



First Korean Case of *Cedecea lapagei* Pneumonia in a Patient With Chronic Obstructive Pulmonary Disease

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To the Editor,

Cedecea, a genus of the *Enterobacteriaceae* family, was named in 1981 from the initials of U.S. Centers for Disease Control and Prevention [1]. To date, a total five species have been identified; currently, three of these have been named (*C. davisae*, *C. lapagei*, and *C. neteri*), whereas two remain unnamed [1, 2]. Infections caused by the *Cedecea* species are infrequent [2-6]. Here, we report a case of *C. lapagei* pneumonia in a patient with chronic obstructive pulmonary disease (COPD).

A 76-yr-old man, with a history of COPD, was admitted with dyspnea. While being treated with empirical antibiotics, he was admitted to the intensive care unit owing to respiratory failure and was provided mechanical ventilator care. After 5-day ventilator care, he was extubated and transferred to a general ward. After 1-week supportive care without antibiotics, he developed an increase in sputum and difficulty in breathing. Physical examination revealed decreased breath sounds and increased wheezing in both lung fields. Chest radiography revealed an infiltration of the left lower lobe. His temperature was 36.8°C; blood pressure, 110/63 mmHg; pulse, 115/min; respiratory rate, 20 breaths/min; and O₂ saturation, 94% without O₂ supply. His hematological tests showed the following findings: Hb, 11.5 g/dL; leukocyte count, 10.0×10⁹/L (neutrophils 72.1%); platelet count, 461×10⁹/L; C-reactive protein (CRP) level, 5.55 mg/dL.

A sputum culture and two sets of blood cultures from separate peripheral veins were performed. The blood cultures tested negative, but many gram-negative rods and some neutrophils containing intracellular organisms were observed on the smear preparation of the sputum sample (Fig. 1A). White colored, non-hemolytic colonies predominantly grew on a blood agar plate (Fig. 1B), and gram-negative coccobacilli were observed on gram stain smear preparations (Fig. 1C). The isolate was colorless on a MacConkey agar plate and catalase-positive and oxidase-negative. Using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (Bruker Daltonik GmbH, Bremen, Germany) and the Vitek2 GN system (bioMérieux, Marcy l'Etoile, France), the organism was identified as *C. lapagei*, with a score of 2.322 in the Bruker system and with a 99.9% probability in the Vitek2 system.

To confirm the identity of the isolate, 16S rRNA gene sequencing was conducted. However, the 1,402 bp 16S rRNA gene sequence of the isolate shared a 99.6% identity with AB086230 (*C. neteri*) in the eZtaxon database (<http://www.ezbiocloud.net>). To solve the discrepancy, additional tests were performed: biochemical tests as well as sequencing of the *dnaJ* gene, which was reported to be useful to identify *Enterobacteriaceae* [7]. The biochemical tests were compatible with the characteristics of *C. lapagei*; ornithine decarboxylase and acid production from su-

