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First Case Report of Human Infection With *Ochrobactrum tritici* Causing Bacteremia and Cholecystitis

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Dear Editor,

Herein, we report the first case of human infection with *Ochrobactrum tritici*, primarily isolated from environmental sources and not previously known to infect humans. A 70-yr-old male patient was admitted to a tertiary-care hospital for jaundice. He had a medical history of cholangiocellular carcinoma (CCC). On the first day of hospitalization, he presented a 38.1°C body temperature, 98/81 mmHg blood pressure, 87 beats per minute heart rate, and abdominal distention. Laboratory findings indicated a white blood cell count of 5.63×10^9/L with a differential of 71% neutrophils, a hemoglobin level of 10 g/dL, a platelet count of 25×10^9/L, and a C-reactive protein level of 48.5 mg/L (reference range, 0.1-6.0 mg/L). Two sets of blood cultures were performed at the time of high fever on admission. Among these four cultures, only one aerobic culture was positive for gram-negative short rods after 4 days of incubation. Intravenous antibiotics with metronidazole (500 mg every 8 hr) and cefoperazone/sulbactam (2,000 mg every 12 hr) were started on the first day of hospitalization. His condition improved after antibiotic therapy and he was discharged from the hospital on day five. The isolate (named GNOT01) was identified as *Ochrobactrum anthropi* by matrix-assisted laser desorption ionization–time of flight mass spectrometer (MALDI-TOF MS; MicroFlex LT, Bruker Daltonics, Bremen, Germany).

Two weeks later, the patient presented with exacerbated jaundice and abdominal pain. Physical examination revealed abdominal distention and ascites. Laboratory analysis indicated a leukocyte count of 6.5×10^9/L with a differential of 71% neutrophils, a platelet count of 83×10^9/L, a C-reactive protein level of 77.4 mg/L, and a total bilirubin of 6.7 mg/dL (reference range, 0.3-1.8 mg/dL). He received intravenous cefoperazone/sulbactam (2,000 mg every 12 hr) from the first day of hospitalization. Culture of the bile specimen collected during percutaneous transhepatic biliary drainage procedure yielded gram-negative rods (isolate GNOT02) and gram-positive cocci, identified as *Ochrobactrum* species and *Enterococcus faecalis*, respectively, by MALDI-TOF MS. The patient fully recovered from cholecystitis without any evidence of infection and was discharged on day 28 without specific complications.

The clinical isolates, GNOT01 and GNOT02, were biochemically identified as *O. anthropi* with >99% probability. However, PCR and sequencing indicated that the 16S rRNA partial se-

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quences of both isolates were 100% identical to those of strain CCUG 47104^T, the *O. tritici* type strain. Scanning electron microscopy (SEM) images of the isolates revealed that they had a single polar flagellum, which was not observed in the type strain CCUG 47104^T (Fig. 1). On bacterial motility test using motility indole ornithine (MIO) agar, GNOT01 and GNOT02 showed upper stab lines that diffused out just beneath the surface of the MIO agar creating an umbrella-shape, which suggests that they are strictly aerobic and motile. No finding related to motility was obtained with CCUG 47104^T.

Pulsed-field gel electrophoresis (PFGE) presented identical XbaI macro-restriction banding patterns between the two isolates, which were different from that of CCUG 47104^T (similarity, 84.2%) indicating that the bacteremia of the patient originated from cholecystitis.

Antimicrobial susceptibility testing showed that CCUG 47104^T was susceptible to ticarcillin, ceftriaxone, and cefepime, while GNOT01 and GNOT02 were resistant to these antimicrobials. Extended-spectrum β-lactamase (ESBL) genes and plasmid-encoded AmpC β-lactamase genes were not detected in GNOT01 and GNOT02 isolates by double disk synergy test and PCR, suggesting that they acquired resistance to β-lactams not by production of plasmid-mediated ESBLs or AmpC β-lactamases, but by overexpression of species-specific intrinsic AmpC β-lactamases.

To date, only four species, *O. anthropi*, *O. intermedium*, *O. haematophilum*, and *O. pseudogrignonense*, have been reported to cause human infections [1-4]. Among these, *O. anthropi* is the most frequently reported human pathogen, especially in immunocompromised patients. Phylogenetic analysis of 16S rRNA gene sequences revealed a high similarity between *O. tritici* and *O. anthropi* with 98% identity [5]. However, *O. tritici* strains exhibit low DNA-DNA re-association values (< 60%) with *O. anthropi* probes and showed different phenotypic characteristics. These genotypic and phenotypic differences resulted in the classification of *O. tritici* as a distinct species.

In summary, we reported the first case of human infection with an *O. tritici* motile strain isolated from the blood and bile. *O. tritici* should be considered as a potential pathogen that can cause bloodstream and biliary tract infections in humans. In addition, both commercial bacterial identification kits and MALDI-TOF MS misidentified *O. tritici* clinical isolates as *O. anthropic*. Thus, 16S rRNA sequencing should be performed when a clinical isolate is identified as *O. anthropi* by routine bacterial identification processes.

