



## Septicemia Caused by *Herbaspirillum huttiense* Secondary to Pneumonia

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Dear Editor,

*Herbaspirillum* species are non-fermenting gram-negative bacilli of the class Betaproteobacteria, found in the environment, including soil, groundwater, and drinking water distribution systems [1]. They are curved or sometimes helical in shape, strict aerobes, motile with polar flagella, and urease-, oxidase-, and catalase-positive [2]. These species are rarely associated with human infections but can cause bacteremia and sepsis in immunocompromised patients [3]. Human disease caused by *Herbaspirillum* species has been previously described in cystic fibrosis patients. *Herbaspirillum* has been reported to be an opportunistic pathogen in patients with cirrhosis and cancer as well as a cause of pneumonia in an immunocompetent farmer in the United States [4]. We report the first case of septicemia caused by *Herbaspirillum huttiense* in Korea. This study was approved by the Institutional Review Board for Human Research, Yonsei University, Severance Hospital (IRB No. 4-2018-0620) with waiver for informed consent.

A 93-year-old male was admitted to the hospital with seizures and fever. Although the patient was of advanced age, he had no remarkable past medical history except for hypertension, for which he was on medication. The patient was suspected to have encephalitis, and vancomycin and ceftriaxone were administered to him immediately. Initial blood, sputum, and cerebrospi-

nal fluid bacterial cultures showed no growth of pathogens. After a few days, dyspnea, O<sub>2</sub> desaturation (85%), tachycardia, and profound hypotension were observed, and radiological examinations showed pneumonia. *Staphylococcus aureus* and a gram-negative bacillus were isolated in subsequent blood cultures. The colony morphology of the gram-negative bacillus on sheep blood agar was grayish, non-hemolytic, circular, smooth, and convex. It was identified as *H. huttiense* by matrix-associated laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS; MicroFlex LT, Bruker Daltonics GmbH, Leipzig, Germany) with an identification log score of 2.30, but as a member of the *Burkholderia cepacia* group by the VITEK 2 system (bioMérieux, Marcy l'Etoile, France). The strain produced acid using adonitol, L-arabitol, D-glucose, and D-mannitol as substrates and could utilize D-mannose and D-sorbitol as carbon sources. Moreover, the strain was positive for malonate, citrate, L-lactate, and succinate alkalization, as well as beta-galactosidase, gamma-glutamyl transferase, L-proline arylamidase, tyrosine arylamidase, and L-malate assimilation, based on the VITEK 2 gram-negative identification card. To confirm the bacterial species, 16S rRNA gene was sequenced with the following primer pairs, according to the CLSI guidelines: forward primer, 4F: 5'-TTG GAG AGT TTG ATC CTG GCT C-3' and reverse primer, 534R: 5'-TAC CGC GGC TGC TGG CAC-3' and forward primer 27F: 5'-AGA GTT

**Received:** August 13, 2018

**Revision received:** September 5, 2018

**Accepted:** December 11, 2018

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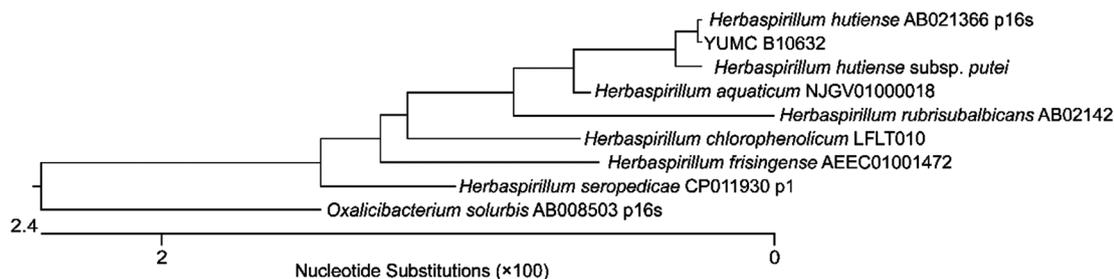
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**Fig. 1.** Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences of *Herbaspirillum* species, including the *H. huttiense* strain isolated in this clinical case. *H. huttiense* is compared with eight other similar organisms.

TGA TCM TGG CTC AG-3' and reverse primer 801R: 5'-CGGC GTG GAC TTC CAG GGT ATC T-3' [5]. When the sequence was submitted in the EzTaxon database v2.1 (<http://www.ezbiocloud.net>), the highest similarity was obtained with *H. huttiense* subsp. *huttiense* (100%), followed by *H. huttiense* subsp. *putei* (99.86%) and *H. aquaticum* (99.58%). Phylogenetic analysis showed that this isolate was very similar to *H. huttiense* subsp. *huttiense* (Fig. 1). Antimicrobial susceptibility tests using VITEK 2 demonstrated ceftazidime, meropenem, minocycline, and trimethoprim/sulfamethoxazole susceptibility and colistin resistance. *H. huttiense* was repeatedly isolated for 10 days from 12 aerobic bottles of 15 pairs of blood culture sets. Meropenem and colistin were administered to the patient for 10 days, and the regimen was changed to ceftazidime, minocycline, and trimethoprim/sulfamethoxazole thereafter. Two months later, the patient's condition deteriorated, and *H. huttiense* was isolated again in the sputum for a week. After approximately one month of conservative treatment, the patient was transferred to a long-term care facility.

Because of the phylogenetic and phenotypic resemblance, current biochemical identification systems, including the VITEK 2 system, are unable to identify the *Herbaspirillum* species and may confuse *Herbaspirillum* with other organisms such as *B. cepacia* complex, *Ralstonia* spp., *Cupriavidus pauculus*, or *Ochrobactrum anthropi* [6, 7]. Therefore, *Herbaspirillum* species may be more prevalent pathogens than previously thought. Antimicrobial susceptibility can serve as a means for differentiating *Herbaspirillum* species from *B. cepacia* complex because the latter are usually multidrug resistant, whereas the former are not [8]. In our case, the strain was susceptible to all antimicrobial drugs except colistin, based on the CLSI Interpretive Guidelines for other non-Enterobacteriaceae [9]. However, despite adequate treatment, microbiological eradication was not achieved, and septicemia lasted for several days, in contrast to a previous report [6].

The *H. huttiense* strain isolated from blood and sputum spec-

imens was successfully identified using MALDI-TOF MS. The rapid identification rate and high discriminatory power of MALDI-TOF MS makes it a useful tool for the characterization of microorganisms that are rarely reported as human pathogens and are difficult to identify using routine methods [10].

In conclusion, we report a case of septicemia due to *H. huttiense* in an immunocompetent patient. Although *Herbaspirillum* species are rarely reported as pathogens, this possibility should be carefully evaluated. The prognosis of *H. huttiense* infection needs to be further studied.

### Authors' Disclosures of Potential Conflicts of Interest

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

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