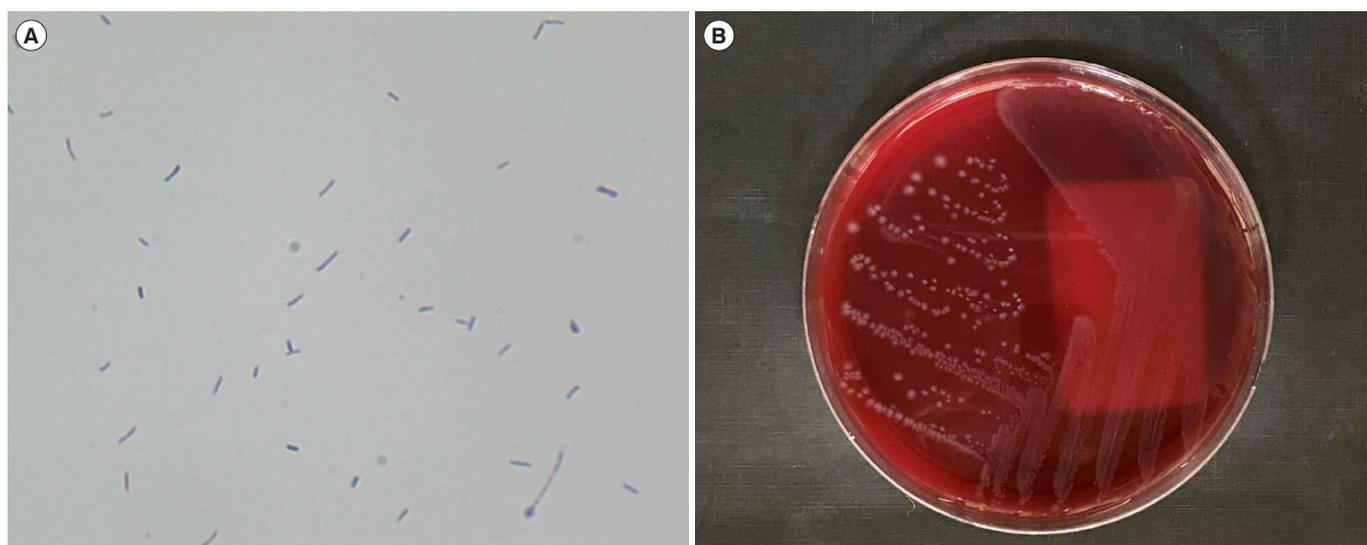
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Fig. 1. Microscopic image and colony morphology of *Coprobacillus catenaformis*. (A) gram-positive non-spore-forming bacilli (Gram stain, ×1,000). (B) small and grayish colonies on a Brucella agar plate.

16S rRNA target sequencing using the universal primers described in the Clinical and Laboratory Standards Institute guidelines [4]. The amplified sequences were compared with sequences in the GenBank database using the basic local alignment search tool algorithm. The 16S rRNA sequence of the isolate exhibited 99.17% (715/721 bp) similarity with *C. catenaformis* (GenBank accession number AB030219.1). The second-best match was *Longibaculum muris*, with 92.18% (672/729 bp) similarity. When the sequence was submitted to the Ez-Taxon database (http://www.ezbiocloud.net), the best-matched strain was *C. catenaformis* (99.86%), which was accepted as the final confirmation of identity.

The patient was successfully treated with a 14-day course of intravenous piperacillin/tazobactam. Follow-up blood cultures from the peripheral veins on days 2, 5, and 14 were negative; the patient's condition improved and he/she was transferred to a long-term care facility.

To date, several studies have elucidated the roles of *Coprobacillus* species in the intestinal microbiota. In the human intestinal microbiota, the abundance of *Coprobacillus* increases with biological age [3] and is diminished in patients with multiple sclerosis [5]. In a mouse experiment, *Coprobacillus* played a role in inhibiting other microorganisms in the intestinal microbiota, including *Clostridioides difficile* [2]. To the best of our knowledge, this is the first case demonstrating the possibility of opportunistic *Coprobacillus* infections. Our patient had a polymicrobial bloodstream infection caused by *C. catenaformis*, *E. callanderi*, and *G. elegans*.

Eubacterium and *Granulicatella* species are present in the human mouth and intestinal tract and have been implicated as the cause of bacteremia [6-8]. The most common source of polymicrobial bloodstream infections is intra-abdominal infection [9]. The loss of intestinal barrier function contributes to systemic infection, and increased gut permeability is associated with the development of multi-organ dysfunction syndrome [10].

In conclusion, we report the first case of bacteremia caused by *Coprobacillus*. Although the information regarding human infections of *Coprobacillus* is limited, *Coprobacillus* should be considered a possible pathogen, especially in patients at high risk of gastrointestinal infections such as mechanical intestinal injury. Our report emphasizes the importance of *Coprobacillus* as a potential human pathogen.

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AUTHOR CONTRIBUTIONS

All authors have accepted their responsibility for the entire content of this manuscript and approved submission.

CONFLICTS OF INTEREST

No potential conflicts of interest relevant to this article were reported.

ORCID

Won Young Heo	https://orcid.org/0000-0003-2695-9634
Jong Kwon Lee	https://orcid.org/0000-0002-6230-1242
Yoo Na Chung	https://orcid.org/0000-0002-4164-6583
In Young Yoo	https://orcid.org/0000-0003-1505-846X
On-Kyun Kang	https://orcid.org/0000-0002-1031-1991
Duk Hyun Sung	https://orcid.org/0000-0002-8261-7199
Sun Young Cho	https://orcid.org/0000-0001-9307-2369
Hee Jae Huh	https://orcid.org/0000-0001-8999-7561
Nam Yong Lee	https://orcid.org/0000-0003-3688-0145

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