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GENOME SEQUENCES

Draft Genome Sequence of *Roseovarius* sp. PS-C2, Isolated from Sekinchan Beach in Selangor, Malaysia

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ABSTRACT *Roseovarius* sp. PS-C2 is a bacterium that was isolated from Sekinchan Beach in Selangor, Malaysia, using an *ex situ* cultivation technique. Here, we present a high-quality annotated draft genome of strain PS-C2 and suggest potential applications of this bacterium.

Roseovarius spp. are halophilic or halotolerant bacteria that thrive in various marine habitats (1). These bacteria have been reported as potential candidates for bioremediation and quorum sensing (2, 3).

Roseovarius sp. PS-C2 was isolated using a modified *ex situ* cultivation technique (4). Wet sediment and mud (0 to 15 cm from the top layer) were collected, using a sterilized laboratory scoop, from Sekinchan Beach in Selangor, Malaysia (3.5029N, 101.0945E). A sterilized corn cob was inserted into a 3-liter bioreactor filled with the collected sediment. After 2 weeks of incubation at 30°C and 80 rpm, samples were taken from the corn cob and spread onto marine agar (Condalab, Madrid, Spain). The PS-C2 strain was isolated, and genomic DNA was extracted using the Monarch genomic DNA purification kit (New England Biolabs, Ipswich, MA, USA), according to the manufacturer's instructions. The 16S rRNA gene was amplified by PCR using 27F and 1492R primers (5), sequenced, and taxonomically identified using the NCBI BLASTn search and the EzBioCloud 16S database (6). The analyses revealed that PS-C2 showed greatest similarity (99.93%) to *Roseovarius pacificus* 81-2^T (GenBank accession number DQ120726.1). Here, we present the genome sequence and analysis of *Roseovarius* sp. PS-C2. The high-quality annotated draft genome of PS-C2 might provide insights into its potential biotechnological applications.

Roseovarius sp. PS-C2 was grown on marine agar (pH 6.5) at 30°C for 24 h. Subsequently, bacterial genomic DNA was extracted using the Monarch genomic DNA purification kit, according to the manufacturer's protocol. A paired-end library was prepared using the standard protocol of the NEBNext Ultra DNA library preparation kit for Illumina (New England BioLabs). Sequencing was performed using the NovaSeq 6000 system with 150-bp paired-end reads (Illumina, San Diego, CA, USA). Sequence adaptors and low-quality reads were filtered using Trimmomatic v0.40 (7). *De novo* assembly of the genome was performed using SOAPdenovo v2.04 (8). The genome was analyzed and annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v5.20 (9). Genome comparison between strain PS-C2 and all 75 available genomes of *Roseovarius* spp. in the NCBI genome database (August 2021) was carried out using digital DNA-DNA hybridization (dDDH) via the Genome-to-Genome Distance Calculator (GGDC) v2.1 (10) and the average nucleotide identity (ANI) function in the EzBioCloud server (11). Carbohydrate-active enzymes (CAZymes) present in the genome of the PS-C2 strain were mined using dbCAN2 (12). Default parameters were used for all software tools, unless otherwise specified.

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The sequencer generated 1,748,493,900 bases from 5,828,313 paired-end reads. The *Roseovarius* sp. PS-C2 genome showed coverage of 362×. The genome was assembled into 39 contigs, with a total size of 3,958,657 bp, an N_{50} value of 411,343 bp, and a G+C content of 62.1%. The PS-C2 genome consisted of 3,920 predicted genes, of which 3,839 were protein-coding sequences, 31 were pseudogenes, 3 were rRNAs, 44 were tRNAs, and 3 were small RNAs. The genome comparison analyses showed that PS-C2 was closely related to *Roseovarius pacificus* 81-2^T (dDDH, 60.7%; ANI, 95.0%). Because the dDDH value was <70% (13) and the ANI value was <96% (11), the results indicated that strain PS-C2 is likely a new species of *Roseovarius*. The PS-C2 genome encoded 56 CAZymes, including 13 glycoside hydrolases (GHs), 31 glycosyl transferases, 8 auxiliary activity enzymes, and 4 carbohydrate esterases. Among the GHs, 4 lytic transglycosylases (LTs) belonged to GH family 103. LTs play an essential role in bacterial cell wall metabolism and present an attractive new target for antibiotic development (14). To date, none of the *Roseovarius* LTs has been characterized. Collectively, the PS-C2 genome contributed to the body of knowledge and possible applications of *Roseovarius* spp.

Data availability. The whole-genome shotgun sequence of *Roseovarius* sp. PS-C2 has been deposited in NCBI GenBank under BioProject accession number PRJNA716475, BioSample accession number SAMN18388700, and GenBank accession number JAHKSQ000000000. The version described in this paper is the first version, JAHKSQ00000000.1. The raw sequencing reads have been deposited in the NCBI Sequence Read Archive (SRA) with accession number SRR15311899. The 16S rRNA gene sequence of *Roseovarius* sp. PS-C2 has been deposited in NCBI GenBank with accession number MW785753.1.

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