

# Draft Genome Sequence of the Human Pathogen *Halomonas stevensii* S18214<sup>T</sup>

Kwang Kyu Kim,<sup>a</sup> Keun Chul Lee,<sup>a</sup> Haeyoung Jeong,<sup>b,c</sup> David A. Stevens,<sup>d,e,f</sup> and Jung-Sook Lee<sup>a</sup>

Korean Collection for Type Cultures, Biological Resource Center, Korea Research Institute of Bioscience and Biotechnology, Daejeon, Republic of Korea<sup>a</sup>; Systems and Synthetic Biology Research Center, Korea Research Institute of Bioscience and Biotechnology, Daejeon, Republic of Korea<sup>b</sup>; Biosystems and Bioengineering Program, University of Science and Technology, Daejeon, Republic of Korea<sup>c</sup>; Division of Infectious Diseases, Department of Medicine, Santa Clara Valley Medical Center, San Jose, California, USA<sup>d</sup>; Department of Infection Prevention, Santa Clara Valley Medical Center, San Jose, California, USA<sup>e</sup>; and Division of Infectious Diseases and Geographic Medicine, Department of Medicine, Stanford University Medical School, Stanford, California, USA<sup>f</sup>

***Halomonas stevensii* is a Gram-negative, moderately halophilic bacterium causing environmental contamination and infections in a dialysis center. Here we present the 3.7-Mb draft genome sequence of the type strain (S18214<sup>T</sup>) of *H. stevensii*, which will give insight into the pathogenic potential of *H. stevensii*.**

The genus *Halomonas* accommodates moderately halophilic/halotolerant microorganisms that typically occur in saline or hypersaline environments. Therefore, many studies on these bacteria have focused on their biotechnological potential and applications (1). However, during the last few decades, several bacterial strains belonging to two different *Halomonas* species, *Halomonas venusta* and “*Halomonas phocaensis*,” have been reported to be a cause of human infections (3, 8). Very recently, a number of *Halomonas* strains were isolated from the blood of two renal care patients that was obtained during dialysis and from the dialysis machines and other environmental sources in a renal care center (6), highlighting the nosocomial infection and pathogenic potential of the genus *Halomonas*. Subsequently, the patient isolates, strains S18214<sup>T</sup> and T49407, have been classified as the novel species *Halomonas stevensii* (5).

The genome sequence of *H. stevensii* S18214<sup>T</sup> was determined using the GS FLX Titanium system (Roche Diagnostics, Branford, CT) with an 8-kb-span paired-end library (218,050 reads, ~43.0 Mb) and Illumina GA Ix (San Diego, CA) with 100 bp paired-end information (14,290,561 reads, ~1,529.1 Mb). All reads were assembled into 53 contigs ( $N_{50}$ , 131,909 bp; maximum contig size, 302,635 bp) using GS Assembler 2.6 (Roche Diagnostics, Branford, CT) and CLC Genomics Workbench 4.9 (CLC bio, Denmark); total coverage over the whole genome reached ~426-fold. The resultant genome sequence was uploaded into the RAST server (2) to predict the open reading frames (ORFs), tRNAs, and rRNAs. The predicted ORFs were annotated by searching against the COG (7) and SEED (4) databases.

The draft genome was 3,693,745 bp in length, with a G+C content of 60.3 mol%. Among 2,286 predicted protein-coding sequences, 1,287 (56.3%) ORFs were assigned to COGs. The genome also contained 56 tRNA genes and 4 rRNA operons.

Putative genomic islands (GIs) were identified based on the algorithm developed by Yoon et al. (9). The length proportion of the GIs to the genome was 24.0%, a value that is much higher than the average proportion of 10.1% for 148 prokaryotic genomes (9). Subsequent detection of potential pathogenicity islands (PAIs) was performed using the PAI Finder (10), a web-based search tool of the pathogenicity island database (PAIDB), and revealed no PAI-like region. However, *H. stevensii* S18214<sup>T</sup> encoded some putative virulence factors, such as the RTX protein, the type I secretion system, the iron uptake system, adhesion-type proteins, stress proteins, flagella, fimbriae, and the resistance-nodulation-cell division (RND) efflux system, which might promote infections in immu-

nocompromised people. In conclusion, this is the first report of the draft genome sequence of a human-pathogenic *Halomonas* strain, which will provide essential information for understanding bacterial pathogenesis and environmental persistence and give new insights into infection control.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [AJTS00000000](http://www.ncbi.nlm.nih.gov/ajts00000000). The version described in this paper is the first version, AJTS01000000.

## ACKNOWLEDGMENT

This research was supported by the Bio & Medical Technology Development Program of the National Research Foundation of Korea (2011-0002202).

## REFERENCES

1. Arahal DR, Ventosa A. 2006. The family *Halomonadaceae*, p 811–835. In Dworkin M, Falkow F, Rosenberg E, Schleifer KH, Stackebrandt E (ed), *The prokaryotes*, 3rd ed, vol 6. Springer, New York, NY.
2. Aziz RK, et al. 2008. The RAST Server: rapid annotations using subsystems technology. *BMC Genomics* 9:75.
3. Berger P, Barguelli F, Raoult D, Drancourt M. 2007. An outbreak of *Halomonas phocaensis* sp. nov. bacteraemia in a neonatal intensive care unit. *J. Hosp. Infect.* 67:79–85.
4. Disz T, et al. 2010. Accessing the SEED genome databases via Web Services API: tools for programmers. *BMC Bioinformatics* 11:319.
5. Kim KK, Lee KC, Oh HM, Lee JS. 2010. *Halomonas stevensii* sp. nov., *Halomonas hamiltonii* sp. nov. and *Halomonas johnsoniae* sp. nov., isolated from a renal care center. *Int. J. Syst. Evol. Microbiol.* 60:369–377.
6. Stevens DA, Hamilton JR, Johnson N, Kim KK, Lee JS. 2009. *Halomonas*, a newly recognized human pathogen, causing infections and contamination in a dialysis center: 3 new species. *Medicine* 88:244–249.
7. Tatusov RL, et al. 2003. The COG database: an updated version includes eukaryotes. *BMC Bioinformatics* 4:41.
8. von Graevenitz A, Bowman J, Del Notaro C, Ritzler M. 2000. Human infection with *Halomonas venusta* following fish bite. *J. Clin. Microbiol.* 38:3123–3124.
9. Yoon SH, et al. 2005. A computational approach for identifying pathogenicity islands in prokaryotic genomes. *BMC Bioinformatics* 6:184.
10. Yoon SH, et al. 2007. Towards pathogenomics: a web-based resource for pathogenicity islands. *Nucleic Acids Res.* 35:D395–D400.

Received 15 June 2012 Accepted 6 July 2012

Address correspondence to Jung-Sook Lee, [jslee@kribb.re.kr](mailto:jslee@kribb.re.kr).

Copyright © 2012, American Society for Microbiology. All Rights Reserved.

doi:10.1128/JB.01071-12