



Genome announcement

Complete genome sequence of *Halocynthiibacter arcticus* PAMC 20958^T from an Arctic marine sediment sampleYung Mi Lee^{a,b}, Kiwoon Baek^c, Jungeun Lee^a, Hong Kum Lee^a, Hyun Park^{a,d}, Seung Chul Shin^{a,*}^a Division of Polar Life Sciences, Korea Polar Research Institute, 26 Songdomirae-ro, Yeosu-gu, Incheon 21990, Republic of Korea^b School of Biological Sciences, College of Natural Science, Seoul National University, 599 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea^c Division of Freshwater Bioresources Culture Research, Nakdonggang National Institute of Biological Resources, 137 Donam 2-gil, Sangju 37242, Republic of Korea^d University of Science & Technology, Yuseong-gu, Daejeon 34113, Republic of Korea

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ABSTRACT

Here, we present the first complete genome sequence of the strain PAMC 20958^T from the genus *Halocynthiibacter*. *Halocynthiibacter arcticus* PAMC 20958^T, isolated from a marine sediment of the Arctic, is a gram-negative, aerobic, and rod-shaped bacterium. The complete genome contains 4,329,554 base pairs with 53.21% GC content and a 44,566 base pair plasmid with 48.72% GC content. This genome contained genes encoding alkaline phosphatase and lipase, and genes that confer resistance to arsenic, cadmium, tellurite, and acriflavin.

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The genus *Halocynthiibacter* (Kim et al., 2014) belongs to the order *Rhodobacterales*, in the class *Alphaproteobacteria*, a major phylogenetic group in the global oceans, and is assumed to significantly impact various biogeochemical cycles (Giovannoni and Rappe, 2000). The genus *Halocynthiibacter* currently consists of two species: *Halocynthiibacter namhaensis*, isolated from sea squirt (*Halocynthia roretzi*), and *Hesperodiptomus arcticus*, isolated from arctic marine sediment (Baek et al., 2015; Kim et al., 2014). Neither *H. arcticus* nor *H. namhaensis* can grow at temperatures over 30 °C, and the optimum growth temperatures are 21 °C and 25 °C, respectively. *H. arcticus* was reported to be positive for alkaline phosphatase, lipase, and alpha-glucosidase and can hydrolyze Tweens 40, 60, and 80 (Baek et al., 2015). Since *Halocynthiibacter* is a newly growing genus, the complete genomic information is not yet known. To evaluate the possibility of industrial applications for this genus and to identify their environmental roles, we performed genome sequencing and present the complete genome sequence of *H. arcticus* PAMC 20958^T.

Genomic DNAs were extracted using a DNeasy Tissue and Blood Kit (Qiagen, USA) according to the manufacturer's instructions. Sequencing was performed using the PacBio RS II (Pacific

Biosciences, USA) by constructing a 20-kb insert library at ChunLab (Seoul, Korea) and 101,402,380 bp were generated from 112,510 subreads. For sequence assemblies, PBCR pipeline in Celera assembler (Ver. 8.3) was used (Berlin et al., 2015; Koren et al., 2012). One complete circular chromosome and one complete circular plasmid were generated. Genome annotation was performed using the Rapid Annotation using Subsystems Technology (RAST) server (Aziz et al., 2008).

The complete genome comprised of 4,329,554 nucleotides with 53.21% GC content. The plasmid comprised of 44,566 nucleotides with 48.72% GC content (Table 1). The predicted protein-coding sequences on the chromosome and the plasmid were 4675 and 40 respectively. The genome contains 45 tRNA genes and 3 rRNA operons (Table 1). A total of 1946 (41.62%) proteins were assigned to 345 RAST subsystem categories. In agreement with the previously reported enzymatic activities (Baek et al., 2015), the genome contained seven alkaline phosphatase, two lipase, two esterase, and one alpha-glucosidase genes. Because the optimal growth temperature of this strain was 21 °C, the heat sensitivity of these enzymes might make this strain valuable in biotechnological applications (Kumar et al., 2011). Interestingly, the genome contained genes that confer resistance to several toxicants, including cadmium, tellurite, and acriflavin. This strain also had three arsenate reductases. Since arsenate reductases reduce arsenate to arsenite in an initial step during arsenic detoxification (Mukhopadhyay and Rosen,

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Table 1
Genome features of *Halocynthiibacter arcticus* PAMC 20958^T.

	Chromosome	Plasmid
Genome size (bps)	4,329,554	46,566
GC content (%)	53.21	48.72
CDSs	4675	40
rRNA operons	3	
tRNA genes	45	

2002), this strain may play a role in bioremediation of arsenic-contaminated environments.

This is the first report of a complete genome sequence in the genus *Halocynthiibacter*. This sequence will be useful for understanding the environmental role of this strain in Arctic marine sediments and will be a basis for comparative genome analysis of the genus *Halocynthiibacter*.

Nucleotide sequence accession numbers

The complete genome sequence of *H. arcticus* PAMC 20958^T has been deposited at DDBJ/EMBL/GenBank under the accession numbers **CP014327** and **CP014328**. This strain is available from Polar and Alpine Microbial Collection (PAMC), Korean Collection for Type Cultures (KCTC), and Japan Collection of Microorganisms (JCM) with the accession number **PAMC 20958**, **KCTC 42129**, and **JCM 30530**, respectively.

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