CrossMark
click for updates

Draft Genome Sequence of *Aeromonas caviae* Strain L12, a Quorum-Sensing Strain Isolated from a Freshwater Lake in Malaysia

Kok-Gan Chan,[a] Pui-San Chin,[a] Kok Keng Tee,[b] Chien-Yi Chang,[c,d] Wai-Fong Yin,[a] Kit-Yeng Sheng[a]

Division of Genetics and Molecular Biology, Institute of Biological Sciences, Faculty of Science, University of Malaya, Kuala Lumpur, Malaysia[a]; Centre of Excellence for Research in AIDS (CERiA), Department of Medicine, Faculty of Medicine, University of Malaya, Kuala Lumpur, Malaysia[b]; Interdisciplinary Computing and Complex BioSystems (ICOS) research group, School of Computing Science, Claremont Tower, Newcastle University, Newcastle upon Tyne, United Kingdom[c]; The Centre for Bacterial Cell Biology, Medical School, Newcastle University, Richardson Road, Newcastle upon Tyne, United Kingdom[d]

Here, we present the draft genome sequence of *Aeromonas caviae* strain L12, which shows quorum-sensing activity. The availability of this genome sequence is important to the research of the quorum-sensing regulatory system in this isolate.

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

Aeromonads are Gram-negative, non-spore-forming, facultative anaerobic, rod-shaped bacteria. Members of *Aeromonas* can be found in aquatic environments. *Aeromonas caviae* is a motile mesophilic species in the *Aeromonas* genus, which is often associated with human infections [1]. *A. caviae* has been isolated from patients with sepsis and wounds, gastroenteritis, and systemic infections [2–4]. A process known as quorum sensing was described to be responsible for the regulation of virulence factors [5–8]. In this work, *A. caviae* strain L12 was isolated from a freshwater lake in Malaysia and subjected to whole-genome sequencing.

Genomic DNA of *A. caviae* strain L12 was extracted using a MasterPure DNA purification kit (Epicentre, Madison, WI, USA) according to the manufacturer's recommended protocol. The quality of the purified genomic DNA was determined using a NanoDrop spectrophotometer (Thermo Scientific) and Qubit 2.0 fluorometer (Life Technologies) [9]. Whole-genome sequencing was done using a paired-end sequencing method with the HiSeq 2500 platform (Illumina, Inc., San Diego, CA, USA) [10]. The sequences were trimmed with a quality threshold of Q30 and *de novo* assembly was done using CLC Genomics Workbench version 7.0 (CLC Bio, Aarhus, Denmark) [11]. The quality trimming yielded a total count of 4,908,771 paired-end reads with an average read length of 80.8 bp. The draft genome size of *A. caviae* strain L12 is 4,376,717 bp with 91 contigs with an average coverage of 100.6-fold. The mean contig read length is 126,255-bp and the maximum contig read length is 294,904 bp. Its G+C content is 61.7%, consisting of 30.7% cytosine and 31.0% guanine. Gene prediction and annotation was done using PROKKA version 1.10 resulting in 3,958 open reading frames (ORFs) and 4,089 genes [12]. The number of RNAs was also predicted using PROKKA version 1.10. There were 3 rRNAs and 84 tRNAs identified.

Genes that were annotated were then searched against the NCBI database using BLAST [13] to confirm their identity and searched against the UniProt database [14] to further understand their functions and characteristics. From the annotated genes of the draft genome of strain L12, several putative quorum-sensing related genes were found, such as transcriptional activator protein LuxR, homoserine and homoserine lactone efflux proteins, regulatory protein LuxO, and autoinducer 2 sensor kinase/phosphatase LuxQ. It is hoped that this genome sequence will provide a better understanding of quorum-sensing regulation in this isolate.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under accession no. JWJP00000000. The version described in this paper is version JWJP01000000.

REFERENCES

1. **Figura N, Guglielmetti P.** 1987. Differentiation of motile and mesophilic *Aeromonas* strains into species by testing for a camp-like factor. J Clin Microbiol **25**:1341–1342.
2. **Beatson SA, das Graças de Luna M, Bachmann NL, Alikhan NF, Hanks KR, Sullivan MJ, Wee BA, Freitas-Almeida AC, Dos Santos PA, de Melo JT, Squire DJ, Cunningham AF, Fitzgerald JR, Henderson IR.** 2011. Genome sequence of the emerging pathogen *Aeromonas caviae*. J Bacteriol **193**:1286–1287. http://dx.doi.org/10.1128/JB.01337-10.
3. **Janda JM, Abbott SL.** 2010. The genus *Aeromonas*: taxonomy, pathogenicity, and infection. Clin Microbiol Rev **23**:35–73. http://dx.doi.org/10.1128/CMR.00039-09.
4. **Tang HJ, Lai CC, Lin HL, Chao CM.** 2014. Clinical manifestations of bacteremia caused by *Aeromonas* species in southern Taiwan. PLoS One **9**:e91642. http://dx.doi.org/10.1371/journal.pone.0091642.
5. **Lim YL, Ee R, Yin WF, Chan KG.** 2014. Quorum sensing activity of *Aeromonas caviae* strain YL12, a bacterium isolated from compost. Sensors (Basel) **14**:7026–7040. http://dx.doi.org/10.3390/s140407026.
6. **Tan WS, Yin WF, Chan KG.** 2015. Insights into the quorum-sensing activity in *Aeromonas hydrophila* strain m013 as revealed by whole-genome sequencing. Genome Announc 3(1):e01372-14. http://dx.doi.org/10.1128/genomeA.01372-14.
7. **Chan XY, Chua KH, Yin WF, Puthucheary SD, Chan KG.** 2014. Whole-genome analysis of *Aeromonas hydrophila* strain 187, exhibiting quorum-sensing activity. Genome Announc 2(6):e01360-14. http://dx.doi.org/10.1128/genomeA.01360-14.
8. **Chan KG, Puthucheary SD, Chan XY, Yin WF, Wong CS, Too WS,**

Chua KH. 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.

9. **Mohamad NI, Yin WF, Chan KG.** 2015. Whole-genome sequence of quorum-sensing *Vibrio tubiashii* strain t33. Genome Announc **3**(1): e01362-14. http://dx.doi.org/10.1128/genomeA.01362-14.

10. **Hong KW, Koh CL, Sam CK, Yin WF, Chan KG.** 2012. Whole-genome sequence of *N*-acylhomoserine lactone-synthesizing and -degrading *Acinetobacter* sp. strain gg2. J Bacteriol **194:**6318. http://dx.doi.org/10.1128/JB.01579-12.

11. **Chong TM, Yin WF, Mondy S, Grandclément C, Dessaux Y, Chan KG.** 2012. Heavy-metal resistance of a France vineyard soil bacterium, *Pseudomonas mendocina* strain S5.2, revealed by whole-genome sequencing. J Bacteriol **194:**6366. http://dx.doi.org/10.1128/JB.01702-12.

12. **Seemann T.** 2014. Prokka: rapid prokaryotic genome annotation. Bioinformatics **30:**2068–2069. http://dx.doi.org/10.1093/bioinformatics/btu153.

13. **Tatusova T, Ciufo S, Fedorov B, O'Neill K, Tolstoy I.** 2014. RefSeq microbial genomes database: new representation and annotation strategy. Nucleic Acids Res **42:**D553–D559. http://dx.doi.org/10.1093/nar/gkt1274.

14. **Leinonen R, Nardone F, Zhu W, Apweiler R.** 2006. UniSave: the UniProtKB sequence/annotation version database. Bioinformatics **22:** 1284–1285. http://dx.doi.org/10.1093/bioinformatics/btl105.