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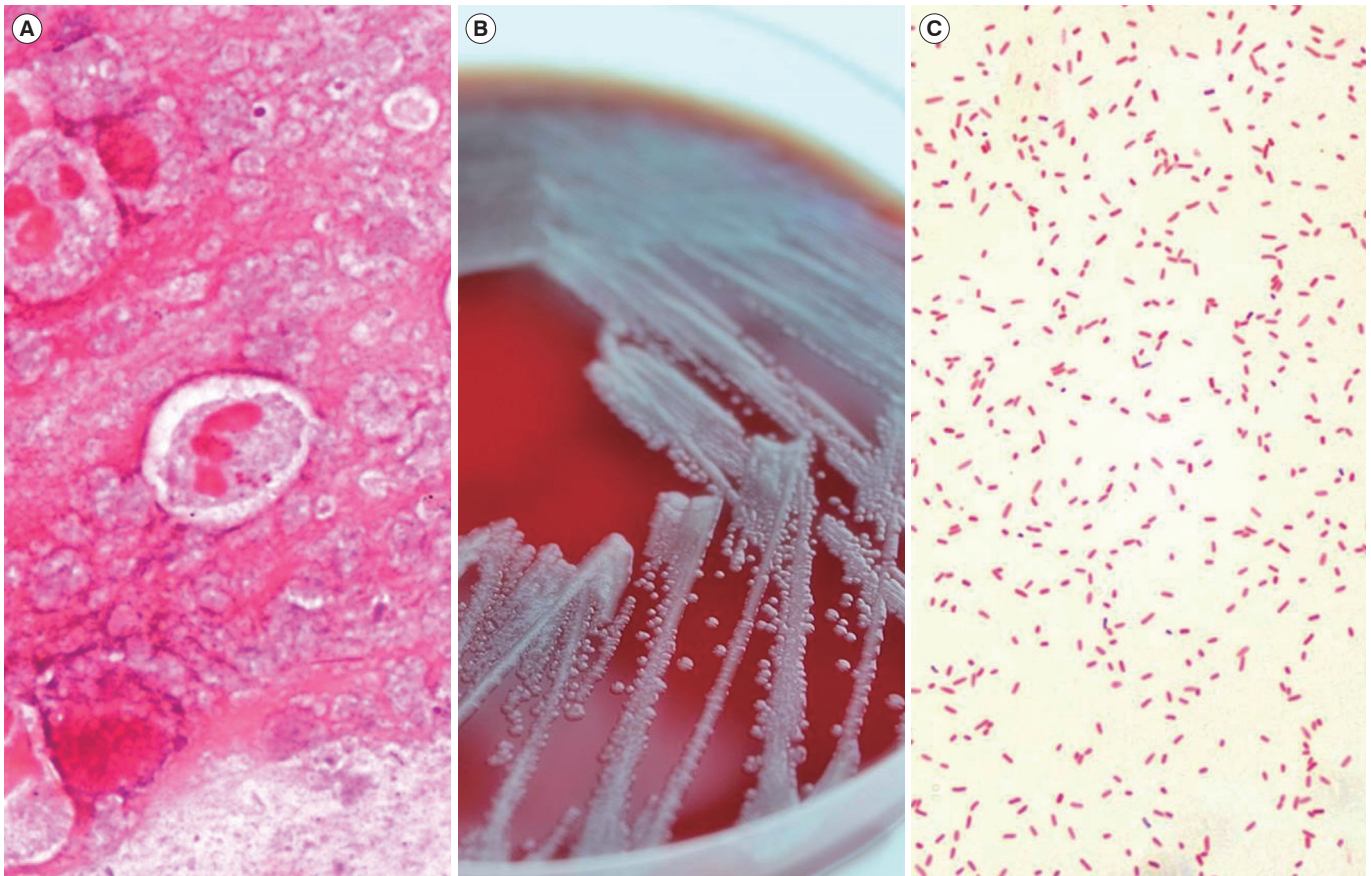


Fig. 1. Colonial and microscopic morphology of *Cedecea lapagei*. (A) Neutrophil containing intracellular gram-negative coccobacilli from smear preparation of the sputum sample (Gram stain, $\times 1,000$). (B) White colored and non-hemolytic colonies on blood agar plate after 48 hr of incubation at 35°C with 5% CO₂. (C) Gram-negative coccobacilli from blood agar plate smear preparation (Gram stain, $\times 1,000$).

crose, D-sorbitol, raffinose, D-xylose, and melibiose were negative [8]. The 719 bp *dnaJ* gene sequence of the isolate shared a 99.3% identity with AB272620 (*C. lapagei*), and a 91.1% identity with AB272621 (*C. neteri*) in the GenBank database. The phylogenetic trees showed that *C. lapagei* has 16S rRNA gene intra-species heterogeneity and this isolate was most close to *C. lapagei*, based on the *dnaJ* gene (Fig. 2).

Antimicrobial susceptibility was tested by using an AST-GN27 card (bioMérieux). Using the CLSI breakpoints for *Enterobacteriaceae* for the interpretation [9], the isolate was determined susceptible to piperacillin, cefotaxime, ceftazidime, cefepime, imipenem, amikacin, ciprofloxacin, tetracycline, and trimethoprim-sulfamethoxazole, but resistant to amoxicillin-clavulanic acid and ceftiofloxacin.

After determining the presence of the pathogen, the patient was treated with cefpodoxime for one week. The pathogen was not observed in follow-up respiratory cultures, and the patient was discharged.

