



Genomics/technical resources

## Draft genome sequence of a denitrifying bacterium *Paracoccus marcusii* PAMC 22219 isolated from Arctic marine sediment



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### ABSTRACT

A denitrifying bacterium, *Paracoccus marcusii* PAMC 22219, was isolated from Arctic marine sediment in Svalbard, Norway. The obtained contigs were 265 with genome size of 4.0 Mb and G + C content of 66.1%. This bacterial genome revealed that it had nitrate and nitrite ammonification genes involved in the denitrification process, suggesting that *P. marcusii* PAMC 22219 is a denitrifying bacterium. This is the first genome that has been sequenced in the genus *Paracoccus*, isolated from an Arctic environment.

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### 1. Introduction

Microorganisms in the genus *Paracoccus*, belonging to the phylum *Alphaproteobacteria*, have been isolated from various environments in diverse geographical locations, and most of the species in this genus are reported to be mesophiles. However, so far, there have been no reports about the isolation of the genus *Paracoccus* in the polar environments such as the Arctic or Antarctic. Members of this genus have been known to exhibit wide metabolic flexibility in respiratory processes, employing nitrate, nitrite and nitrous oxide as electron acceptors in a process called denitrification. Accordingly, a strain of *Paracoccus denitrificans*, the type species of this genus, has nitrate reductase (catalyzing the reduction of nitrate to nitrite), nitrite reductase and nitrate transporter as well, which are responsible for denitrification (Siddavattam et al., 2011).

Microorganism in the genus *Paracoccus* (*Paracoccus marcusii* PAMC 22219) has been previously isolated from Arctic marine sediment of

Kongsfjorden in Svalbard, Norway (N 78.92267, E 11.89147). Growth temperature range of this strain was 4–37 °C, with optimum 25 °C. Although it was isolated from the Arctic marine sediment, the optimal growth temperature range was within the mesophile limit. Phylogenetic analysis based on the 16S rRNA gene of this strain was shown in Fig. 1. According to the tree, the strain PAMC 22219 was most closely related to *P. marcusii* DSM 11574<sup>T</sup> (99.2%) that is not able to reduce nitrate to nitrite (Harker et al., 1998). However, the genome of *P. marcusii* PAMC 22219 was revealed to have nitrate and nitrite reducing genes (Nas and Nap) that are important in environmental remediation (Mellor et al., 1992). In addition, the previous study reporting the isotope evidence for denitrification in high Arctic glacial ecosystem of Svalbard (Ansari et al., 2013), challenged this study on the genome sequence information of *P. marcusii* PAMC 22219 that could provide the denitrification-related gene information useful to understand the Arctic ecosystem.

