



Draft Genome Sequence of Heavy Metal-Resistant *Aeromonas veronii* CTe-01, Isolated from a Peruvian Wastewater Treatment Plant

 Luis Tataje-Lavanda,^a Phillip Ormeño-Vásquez,^a Rosa Altamirano-Díaz,^c Lucy Espinoza-Salazar,^c Mirko Zimic,^{a,b} Manolo Fernández-Sánchez,^a Manolo Fernández-Díaz,^a Claudio C. Vásquez,^d  Juan C. Tantaleán^c

^aLaboratorios de Investigación y Desarrollo, FARVET, Chíncha Alta, Ica, Peru

^bLaboratorio de Bioinformática, Biología Molecular y Desarrollos Tecnológicos, Laboratorios de Investigación y Desarrollo, Facultad de Ciencias, Universidad Peruana Cayetano Heredia, Lima, Peru

^cLaboratorio de Biología Molecular y Biotecnología, Facultad de Ciencias Biológicas, Universidad Nacional San Luis Gonzaga, Ica, Peru

^dLaboratorio de Microbiología Molecular, Facultad de Química y Biología, Universidad de Santiago de Chile, Santiago, Chile

ABSTRACT Here, we report a draft genome sequence of *Aeromonas veronii* strain CTe-01 (4.5 Mb), a hemolytic, heavy metal-resistant bacterium isolated from a wastewater treatment plant located at Cachiche, Ica, Peru. These characteristics could be used for bioremediation of contaminated environments.

Aeromonas veronii causes infections and death in fish (1, 2) and other freshwater animals (3). It is an emerging pathogen involved in enteric (4) and extraintestinal infections in humans (5–8), and its pathogenicity is usually multifactorial (6). Additionally, it is routinely oxacillin, ampicillin, tetracycline, streptomycin, chloramphenicol, and erythromycin resistant (1, 9). It is typically a Gram-negative, lactose-negative, and oxidase-positive bacterium that has been isolated from soils, food, animals, and different aquatic sources (10, 11). Studies of heavy metal resistance genes in *A. veronii* are limited, so the study of its genome is important because, like other *Aeromonas* species, it harbors heavy metal resistance genes, including those for mercury, cobalt, zinc, cadmium, and chromium resistance, among others (12). Frequently, *A. veronii* harbors mobile elements, such as plasmids, insertion sequences (IS), transposons, genes associated with integrons, and bacteriophages (12–14), which participate in horizontal transfer and diffusion of heavy metal resistance and antibiotic resistance to other environmental bacteria (15–17).

A. veronii CTe-01 was isolated from a wastewater sample at Cachiche, Ica, Peru (14°07'06.00"S, 75°43'34.89"W; 391 m above sea level [masl]) using Luria Bertani (LB) medium supplemented with potassium tellurite (75 µg/ml). It is a hemolytic bacterium which grows in the presence of HgCl₂ (10 µg/ml). For its identification, biochemical characteristics were evaluated using an automatic Vitek 2 compact system with Gram-negative (GN) bacterial identification (ID) cards (bioMérieux), and the 16S rRNA gene was sequenced by Macrogen, Inc. (USA) (GenBank accession number MK876839.1).

Pure cultures were grown in Luria Bertani broth containing 100 µg/ml ampicillin and incubated at 37°C for 12 h. Genomic DNA was extracted using a DNeasy blood and tissue kit (Qiagen, Germany) and sequenced at Macrogen, Inc. (South Korea) using a HiSeq 2000 platform with 101-bp paired-end reads (TruSeq DNA PCR-free library), producing 2,145,830,850 bp with a total of 21,245,850 reads. Unless otherwise stated, default parameters were used for all software. Reads were checked for quality using FastQC version 0.11.5 (Babraham Bioinformatics, Cambridge, UK) and assembled *de novo* using SPAdes version 3.11 (with the “-careful” and “-plasmid” settings) (18) without trimming the reads to avoid losing information; contigs were reordered with Mauve

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Address correspondence to Juan C. Tantaleán, jtantalean@unica.edu.pe.

