

Genome Sequences of Six *Pseudoalteromonas* Strains Isolated from Arctic Sea Ice

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Yu et al. (*Polar Biol.* 32:1539–1547, 2009) isolated 199 *Pseudoalteromonas* strains from Arctic sea ice. We sequenced the genomes of six of these strains, which are affiliated to different *Pseudoalteromonas* species based on 16S rRNA gene sequences, facilitating the study of physiology and adaptation of Arctic sea ice *Pseudoalteromonas* strains.

Bacteria from the genus *Pseudoalteromonas* (*Gammaproteobacteria*, *Alteromonadales*, *Alteromonadaceae*) are found in various habitats in global oceans, including seawater (see, e.g., references 1 and 5), sediment (6, 11), and sea ice (3), ranging from the Antarctic (3, 4) to the Arctic (2). Currently, there are 38 recognized species in this genus. Complete genome sequences of three strains, Antarctic seawater strain *Pseudoalteromonas haloplanktis* TAC125 (9), deep-sea sediment strain *Pseudoalteromonas* sp. SM9913 (12), and strain *P. atlantica* T6c (<http://genome.jgi-psf.org/pseat/pseat.home.html>), and draft genome sequences of some other strains (e.g., *P. tunicata* D2 [13]) have been reported or released to public databases, revealing a number of features that are related to the adaptation to their habitats.

Recently, Yu et al. (14) screened 338 bacterial strains from Arctic sea ice, Canada Basin (77°30'N to 80°12'N), and it was unexpected that more than half (199 strains) of the total strains were closely related to eight *Pseudoalteromonas* species based on 16S rRNA gene sequences (14). This study indicates that many species in the *Pseudoalteromonas* genus have the ability to adapt to the Arctic sea ice environment. Here we reported the draft genome sequences of six of these Arctic sea ice strains, BSi20311, BSi20429, BSi20439, BSi20480, BSi20495, and BSi20652, which are affiliated with different *Pseudoalteromonas* species based on 16S rRNA gene sequences.

The genomes of the six strains were sequenced using Roche/454 technology (8). A 454 shotgun library was prepared for each strain. The sequencing generated 230,516 reads (totaling 90.6 Mb) for BSi20311, 212,278 reads (totaling 84.2 Mb) for BSi20429, 251,763 reads (totaling 82.3 Mb) for BSi20439, 238,953 reads (totaling 72.1 Mb) for BSi20480, 242,584 reads (totaling 87.6 Mb) for BSi20495, and 243,786 reads (totaling 67.4 Mb) for BSi20652. The average sequencing coverage ranges from 16-fold to 23-fold. Reads of each strain were assembled into contigs using Newbler, version 2.3. The numbers of large contigs (>500 bp) were 165 for BSi20311, 102 for BSi20429, 192 for BSi20439, 162 for BSi20480, 171 for BSi20495, and 242 for BSi20652. The protein-coding open reading frames (ORFs) were predicted using Glimmer, version 3.02 (7), and were annotated using the Swiss-Prot, NCBI nr, and Kyoto Encyclopedia of Genes and Genomes (KEGG) (10) databases. A comprehensive comparative genome analysis is under way.

The genome sizes range from 3.88 Mb (for BSi20439) to 4.82 Mb (for BSi20495). The G+C contents range from 38.85% to

40.33%. The ORF numbers range from 3,612 (for BSi20439) to 4,365 (for BSi20495).

These six genomes represent the first reported genomes for Arctic sea ice *Pseudoalteromonas* strains. These strains are closely related to different species in the *Pseudoalteromonas* genus, making them good models to study the physiology and adaptation of the Arctic sea ice strains.

Nucleotide sequence accession numbers. The contig sequences (>100 bp) of the six strains were deposited in DDBJ under the accession numbers [BADT000000000](#), [BADU000000000](#), [BADV000000000](#), [BADW000000000](#), [BADX000000000](#), and [BADY000000000](#).

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