Authors' Disclosures of Potential Conflicts of Interest

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

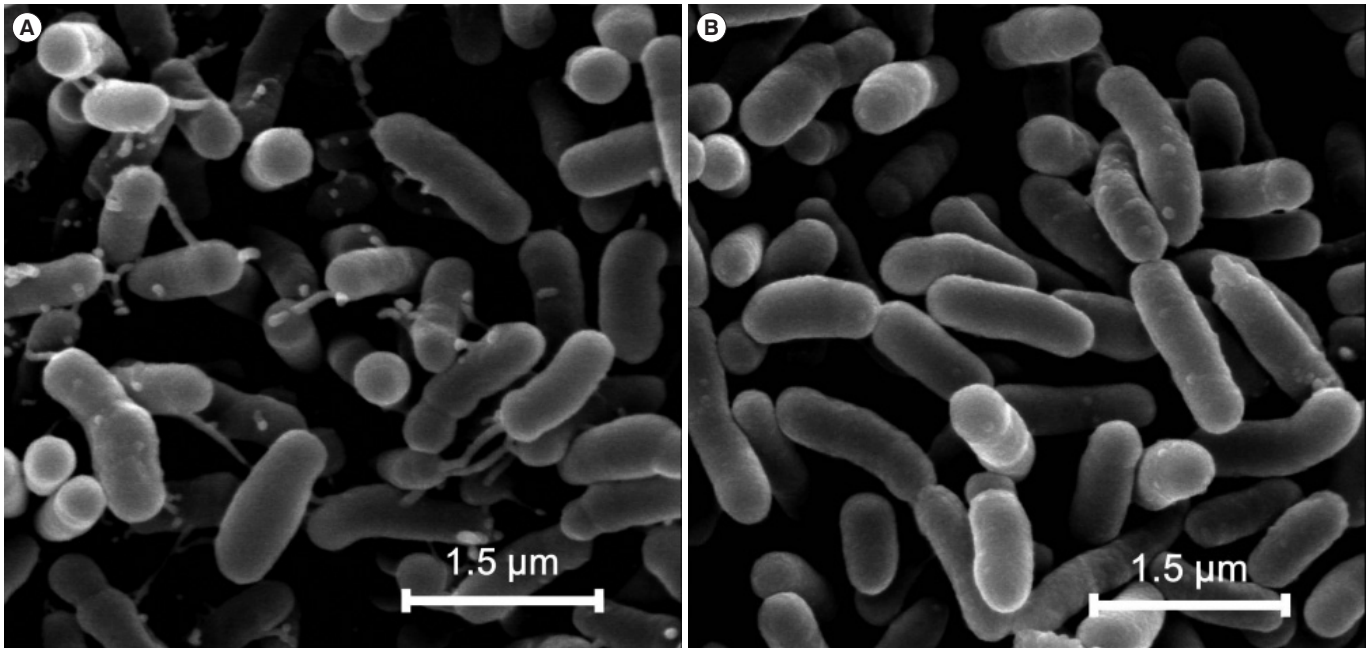

Fig. 1. Scanning electron micrographs of *Ochrobactrum tritici* clinical isolate GNOT01 (A) and the type strain CCUG 47104^T (B). GNOT01 isolate presented a single polar flagellum, while CCUG 47104^T strain did not (Magnification, ×20,000).

Acknowledgments

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REFERENCES

1. Holmes B, Popoff M, Kiredjian M, Kersters K. *Ochrobactrum anthropi* gen. nov., sp. nov. from human clinical specimens and previously known as group Vd. Int J Syst Evol Microbiol 1988;38:406-16.
2. Velasco J, Romero C, López-Goñi I, Leiva J, Díaz R, Moriyón I. Evaluation of the relatedness of *Brucella* spp. and *Ochrobactrum anthropi* and description of *Ochrobactrum intermedium* sp. nov., a new species with a closer relationship to *Brucella* spp. Int J Syst Bacteriol 1998;48:759-68.
3. Teyssier C, Marchandin H, Jean-Pierre H, Masnou A, Dusart G, Jumas-Bilak E. *Ochrobactrum pseudintermedium* sp. nov., a novel member of the family *Brucellaceae*, isolated from human clinical samples. Int J Syst Evol Microbiol 2007;57:1007-13.
4. Kämpfer P, Scholz HC, Huber B, Falsen E, Busse HJ. *Ochrobactrum haematophilum* sp. nov. and *Ochrobactrum pseudogrignonense* sp. nov., isolated from human clinical specimens. Int J Syst Evol Microbiol 2007;57:2513-8.
5. Scholz HC, Tomaso H, Al Dahouk S, Witte A, Schloter M, Kämpfer P, et al. Genotyping of *Ochrobactrum anthropi* by *recA*-based comparative sequence, PCR-RFLP, and 16S rRNA gene analysis. FEMS Microbiol Lett 2006;257:7-16.

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