


Whole-Genome Analysis of *Aeromonas hydrophila* Strain 187, Exhibiting Quorum-Sensing Activity

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***Aeromonas hydrophila* is a quorum-sensing (QS) bacterium that causes diarrhea in humans upon infection. Here, we report the genome of pathogenic *Aeromonas hydrophila* strain 187, which possesses a QS gene responsible for signaling molecule *N*-acyl homoserine lactone (AHL) synthesis and has been found to be located at contig 36.**

Received 15 November 2014 Accepted 19 November 2014 Published 24 December 2014

Citation Chan X-Y, Chua KH, Yin W-F, Puthuchery SD, Chan K-G. 2014. Whole-genome analysis of *Aeromonas hydrophila* strain 187, exhibiting quorum-sensing activity. *Genome Announc.* 2(6):e01360-14. doi:10.1128/genomeA.01360-14.

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Aeromonas hydrophila is a quorum-sensing (QS) bacterium that causes human gastrointestinal and extra-intestinal diseases (1, 2). The expressions of its virulence factor, including the exoprotease, biofilm formation, and hemolysin coregulated protein, are QS regulated (3–5). In a previous study, the QS signaling molecule *N*-acyl homoserine lactone (AHL) profile of *A. hydrophila* 187 was characterized. However, the gene coding for its AHL synthase remains unknown. In this study, we report the whole genome and QS gene of *A. hydrophila* 187.

A. hydrophila strain 187 was isolated from a patient's pus at the University Hospital, University of Malaya, Kuala Lumpur, Malaysia (6). The isolate was maintained using LB media at 37°C. Genomic DNA of the *A. hydrophila* strain was extracted using a QIAamp DNA MiniKit (Qiagen, Germany) (7). Subsequently, the DNA was quantified and qualified using a Qubit 2.0 fluorometer (Invitrogen, USA) and Nanodrop (Thermo Scientific, USA) prior to next generation sequencing library preparation with a Nextera DNA sample preparation kit (Illumina, USA). The whole-genome sequencing was performed using MiSeq (Illumina, USA) (8). Paired-end reads were trimmed and *de novo* assembled with CLC genomic workbench v5.1 (9). The contigs were subjected to gene prediction with Prodigal followed by gene annotation by BLAST against the Uniprot database (10, 11).

A total of 3.48 million reads were generated from this whole-genome sequencing. After quality trimming, the reads were assembled into 59 contigs, with an average coverage of 111-fold and N_{50} of 197 kbp. The draft genome of *A. hydrophila* strain 187 is 4.7 Mbp and the G+C content of its genome is 61.63%. Gene prediction has identified 4,339 coding DNA sequences (CDS) from the genome.

Based on the annotation result, *luxI* homolog (*ahyI*) of *A. hydrophila* 187 was detected in contig 37. The length of this gene is 621 bp located at 45,853 bp to 48,473 bp of contig 37. The *ahyI* gene encodes for *A. hydrophila* AHL synthase, which is responsible for the production of its QS signaling molecule (12). Recently, another member of *Aeromonas* that exhibits QS properties,

A. caviae, has been isolated from garden compost samples (13). With the availability of this genome sequence, further characterization of the *A. hydrophila* strain 187 could be carried out using our whole-genome data, which could lead to an understanding of the relation of QS and the virulence factor of this bacterium.

Nucleotide sequence accession numbers. This draft genome was deposited into DDBJ/EMBL/GenBank under the accession no. [AOBO00000000](https://www.ncbi.nlm.nih.gov/nuccore/AOBO00000000). The version described in this paper is the first version, [AOBO10000000](https://www.ncbi.nlm.nih.gov/nuccore/AOBO10000000).

ACKNOWLEDGMENT

We are thankful for the High Impact Research Grant (UM-MOHE HIR grant UM.C/625/1/HIR/MOHE/CHAN/01, H-50001-A000001) that supported this project. This grant was granted to K.-G.C. by the University of Malaya.

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