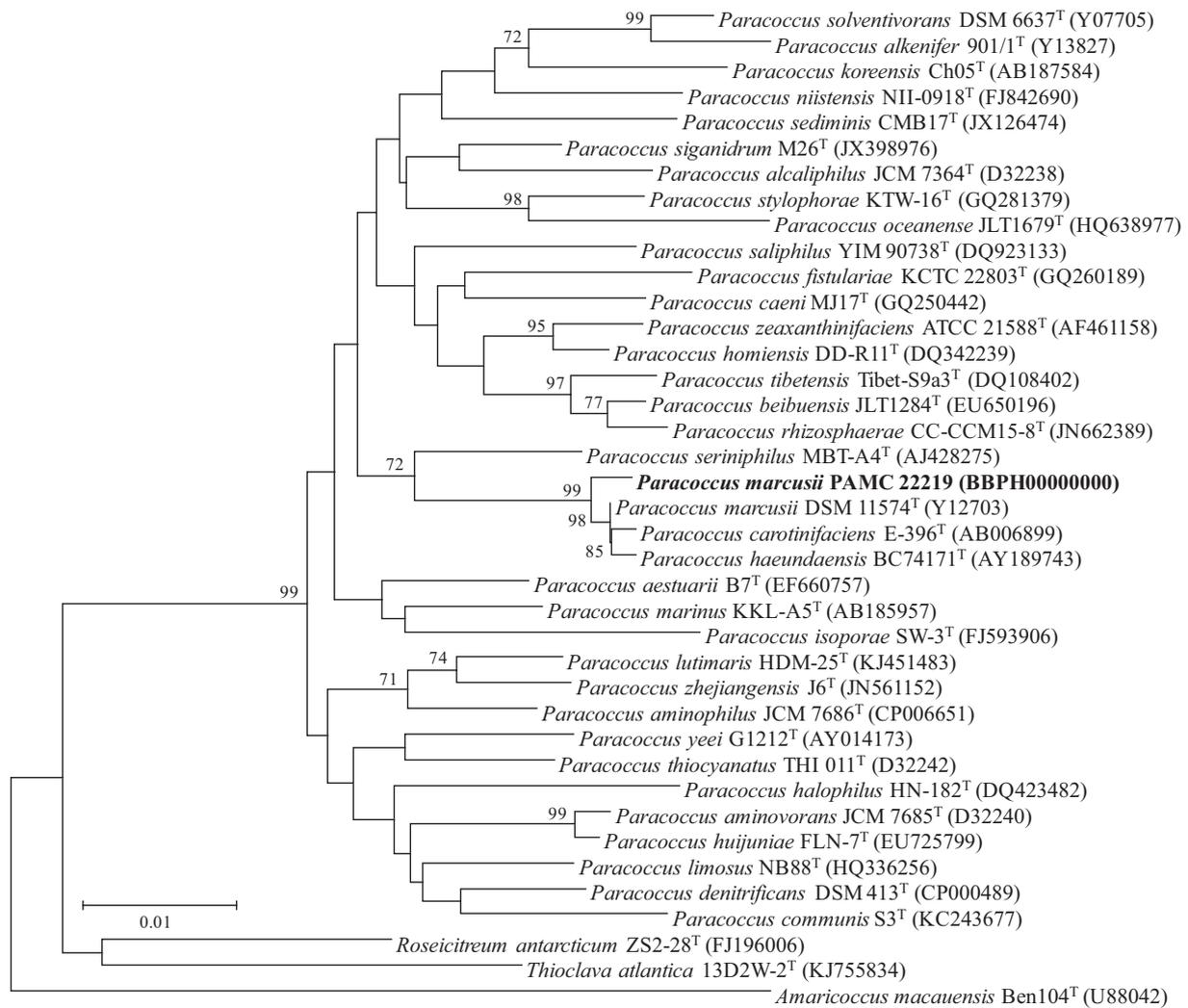
Genomic DNA of *P. marcusii* PAMC 22219 was extracted and purified with the G-spin™ Total DNA Extraction Kit (iNTRON Biotechnology, Seongnam, Korea). For whole genome sequencing, the 400-bp length sequencing library was constructed and sequenced with Ion Torrent PGM (318D sequencing Chip) according to the manufacturer's instructions (Rothberg et al., 2011). The draft genome sequence for *P. marcusii* PAMC 22219 was obtained from 1,959,079 reads spanning 4.01 Mb (108.3-fold coverage of the genome). The genome sequences

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**Fig. 1.** Phylogenetic analysis based on the 16S rRNA gene sequences of *P. marcusii* PAMC 22219 and closely related species. Numbers at branch points are bootstrap values (1000 replication; only values above 70% are shown). Bar, 0.01 accumulated changed per nucleotide.

were assembled into 265 contigs (> 1 kb in size) by using CLC Genomics Workbench 6.5 analysis software (CLC Bio, Aarhus, Denmark). Gene prediction and annotation were performed with RNAMmer 1.2 (Lagesen et al., 2007), tRNAscan-SE 1.21 (Lowe and Eddy, 1997), and the Rapid Annotation using Subsystem Technology (RAST) pipeline (Aziz et al., 2008).

The genome features of *P. marcusii* PAMC 22219 are summarized in Table 1. The genome is 4,010,486 bp in length, with a G + C content of 66.1%. One 16S rRNA, one 23S rRNA, two 5S rRNA and 46 tRNA genes were identified. Based on the RAST results, the draft genome contains 4089 coding sequences and, among the predicted CDSs, 9 genes were related to nitrate and nitrite ammonification: nitrate ABC transporter

(3 genes), response regulator *NasT*, and assimilatory nitrate reductase (2 genes), and nitrite reductase (3 genes). So far, the microorganisms mediating denitrification have been poorly isolated in cold environments, even though reactive nitrogen such as nitrate in cold regions has been known to be mostly lost via denitrification. However, novel psychrophilic denitrifying bacteria such as *Acrobacter* and *Hermiimonas* were isolated and characterized in Arctic fjords in Svalbard (Canion et al., 2013). Our results show that the first genome of *P. marcusii* isolated from Arctic marine sediment has the genes involved in the denitrification process. It strongly implies that it could be one of the polar-derived denitrifying bacteria, providing the basis for analyzing the nitrate reductase family enzymes that would be contributing to the supply of nitrogen sources in Arctic environments.

## 2. Nucleotide sequence accession number

The genome sequences of *P. marcusii* PAMC 22219 have been deposited at DDBJ/EMBL/GenBank under the accession number BBPH00000000.

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**Table 1**

General features of *Paracoccus marcusii* PAMC 22219 draft genome.

	<i>Paracoccus marcusii</i> PAMC 22219
Assembly size (bp)	4,010,486
G + C content (%)	66.1
Contigs	265
Coding sequence	4089
16S rRNA genes	1
23S rRNA genes	1
5S rRNA genes	2
tRNA genes	46

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