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version 2015-02-26 (19). After removal of small contigs (<200 bp) and contaminants, 272 contigs were obtained (total length, 4,641,822 bp; N_{50} , 79,963 bp; L_{50} , 22; GC content, 58.64%; genome coverage, $\sim 383\times$) (QUAST Web interface [20]). Annotation was carried out using the NCBI Prokaryotic Genome Automatic Annotation Pipeline version 4.8 (21) and predicted 4,332 genes, 4,283 coding DNA sequences (CDS), 49 RNA genes (4 rRNAs, 40 tRNAs, 5 noncoding RNAs [ncRNAs]), 162 pseudogenes, and 1 CRISPR array. ResFinder version 3.2 analyses (DTU, Denmark) (22) identified 34 beta-lactam resistance genes and 1 colistin resistance gene (see Table I at <https://doi.org/10.6084/m9.figshare.9828173>).

Analyses of metal resistance were performed using BLASTX with the BacMet2 experimentally confirmed resistance gene database version 2.0 (http://bacmet.biomedicine.gu.se/download/BacMet2_EXP_database.fasta) (23). A total of 195 genes were found to be associated with the bacterial chromosome, 25 genes were associated with plasmids, and 5 genes were present in both genetic elements. Resistance genes for Cu ($n = 30$), Zn ($n = 23$), Co ($n = 19$), Ni ($n = 17$), As ($n = 13$), Cd ($n = 12$), Fe ($n = 11$), Te ($n = 10$), and others (Sb, Ag, Cr, Hg, Mn, W, Mg, Se, Au, Mo, Al, V, Ga, and Pb) were identified (see Table II at <https://doi.org/10.6084/m9.figshare.9828173>).

Data availability. The genome sequence of CTe-01 has been deposited at the GenBank database under the accession number [VATZ00000000](https://www.ncbi.nlm.nih.gov/nuclseq/VATZ00000000). The raw data are available at the SRA under run number [SRR9052997](https://www.ncbi.nlm.nih.gov/sra/SRR9052997).

