



Data in Brief

Novel quorum quenching enzymes identified from draft genome of *Roseomonas* sp. TAS13



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ABSTRACT

Roseomonas sp. strain TAS13 isolated from an activated sludge sample degrades *N*-acylhomoserine lactones (AHLs) that are widely utilized as a signal in bacterial quorum sensing systems. The draft genome of *Roseomonas* sp. TAS13 contains 816 contigs (total 5,078,941 bp) which carries 4760 protein-coding genes and 52 tRNA genes (DDBJ/EMBL/GenBank accession numbers BDLP01000001 through BDLP01000016).

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Specifications

Organism/cell line/tissue	<i>Roseomonas</i> sp.
Strain	TAS13
Sequencer or array type	Illumina MiSeq sequencer
Data format	Processed
Experimental factors	Bacterial DNA
Experimental features	Draft genome sequence of <i>Roseomonas</i> sp. strain TAS13, assembly and annotation
Consent	Level of consent allowed for reuse if applicable
Sample source location	The activated sludge obtained from wastewater treatment plant (Tochigi, Japan)

1. Direct link to deposited data

<https://www.ncbi.nlm.nih.gov/nucleotide/BDLP00000001>.

2. Introduction

N-Acylhomoserine lactones (AHLs) are the major signaling molecules for quorum sensing (QS) in Gram-negative bacteria [1]. Several

opportunistic pathogens produce AHLs to regulate the expression of various genes related to their pathogenicity, biofilm formation, and antibiotic production [2,3]. Currently, novel AHL lactonase and/or acylase-producing bacteria have been screened from various environments to hydrolyze AHLs for inactivation [4]. There is considerable interest in techniques that selectively interrupt bacterial pathogenicity or biofilm formation using these AHL degrading enzymes [5].

An activated sludge is an important source of AHL-degrading enzymes because of the abundance of AHL producing bacteria [6]. The gene encoding AHL lactonase was identified from the whole genome of *Roseomonas* sp. strain B5 [7]; however, *Roseomonas* sp. producing AHL acylase was not identified. Bacteria belonging to the genus *Roseomonas*, a member of the family *Acetobacteraceae* within class *Alphaproteobacteria*, are aerobic, pink-pigmented, and coccoid- or short-rod-shaped. This genus was first proposed by Rihs et al. [8], and 25 species with 2 subspecies have been isolated (<http://www.bacterio.net/roseomonas.html>) from various environments including clinical specimens [9], water [10], soil [11], and air [12,13].

3. Experimental design, material and methods

3.1. Strain isolation

The activated sludge was obtained from wastewater treatment plants in Tochigi Prefecture, Japan. The bacteria in the sludge suspension were isolated on the agar plate of one half of Luria-Bertani (LB) medium

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after incubation at 30 °C for 3 to 5 days. The bacterial individual colonies formed were picked and cultured over night by liquid LB medium at 30 °C and stored at −80 °C with glycerol. The AHL-degrading *Roseomonas* sp. strain TAS13 was successfully identified from collection of the isolated and stored bacterial strains by bioassay using the representative AHL reporter strain *Chromobacterium violaceum* CV026 [14] which responds to the additive AHLs with length of the acyl chain from C4 to C8.

3.2. DNA extraction and sequencing

The genomic DNA of *Roseomonas* sp. strain TAS13 was extracted, purified, and concentrated by DNeasy blood and Tissue Kit (Qiagen) and Genomic DNA Clean and Concentrator Kit (Zymo Research). A DNA library was constructed using SureSelect QXT (Agilent Technologies) according to the manufacturer's instructions and its quality and concentration was evaluated using the Qubit double-stranded DNA BR Assay Kit with a Qubit fluorometer (Thermo Fisher Scientific). Draft genome sequencing was performed by the Illumina MiSeq sequencer (Illumina).

3.3. Genome assembly and annotation

The read pairs were assembled using SPAdes genome assembler software (version 3.9.0) [15]. The tRNA was predicted by tRNA scan-SE 2.0 program. The generated 816 contigs (214 to 63,315 bp) were annotated using Prokka 1.11 [16].

4. Data description

4.1. General features of the genome

The annotated genome contains 4760 protein-coding sequences (CDSs) and 52 tRNA genes totaling 5,078,941 bp with an average G + C content of 69.9%.

4.2. CDSs sharing relatively high homology with the known AHL acylases

On searching for the sequences sharing homology with all known AHL acylases in the draft genome sequence of TAS13, 11 predicted CDSs showed relatively high identity to the known AHL acylases. One of the predicted AHL acylases had high homology (e-value $2e^{-13}$; identities 30%; positives 41%) with penicillin acylase from *Kluyvera citrophila*. Penicillin G acylase having amidase activity, isolated from *K. citrophila*, showed an ability to degrade AHLs with C6–C8 acyl chains [17]. Therefore, the draft genome sequence of AHL-degrading *Roseomonas* sp. strain TAS13 provides valuable insights into the AHL acylase activity of this bacterium.

5. Nucleotide sequence accession numbers

The draft genome sequences of *Roseomonas* sp. TAS13 have been deposited in the DDBJ/Genbank/EMBL databases under accession numbers BDLP01000001 through BDLP01000816.

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