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First Korean Case of *Helcococcus kunzii* Bacteremia in a Patient with Diabetes

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Dear Editor

Members of the *Helcococcus* genus are non-motile, catalase-negative, facultatively anaerobic gram-positive cocci. To date, a total of 5 species have been assigned to *Helcococcus*, including *H. kunzii*, *H. ovis*, *H. pyogenes*, *H. seattlensis*, and *H. suecien-sis*; however, *H. pyogenes* has not yet received official taxo-nomic classification [1, 2]. *H. kunzii* has been identified as a causative pathogen of abscess, bacteremia, cellulitis, empyema, implantable cardiac device infection, osteomyelitis, prosthetic joint infection, and sebaceous cyst infection; however, *H. kunzii*-associated bacteremia is not common [3-7]. We report a case of *H. kunzii* bacteremia in a patient with diabetes.

A 58-yr-old man complained of redness in his left foot with abrasions on the third and fourth toes and pain 8 days prior to admission to the emergency room. His diabetes was diagnosed 20 yr ago and he was receiving hemodialysis for treatment of end-stage renal disease. Physical examination revealed an ul-cerative lesion on the dorsum and sole of his left foot. The pa-tient had temperature of 38.0°C, blood pressure of 195/86 mm Hg, pulse of 62/min, and respiratory rate of 20 breaths/min. Laboratory investigation showed Hb of 9.1 g/dL, leukocyte count of 7.6×10^9/L, platelet count of 267×10^9/L, C-reactive protein level of 7.42 mg/dL, erythrocyte sedimentation rate of 112 mm/hr, glucose level of 251 mg/dL, Hb A_{1c} level of 7.1%, blood urea nitrogen/creatinine of 18/4.4 mg/dL, and total protein/albumin level of 7.4/3.2 g/dL. Magnetic resonance imaging of the left foot revealed a soft tissue abscess in the third webspace and infec-tious arthritis at the third and fourth metatarsophalangeal joints.

A wound swab sample and 2 sets of blood samples were col-lected, and the patient received empirical antibiotic therapy with intravenous piperacillin/tazobactam. Cultured swab samples were positive for *Proteus mirabilis*. After 48 hr of incubation, gram-positive cocci grew in 2 anaerobic blood culture bottles. The positive culture broth was streaked onto a blood agar plate (BAP) and incubated for 24 hr at 35°C in a 5% CO_2 atmo-sphere, but few colonies were observed. The positive culture broth was also streaked onto a BAP and cultured anaerobically for 48 hr. Tiny gray-colored, non-hemolytic colonies were ob-served on the BAP cultured anaerobically; Gram staining of this microorganism revealed gram-positive cocci (Fig. 1). The isolate was positive for pyrrolidonyl arylamidase production, but was negative for leucine aminopeptidase production.

The isolate was identified as *H. kunzii* by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-