Clinical significance and disease spectrum of *Cedecea* have not yet been clearly elucidated; however, in elderly patients (age >60 yr) who are immunocompromised or have multiple comorbidities, *Cedecea* has been reported to cause bacteremia and pneumonia [2]. Accurate identification at species level is important in understanding *Cedecea* infections. Identification of *Cedecea* at the species level is possible by using conventional biochemical tests [8]; so its identification using molecular characteristics is not well established. Therefore, thus far, the number of sequences on GenBank is small, and whole genome analyses have not been established. This case study showed that sequencing the *dnaJ* gene could be useful in the molecular identification of *Cedecea*, as it has 16S rRNA gene intra-species heterogeneity.

Although *C. lapagei* was isolated only in a sputum sample from the patient, we concluded that the patient had *C. lapagei* pneumonia on the basis of his respiratory symptoms, elevated CRP levels, and the phagocytosis by neutrophils. Therefore, we

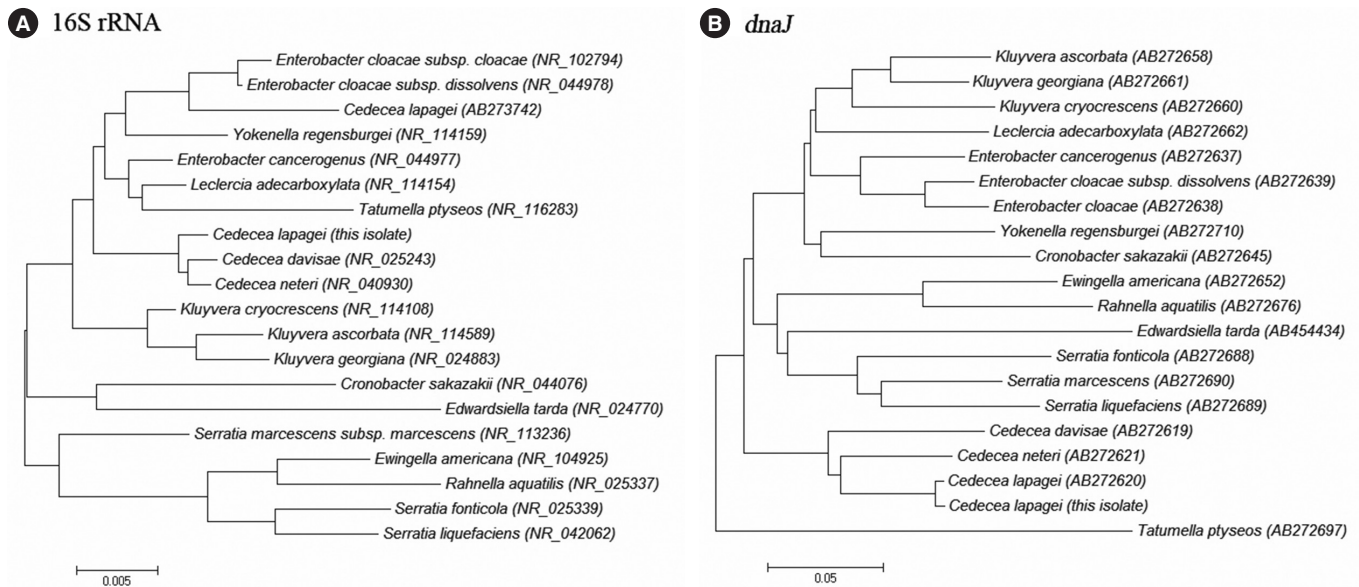


Fig. 2. Neighbor-joining phylogenetic trees based on partial 16S rRNA (1,300 bp) and *dnaJ* (719 bp) gene sequences of rare *Enterobacteriaceae* strains. (A) Phylogenetic tree of 16S rRNA gene showed that *Cedecea lapagei* has 16S rRNA gene intra-species heterogeneity. (B) Phylogenetic tree of *dnaJ* gene showed that this isolate was most closely related to *C. lapagei* (AB272620).

report the first case of *C. lapagei* pneumonia in Korea. The present findings indicate that good care must be taken in its molecular identification, as it has intra-species heterogeneity due to the 16S rRNA gene.

Authors' Disclosures of Potential Conflicts of Interest

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

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