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REFERENCES

- de Jagoda SS, Wijewardana TG, Arulkanthan A, Igarashi Y, Tan E, Kinoshita S, Watabe S, Asakawa S. 2014. Characterization and antimicrobial susceptibility of motile aeromonads isolated from freshwater ornamental fish showing signs of septicemia. *Dis Aquat Organ* 109:127–137. <https://doi.org/10.3354/dao02733>.
- Walczak N, Puk K, Guz L. 2017. Bacterial flora associated with diseased freshwater ornamental fish. *J Vet Res* 61:445–449. <https://doi.org/10.1515/jvetres-2017-0070>.
- Liu ZG, Zheng AF, Chen MM, Lian YX, Zhang XK, Zhang SZ, Yu D, Li JK. 2018. Isolation and identification of pathogenic *Aeromonas veronii* from a dead Yangtze finless porpoise. *Dis Aquat Organ* 132:13–22. <https://doi.org/10.3354/dao03288>.
- da Silva LCA, Leal-Balbino TC, de Melo BST, Mendes-Marques CL, Rezende AM, de Almeida AMP, Leal NC. 2017. Genetic diversity and virulence potential of clinical and environmental *Aeromonas* spp. isolates from a diarrhea outbreak. *BMC Microbiol* 17:179. <https://doi.org/10.1186/s12866-017-1089-0>.
- Janda JM, Abbott SL. 2010. The genus *Aeromonas*: taxonomy, pathogenicity, and infection. *Clin Microbiol Rev* 23:35–73. <https://doi.org/10.1128/CMR.00039-09>.
- Igbinosa IH, Igumbor EU, Aghdasi F, Tom M, Okoh AI. 2012. Emerging *Aeromonas* species infections and their significance in public health. *ScientificWorldJournal* 2012:625023. <https://doi.org/10.1100/2012/625023>.
- Monti M, Torri A, Amadori E, Rossi A, Bartolini G, Casadei C, Frassinetti GL. 2019. *Aeromonas veronii* biovar *veronii* and sepsis—infrequent complication of biliary drainage placement: a case report. *World J Clin Cases* 7:759–764. <https://doi.org/10.12998/wjcc.v7.i6.759>.
- Zhou Y, Yu L, Nan Z, Zhang P, Kan B, Yan D, Su J. 2019. Taxonomy, virulence genes and antimicrobial resistance of *Aeromonas* isolated from extra-intestinal and intestinal infections. *BMC Infect Dis* 19:158. <https://doi.org/10.1186/s12879-019-3766-0>.
- Vincent AT, Trudel MV, Paquet VE, Boyle B, Tanaka KH, Dallaire-Dufresne S, Daher RK, Frenette M, Derome N, Charette SJ. 2014. Detection of variants of the pRAS3, pAB559, and pSN254 plasmids in *Aeromonas salmonicida* subsp. *salmonicida*: multidrug resistance, interspecies exchanges, and plasmid reshaping. *Antimicrob Agents Chemother* 58:7367–7374. <https://doi.org/10.1128/AAC.03730-14>.
- Skwor T, Shinko J, Augustyniak A, Gee C, Andraso G. 2014. *Aeromonas hydrophila* and *Aeromonas veronii* predominate among potentially pathogenic ciprofloxacin- and tetracycline-resistant *Aeromonas* isolates from Lake Erie. *Appl Environ Microbiol* 80:841–848. <https://doi.org/10.1128/AEM.03645-13>.
- Neupane S, Modry D, Pafčo B, Zurek L. 2019. Bacterial community of the digestive tract of the European medicinal leech (*Hirudo verbana*) from the Danube River. *Microb Ecol* 77:1082–1090. <https://doi.org/10.1007/s00248-019-01349-z>.
- Abdelhamed H, Lawrence ML, Waldbieser G. 2019. Complete genome sequence data of multidrug-resistant *Aeromonas veronii* strain MS-18–37. *Data Brief* 23:103689. <https://doi.org/10.1016/j.dib.2019.01.037>.
- Piotrowska M, Popowska M. 2015. Insight into the mobilome of *Aeromonas* strains. *Front Microbiol* 6:494. <https://doi.org/10.3389/fmicb.2015.00494>.
- Roh HJ, Kim B-S, Kim A, Kim NE, Lee Y, Chun W-K, Ho TD, Kim D-H. 2019. Whole-genome analysis of multi-drug-resistant *Aeromonas veronii* isolated from diseased discus (*Symphysodon discus*) imported to Korea. *J Fish Dis* 42:147–153. <https://doi.org/10.1111/jfd.12908>.
- Bennett PM. 2008. Plasmid encoded antibiotic resistance: acquisition and transfer of antibiotic resistance genes in bacteria. *Br J Pharmacol* 153:S347–S357. <https://doi.org/10.1038/sj.bjp.0707607>.
- Aminov RI. 2011. Horizontal gene exchange in environmental microbiota. *Front Microbiol* 2:158. <https://doi.org/10.3389/fmicb.2011.00158>.
- Rodríguez-Blanco A, Lemos ML, Osorio CR. 2012. Integrating conjugative elements as vectors of antibiotic, mercury, and quaternary ammonium compound resistance in marine aquaculture environments. *Antimicrob Agents Chemother* 56:2619–2626. <https://doi.org/10.1128/AAC.05997-11>.
- Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Pribelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell se-

- quencing. *J Comput Biol* 19:455–477. <https://doi.org/10.1089/cmb.2012.0021>.
19. Darling ACE, Mau B, Blattner FR, Perna NT. 2004. Mauve: multiple alignment of conserved genomic sequence with rearrangements. *Genome Res* 14:1394–1403. <https://doi.org/10.1101/gr.2289704>.
 20. Gurevich A, Saveliev V, Vyahhi N, Tesler G. 2013. QUILT: quality assessment tool for genome assemblies. *Bioinformatics* 29:1072–1075. <https://doi.org/10.1093/bioinformatics/btt086>.
 21. Tatusova T, DiCuccio M, Badretdin A, Chetvermin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI Prokaryotic Genome Annotation Pipeline. *Nucleic Acids Res* 44:6614–6624. <https://doi.org/10.1093/nar/gkw569>.
 22. Zankari E, Hasman H, Cosentino S, Vestergaard M, Rasmussen S, Lund O, Aarestrup FM, Larsen MV. 2012. Identification of acquired antimicrobial resistance genes. *J Antimicrob Chemother* 67:2640–2644. <https://doi.org/10.1093/jac/dks261>.
 23. Pal C, Bengtsson-Palme J, Rensing C, Kristiansson E, Larsson D. 2014. BacMet: antibacterial biocide and metal resistance genes database. *Nucleic Acids Res* 42:D737–D43. <https://doi.org/10.1093/nar/gkt1252>.