

Draft Genome Sequence of *Aeromonas hydrophila* TN97-08

Hasan C. Tekedar,^a Salih Kumru,^a Attila Karsi,^a Geoffrey C. Waldbieser,^b Tad Sonstegard,^c Steven G. Schroeder,^c Mark R. Liles,^d Matt J. Griffin,^a Mark L. Lawrence^a

College of Veterinary Medicine, Mississippi State University, Mississippi State, Mississippi, USA^a; Warmwater Aquaculture Research Unit, Agriculture Research Service, United States Department of Agriculture, Stoneville, Mississippi, USA^b; Bovine Functional Genomics Laboratory, Agricultural Research Service, United States Department of Agriculture, Beltsville, Maryland, USA^c; Department of Biological Sciences, Auburn University, Auburn, Alabama, USA^d

***Aeromonas hydrophila* is an opportunistic pathogen residing in freshwater environments that causes infection in fish and mammals. Here, we report the draft genome sequence of *A. hydrophila* strain TN97-08 isolated from a diseased bluegill (*Lepomis macrochirus*) in 1997.**

Received 8 April 2016 Accepted 12 April 2016 Published 26 May 2016

Citation Tekedar HC, Kumru S, Karsi A, Waldbieser GC, Sonstegard T, Schroeder SG, Liles MR, Griffin MJ, Lawrence ML. 2016. Draft genome sequence of *Aeromonas hydrophila* TN97-08. *Genome Announc* 4(3):e00436-16. doi:10.1128/genomeA.00436-16.

Copyright © 2016 Tekedar et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Mark L. Lawrence, lawrence@cvm.msstate.edu.

Aeromonas hydrophila is an opportunistic Gram-negative species causing disease in fish and mammals. The genus *Aeromonas* affects a variety of aquatic organisms and lives in diverse aquatic ecosystems (1). There are 45 *A. hydrophila* genomes currently available in GenBank. Our research group released the genomes of strains ML09-119 and AL06-06 (accession numbers CP005966 and CP010947). Strain ML09-119 was isolated from an outbreak of bacterial septicemia in a commercial channel catfish pond in the southeastern United States (2). Strain AL06-06 was isolated from a diseased goldfish in 2006 (3). Here, we report the draft genome sequence of strain TN97-08, which was isolated in 1997 from diseased bluegill (*Lepomis macrochirus*).

The *A. hydrophila* TN97-08 genome was sequenced using an Illumina Genome Analyzer IIx (9,280,112 reads with 243× coverage). Adaptor trimming, contig creation, and quality control of sequence reads were conducted using CLC Workbench 6.5.1 (CLC bio) and Sequencher 5.3 (Gene Codes Corporation). *De novo* assembly was performed by CLC Workbench 6.5.1. To reduce contig numbers, some of the scaffolded gaps were closed by Sanger sequencing of PCR amplicons. Additionally, some of the unscaffolded gaps were closed by single-primer PCR (4).

Two different methods were used to annotate the draft genome: RAST (5) and the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP) (6). The draft genome of *A. hydrophila* TN97-08 is composed of 16 contigs and 5,087,310 bp. It contains 4,602 predicted genes, of which 4,445 are protein-coding genes.

The annotated *A. hydrophila* TN97-08 genome was compared against the genomes of *A. hydrophila* ML09-119 and AL06-06. The results indicated that *A. hydrophila* TN97-08 has 100 and 74 unique elements compared to strains ML09-119 and AL06-06, respectively. One of the unique features identified is a type VI secretion system, which is considered a virulence factor involved in the translocation of potential effector proteins into the host (7). Other unique elements include multidrug resistance efflux pumps, cobalt zinc cadmium resistance, stress response proteins, phage and prophage elements, and toxin-antitoxin replicon stabi-

lization system elements. In contrast to the AL06-06 genome, TN97-08 does not carry any plasmids. The estimated average nucleotide identity (<http://enve-omics.ce.gatech.edu/ani/>) between the strain TN97-08 genome and the strain ML09-199 genome was 96.61%, and it was 96.72% between TN97-08 and AL06-06 (8).

Nucleotide sequence accession numbers. The draft genome sequence of *A. hydrophila* TN97-08 was deposited in GenBank under accession no. [LNUR000000000](https://www.ncbi.nlm.nih.gov/nuccore/LNUR000000000), version LNUR000000000.1, genomic ID 982545319.

ACKNOWLEDGMENTS

This work was supported by USDA NIFA grant 2013-67015-21313, Mississippi State University College of Veterinary Medicine, and USDA Agricultural Research Service CRIS project 6402-31000-009-00D.

FUNDING INFORMATION

This work, including the efforts of Hasan C. Tekedar, Salih Kumru, and Mark L. Lawrence, was funded by Mississippi State University College of Veterinary Medicine. This work, including the efforts of Attila Karsi, Mark R. Liles, Matt J. Griffin, and Mark L. Lawrence, was funded by USDA | National Institute of Food and Agriculture (NIFA) (2013-67015-21313). This work, including the efforts of Geoffrey C. Waldbieser, Tad Sonstegard, and Steven G. Schroeder, was funded by USDA | Agricultural Research Service (ARS).

REFERENCES

- 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>.
- Tekedar HC, Waldbieser GC, Karsi A, Liles MR, Griffin MJ, Vamenta S, Sonstegard T, Hossain M, Schroeder SG, Khoo L, Lawrence ML. 2013. Complete genome sequence of a channel catfish epidemic isolate, *Aeromonas hydrophila* strain ML09-119. *Genome Announc* 1(5):e00755-13. <http://dx.doi.org/10.1128/genomeA.00755-13>.
- Tekedar HC, Karsi A, Akgul A, Kalindamar S, Waldbieser GC, Sonstegard T, Schroeder SG, Lawrence ML. 2015. Complete genome sequence of fish pathogen *Aeromonas hydrophila* AL06-06. *Genome Announc* 3(2):e00368-15. <http://dx.doi.org/10.1128/genomeA.00368-15>.

4. Karlyshev AV, Pallen MJ, Wren BW. 2000. Single-primer PCR procedure for rapid identification of transposon insertion sites. *Biotechniques* 28: 1078, 1080, 1082.
5. Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Disz T, Edwards RA, Gerdes S, Parrello B, Shukla M, Vonstein V, Wattam AR, Xia F, Stevens R. 2014. The SEED and the rapid annotation of microbial genomes using subsystems technology (RAST). *Nucleic Acids Res* 42:D206–D214. <http://dx.doi.org/10.1093/nar/gkt1226>.
6. Angiuoli SV, Gussman A, Klimke W, Cochrane G, Field D, Garrity G, Kodira CD, Kyrpides N, Madupu R, Markowitz V, Tatusova T, Thomson N, White O. 2008. Toward an online repository of Standard Operating Procedures (SOPs) for (meta)genomic annotation. *Omic* 12:137–141. <http://dx.doi.org/10.1089/omi.2008.0017>.
7. Bingle LE, Bailey CM, Pallen MJ. 2008. Type VI secretion: a beginner's guide. *Curr Opin Microbiol* 11:3–8. <http://dx.doi.org/10.1016/j.mib.2008.01.006>.
8. Goris J, Konstantinidis KT, Klappenbach JA, Coenye T, Vandamme P, Tiedje JM. 2007. DNA-DNA hybridization values and their relationship to whole-genome sequence similarities. *Int J Syst Evol Microbiol* 57:81–91. <http://dx.doi.org/10.1099/ijs.0.64483-0>.