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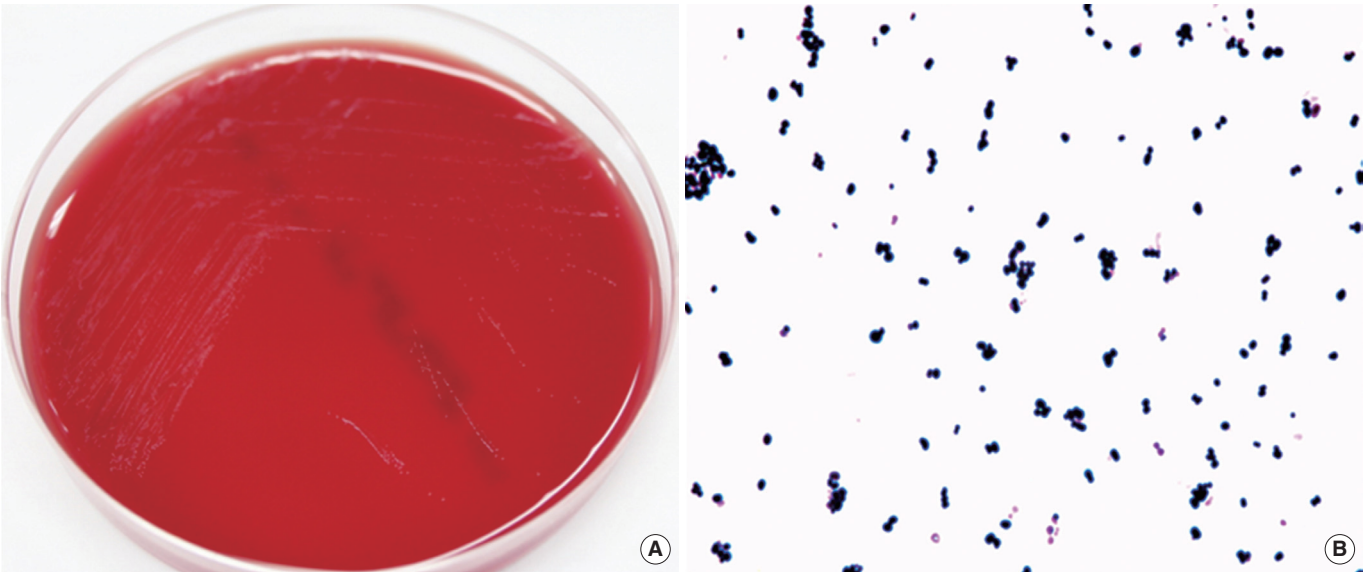

Fig. 1. Colony and microscopic characteristics of *Helcococcus kunzii*. (A) Tiny, gray-colored colonies were observed on a blood agar plate after 48 hr of anaerobic incubation. (B) Gram-positive cocci from a smear of colonies obtained from the blood agar plate (×1,000).

TOF MS; Bruker Daltonik GmbH, Bremen, Germany), which yielded a score of 2.299. In addition, Vitek2 GP system (bioMérieux, Marcy l'Etoile, France) identified the organism as either *H. kunzii* or *Erysipelothrix rhusiopathiae* with equal probability. To confirm the isolate identity, 16S rRNA gene was sequenced. The 1,450 bp 16S rRNA gene sequence of the isolate shared a 99.8% identity with GenBank sequence DQ082898 (*H. kunzii*) and 95.6% identity with NR_027228 (*H. ovis*). Antimicrobial susceptibility testing (AST) of the isolate was performed by Etest (AB Biodisk, Stockholm, Sweden) on BAPs incubated anaerobically for 48 hr since the isolate grew poorly at 35°C in 5% CO_2 atmosphere. Breakpoints for anaerobes published by the Clinical and Laboratory Standards Institute were used to determine susceptibility, those of erythromycin for *Streptococcus* spp. viridans group [8]. The isolate was susceptible to penicillin, ampicillin, ampicillin/sulbactam, ertapenem, meropenem and piperacillin, but was resistant to clindamycin, erythromycin and metronidazole.

On the second day of hospitalization, the patient underwent an amputation of the third toe and debridement of the left foot. Treatment with intravenous piperacillin/tazobactam had been maintained for 3 weeks; follow-up blood cultures from the periphery on day 3 were negative, and the patient was cured without further complications.

Bloodstream infection caused by *H. kunzii* is extremely rare; only one patient with prior history of intravenous drug abuse has been reported [4]. This isolate was identified as *H. kunzii* by both 16S rRNA gene sequencing and MALDI-TOF MS. Although 16S rRNA gene sequence analysis remains the gold standard, the MALDI-TOF MS systems have also been successfully used to identify *H. kunzii* [7, 9]. The AST pattern indicated that the isolate was resistant to clindamycin and erythromycin. This finding corroborates previous reports on *H. kunzii* resistance to both of these drugs [3, 4].

In conclusion, we report the first Korean case of *H. kunzii* bacteremia confirmed by 16S rRNA gene analysis and MALDI-TOF MS. *H. kunzii* may be an opportunistic pathogen in humans, especially in patients with diabetes.

Authors' Disclosure of Potential Conflicts of Interest

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

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