



Genome announcement

Complete genome sequence of thiosulfate-oxidizing *Bosea* sp. strain PAMC26642 isolated from an Arctic lichen

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ABSTRACT

Thiosulfate-oxidizing *Bosea* sp. strain PAMC26642 was isolated from the Arctic lichen *Stereocaulon* sp. Complete genome sequencing of *Bosea* sp. PAMC26642 revealed several genes involved in thiosulfate oxidation. An analysis of the *Bosea* sp. PAMC26642 genome will provide novel insight into the genetic basis of its physiology and enable further analysis of key genes in the thiosulfate oxidation pathway.

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Bacteria of the genus *Bosea*, class *Alphaproteobacteria*, family *Bradyrhizobiaceae*, were first described by Das et al. (1996), and then in greater detail by La Scola et al. (2003). *Bosea* species, which were first isolated from plant rhizospheres, are mostly Gram-negative rods with unique metabolic features such as the ability to oxidize thiosulfate (Das et al., 1996; Deb et al., 2003). Well-known members of the genus include *Bosea massiliensis* (La Scola et al., 2003), *Bosea enaeae* (La Scola et al., 2003), *Bosea minatitlanensis* (Ouattara et al., 2003), *Bosea thiooxidans* (Das et al., 1996), and *Bosea vestrii* (La Scola et al., 2003). However, until now, only the taxonomy and thiosulfate-oxidizing ability of *Bosea* were known. In addition, the complete genome sequence of a *Bosea* species has not been reported. Here, we report the first complete genome sequence of *Bosea* sp. strain PAMC26642.

The thiosulfate-oxidizing bacterium *Bosea* sp. PAMC26642 (deposited as PAMC26642 in the Polar and Alpine Microbial Collection, Korea Polar Research Institute, Incheon, Korea) was isolated from *Stereocaulon* sp., an Arctic lichen collected from Ny-Ålesund, Svalbard, Arctic (78°55'N, 11°56'E). Genomic DNA was extracted from *Bosea* sp. PAMC26642 using a QIAamp DNA Mini Kit (Qiagen Inc., Valencia, CA), and the quantity and purity were determined using an Agilent 2100 Bioanalyzer (Agilent Technologies, Santa

Clara, CA). Genome sequencing was performed using PacBio RS II single-molecule real-time (SMRT) sequencing technology (Pacific Biosciences, Menlo Park, CA). Ten-kilobase SMRTbell library inserts were sequenced using SMRT cells. Raw sequence data were generated from 98,259 reads and 1,308,437,307 bp that were *de novo* assembled using the hierarchical genome-assembly process (HGAP) protocol (Chin et al., 2013) and RS HGAP Assembly 2 in SMRT analysis version 2.3 software (Pacific Biosciences; <https://github.com/PacificBiosciences/SMRT-Analysis>).

The resulting genome sequence has a size of 5,503,156 bp with a G+C content of 65.16%. Coding DNA sequences (CDSs) were predicted and annotated using NCBI Prokaryotic Genome Annotation Pipeline (PGAP) and the Rapid Annotation using Sub-system Technology (RAST) server (Aziz et al., 2008). Predicted gene sequences were translated and searched against National Center for Biotechnology Information (NCBI) non-redundant database, Clusters of Orthologous Groups (COG), and Kyoto Encyclopedia of Genes and Genomes (KEGG). A total of 5197 CDSs were predicted; the coding region accounted for 86.48% of the genome. In addition, 3 rRNA and 50 tRNA were predicted in the complete genome (Table 1). In total, 3936 genes were assigned a putative function. The genes were classified into 23COG functional categories. Sequence analyses revealed four rhodanese homologs (AXW83.07360, AXW83.07740, AXW83.24815 and AXW83.11195) and two sulfite oxidase homologs (AXW83.04245 and AXW83.11000), which are associated with thiosulfate oxidation via the tetrathionate intermediate (S₄-I) pathway. An analysis of the *Bosea* sp. PAMC26642 genome will lead to a better under-

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Table 1
Genome features of *Bosea* sp. PAMC26642.

Features	Chromosome	Plasmid
Genome size (bp)	5,503,156	7,199
Contig numbers	1	1
G + C content (%)	65.16	66.38
Protein coding genes	5197	8
rRNA number	3	–
tRNA genes	50	–
Rhodanese gene number	4	–
Sulfite oxidase gene number	2	–

standing of its evolution and the development of biotechnological applications using the thiosulfate oxidation pathway.

Nucleotide sequence accession numbers

The complete genome sequence has been deposited at GenBank/EMBL/DDBJ under the accession number CP014301 and CP014302.

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