


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

Xin-Yue Chan,<sup>a</sup> Kek Heng Chua,<sup>b</sup> Wai-Fong Yin,<sup>a</sup> S. D. Puthuchery,<sup>c</sup>  Kok-Gan Chan<sup>a</sup>

Division of Genetics and Molecular Biology, Institute of Biological Sciences, Faculty of Science, University of Malaya, Kuala Lumpur, Malaysia<sup>a</sup>; Department of Biomedical Science, Faculty of Medicine, University of Malaya, Kuala Lumpur, Malaysia<sup>b</sup>; Department of Medical Education, Research and Evaluation, Duke-NUS Graduate Medical School Singapore, Singapore<sup>c</sup>

***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.

Copyright © 2014 Chan et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/3.0/).

Address correspondence to Kok-Gan Chan, kokgan@um.edu.my.

*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. [AOBO0000000](https://doi.org/10.1093/nucleotide/AOBO0000000). The version described in this paper is the first version, AOBO01000000.

## 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.

## REFERENCES

- Vila J, Ruiz J, Gallardo F, Vargas M, Soler L, Figueras MJ, Gascon J. 2003. *Aeromonas* spp. and traveler's diarrhea: clinical features and antimicrobial resistance. *Emerg. Infect. Dis.* 9:552–555. [http://dx.doi.org/10.3201/eid0905.020451](https://doi.org/10.3201/eid0905.020451).
- Parker JL, Shaw JG. 2011. *Aeromonas* spp. clinical microbiology and disease. *J. Infect.* 62:109–118. [http://dx.doi.org/10.1016/j.jinf.2010.12.003](https://doi.org/10.1016/j.jinf.2010.12.003).
- Khajanchi BK, Sha J, Kozlova EV, Erova TE, Suarez G, Sierra JC, Popov VL, Horneman AJ, Chopra AK. 2009. *N*-acylhomoserine lactones involved in quorum sensing control the type VI secretion system, biofilm formation, protease production, and in vivo virulence in a clinical isolate of *Aeromonas hydrophila*. *Microbiology* 155:3518–3531. [http://dx.doi.org/10.1099/mic.0.031575-0](https://doi.org/10.1099/mic.0.031575-0).
- Swift S, Lynch MJ, Fish L, Kirke DF, Tomás JM, Stewart GS, Williams P. 1999. Quorum sensing-dependent regulation and blockade of exoprotease production in *Aeromonas hydrophila*. *Infect. Immun.* 67:5192–5199.
- Lynch MJ, Swift S, Kirke DF, Keevil CW, Dodd CE, Williams P. 2002. The regulation of biofilm development by quorum sensing in *Aeromonas hydrophila*. *Environ. Microbiol.* 4:18–28. [http://dx.doi.org/10.1046/j.1462-2920.2002.00264.x](https://doi.org/10.1046/j.1462-2920.2002.00264.x).
- Chan K-G, Puthuchery SD, Chan X-Y, Yin W-F, Wong C-S, See Too WS, Chua K-H. 2011. Quorum sensing in *Aeromonas* species isolated from patients in Malaysia. *Curr. Microbiol.* 62:167–172. [http://dx.doi.org/10.1007/s00284-010-9689-z](https://doi.org/10.1007/s00284-010-9689-z).

7. Chan XY, Chua KH, Puthuchery SD, Yin W-F, Chan K-G. 2012. Draft genome sequence of an *Aeromonas* sp. strain 159 clinical isolate that shows quorum-sensing activity. *J. Bacteriol.* **194**:6350. <http://dx.doi.org/10.1128/JB.01642-12>.
8. Chan XY, Chang CY, Hong KW, Tee KK, Yin WF, Chan KG. 2013. Insights of biosurfactant producing *Serratia marcescens* strain W2.3 isolated from diseased tilapia fish: a draft genome analysis. *Gut Pathog.* **5**:29. <http://dx.doi.org/10.1186/1757-4749-5-29>.
9. Hong K-W, Gan HM, Low S-M, Lee PKY, Chong Y-M, Yin W-F, Chan K-G. 2012. Draft genome sequence of *Pantoea* sp. strain A4, a *Rafflesia*-associated bacterium that produces *N*-acylhomoserine lactones as quorum-sensing molecules. *J. Bacteriol.* **194**:6610. <http://dx.doi.org/10.1128/JB.01619-12>.
10. Hyatt D, Chen G-L, LoCascio PF, Land ML, Larimer FW, Hauser LJ. 2010. Prodigal: prokaryotic gene recognition and translation initiation site identification. *BMC Bioinformatics* **11**:119. <http://dx.doi.org/10.1186/1471-2105-11-119>.
11. UniProt Consortium. 2010. The universal protein resource (UniProt) in 2010. *Nucleic Acids Res.* **38**:D142–D148. <http://dx.doi.org/10.1093/nar/gkp846>.
12. Swift S, Karlyshev AV, Fish L, Durant EL, Winson MK, Chhabra SR, Williams P, Macintyre S, Stewart GS. 1997. Quorum sensing in *Aeromonas hydrophila* and *Aeromonas salmonicida*: identification of the LuxRI homologs AhyRI and AsaRI and their cognate *N*-acylhomoserine lactone signal molecules. *J. Bacteriol.* **179**:5271–5281.
13. Lim Y-L, Ee R, Yin W-F, Chan K-G. 2014. Quorum sensing activity of *Aeromonas caviae* strain YL12, a bacterium isolated from compost. *Sensors* **14**:7026–7040. <http://dx.doi.org/10.3390/s140407026>.