

Genome Sequence Analysis Reveals Evidence of Quorum-Sensing Genes Present in *Aeromonas hydrophila* Strain M062, Isolated from Freshwater

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***Aeromonas hydrophila* has emerged worldwide as a human pathogen. Here, we report the draft whole-genome sequence of a freshwater isolate from Malaysia, *A. hydrophila* strain M062, and its *N*-acylhomoserine lactone genes are also reported here.**

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Quorum sensing (QS) is a term coined by Fuqua and coworkers to define the phenomenon of a bacterial cell-to-cell communication system that controls bacterial physiological processes in a population density-dependent manner (1). This process describes the event whereby an increase in the population density of the bacterial cell is proportional to an increase in the concentration of signal molecule(s) in the extracellular environment (2, 3). *Aeromonas hydrophila* is QS bacterium and is a known pathogen, as it can cause minor skin infections and gastroenteritis in humans (4, 5). In this study, we report the whole-genome sequence and the QS genes of *A. hydrophila* strain M062.

A. hydrophila M062 was isolated from the Sungai Tua waterfall, Selangor, Malaysia. The genomic DNA of *A. hydrophila* M062 was extracted using the MasterPure DNA purification kit (Epicentre, Inc., Madison, WI, USA). A Qubit 2.0 fluorometer (Invitrogen, USA) and NanoDrop spectrophotometer (Thermo Scientific, USA) were used to quantify and qualify the DNA preceding whole-genome shotgun sequencing on an Illumina MiSeq personal sequencer (Illumina, Inc., San Diego, CA, USA) and generated 4,984,734 paired-end reads. Subsequently, the paired-end reads were trimmed and *de novo* assembled with CLC Genomics Workbench version 5.1 (CLC bio, Denmark). Gene prediction was conducted using Prodigal (version 2.60) (6), followed by gene annotation using RAST (7). Next, tRNAs and rRNAs were predicted with tRNAscan-SE version 1.21 (8) and RNAmmer (9), respectively.

From this whole-genome sequencing, a total of 4,974,350 reads were generated. After trimming (1,548,021 quality reads), the reads were assembled into 140 contigs, with an N_{50} of 93,561 and an average coverage of 51.4-fold. The G+C content of the draft genome of *A. hydrophila* strain M062 is 60.5%. An analysis of its genome sequences led to the identification of 4,392 coding DNA sequences (CDSs), 95 tRNAs, two copies of 5S rRNA, and one copy each of 16S rRNA and 23S rRNA.

The annotation result showed that the *luxI* and *luxR* homo-

logues of *A. hydrophila* strain M062 are located at contig 35. With the availability of the whole-genome sequence of *A. hydrophila* strain M062, it may provide a better understanding of the QS system in this strain.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [JSXE00000000](#). The version described in this paper is the first version, JSXE01000000.

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