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GENOME ANNOUNCEMENT

Draft Genome Sequence of the Human Pathogen *Halomonas stevensii* S18214^T

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***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^T) 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 phocaeensis*," 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^T and T49407, have been classified as the novel species *Halomonas stevensii* (5).

The genome sequence of *H. stevensii* S18214^T 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 IIx (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^T 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 immunocompromised 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. The version described in this paper is the first version, AJTS01000000.

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