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GENOME ANNOUNCEMENT

Genome Sequence of *Roseomonas* sp. Strain B5, a Quorum-Quenching *N*-Acylhomoserine Lactone-Degrading Bacterium Isolated from Malaysian Tropical Soil

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***Roseomonas* sp. strain B5 was isolated from Malaysian tropical soil that showed *N*-acylhomoserine lactone degradation. This is the first genome announcement of a member from the genus of *Roseomonas* and the first report on the quorum-quenching activity of *Roseomonas* spp.**

Members of the genus *Roseomonas* belong to *Alphaproteobacteria* and are pale-pink-pigmented, aerobic, nonmotile, Gram-negative bacteria (6, 17). Although the natural reservoir of *Roseomonas* spp. remains unknown, they have been recovered from environmental sources such as water and soil (7, 13, 18). *Roseomonas* spp. have also been isolated from clinical samples, including blood, wounds, peritoneal dialysis fluid, and bone (2, 3, 6, 8, 10, 17). *Roseomonas* spp. appear to have low pathogenic potential for humans, but some species may cause clinically serious or even fatal diseases, especially in immunocompromised patients (10).

Quorum sensing refers to the phenomenon of regulation of gene expression in a population-dependent manner. Quorum sensing in proteobacteria usually involves production, secretion, and binding of signaling molecules called *N*-acylhomoserine lactones (AHL) to the cognate receptor protein (11). Interference of AHL-dependent quorum sensing, commonly known as quorum quenching, may be the novel way to attenuate bacterial virulence production (11), but such activity has not been reported in members of the *Roseomonas* genus. Here, we present the draft genome of *Roseomonas* sp. strain B5, a quorum-quenching bacterium isolated from Malaysian tropical soil enriched using a published method (4). We sequenced the whole genome of *Roseomonas* sp. strain B5 as a step toward understanding quorum-quenching activity in this bacterium.

Genomic DNA of *Roseomonas* sp. strain B5 was isolated using the QIAamp DNA minikit (Qiagen, Germany) according to the manufacturer's recommended protocol. The quality of DNA was examined by using both a NanoDrop spectrophotometer (Thermo Scientific) and a Qubit 2.0 fluorometer (Life Technologies). Whole-genome shotgun sequencing was performed by using the Illumina MiSeq personal sequencer platform (Illumina, Inc., CA). The resulting nucleotide sequences were trimmed and *de novo* assembled using Genomics Workbench version 5.1 (CLC bio, Aarhus, Denmark), which yielded 4,242,856 reads from 245 contigs with approximately 98-fold coverage. An N_{50} quality measurement of the contig was 49 kb, with an average contig size of 19 kb, and the largest contig assembled was approximately 202 kb. The genome contains 471,409,596 bp with a G+C content of 70.5%. Prodigal version 2.60 (12) was performed to predict open reading frames (ORFs), resulting in 4,365 ORFs. These ORFs were further annotated by comparison with NCBI-NR and Blast2GO (5). A total of 51 tRNAs were predicted using tRNAscan-SE (v.1.21) (16). One complete rRNA operon, one copy each of a 5S rRNA gene, 23S rRNA gene, and 16S rRNA gene, was identified by using RNAmmer (15).

BLASTX against a quorum-quenching lactonase database acquired from the UniProtKB protein knowledgebase (1) was performed to search for possible AHL-degrading genes. One predicted protein-coding sequence (CDS) encoding 263 amino acids that shows 84% similarity to the reported *attM* gene, an AHL-degrading gene (9, 14), was detected. Hence, the genome sequence of *Roseomonas* sp. strain B5 may provide insights into the quorum-quenching activity of this soil bacterium.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number ALOX00000000. The version described in this paper is the first version, ALOX01000000.

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