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Data Article

Complete genome sequence data of multidrug-resistant *Aeromonas veronii* strain MS-18-37

Hossam Abdelhamed [a,*], Mark L. Lawrence [a], Geoffrey Waldbieser [b]

[a] College of Veterinary Medicine, Mississippi State University, Mississippi State, MS, USA
[b] USDA-ARS Warmwater Aquaculture Research Unit, Thad Cochran National Warmwater Aquaculture Center, Stoneville, MS, USA

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ABSTRACT

Aeromonas are Gram-negative, non-spore forming rods belonging to the family *Aeromonadaceae* within the class *Gammaproteobacteria*. These facultative anaerobic bacteria are ubiquitous in aquatic environments and have a broad host range. We present here the complete genome sequence of multidrug-resistant *A. veronii* strain MS-18-37 isolated from diseased catfish. The genome size of this strain is 4,683,931, with a G+C content of 58.60%. Annotation reveals multiple genes that encode antibiotic resistance. The complete genome sequence of *A. veronii* strain MS-18-37 will provide a genetic basis for understanding molecular mechanisms of antimicrobial resistance and exchange in *Aeromonas*.

* Corresponding author.
E-mail addresses: Abdelhamed@cvm.msstate.edu (H. Abdelhamed), Lawrence@cvm.msstate.edu (M.L. Lawrence), Geoff.Waldbieser@ARS.USDA.GOV (G. Waldbieser).

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Specifications table

Subject area	Biology
More specific subject area	Microbiology and genomics.
Type of data	Complete genome sequence data in FASTA format.
How data was acquired	Nanopore GridION instrument and Illumina MiSeq.
Data format	Analyzed and assembled genome sequences.
Experimental factors	Genomic DNA was extracted from pure culture of *Aeromonas veronii* strain MS-18-37.
Experimental features	Whole genome sequencing, assembly, and annotation
Data source location	Strain MS-18-37 was isolated from a diseased catfish in 2018 from the Aquatic Diagnostic Laboratory at College of Veterinary Medicine, Mississippi State University, Mississippi State, USA.
Data accessibility	The complete genome sequence of *A. veronii* strain MS-18-37 is available in the National Center for Biotechnology Information (NCBI) under accession number CP033604 (https://www.ncbi.nlm.nih.gov/nuccore/CP033604.1/), BioProject number PRJNA504296 (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA504296/), and BioSample number SAMN10389897 (https://www.ncbi.nlm.nih.gov/assembly/GCA_003722175.1).
Related research	Abdelhamed et al. 2018. Complete Genome Sequence of Multidrug-Resistant *Edwardsiella ictaluri* Strain MS-17–156. Genome Announc [1] Abdelhamed et al. 2018. Complete Genome Sequence of Multidrug-Resistant *Plesiomonas shigelloides* Strain MS-17–188. Genome Announc [2]

Value of the data

- This genome sequence and annotation will be utilized to understand mechanisms of antimicrobial resistance in *Aeromonas* and *Gammaproteobacteria*.
- *Aeromonas* are regarded not only as important pathogens causing disease in fish and other poikilothermic species, but also as etiologic agents for clinical infections in mammals, including humans. The current sequence data will be useful for comparative genomics to determine genes and pathways involved in the pathogenicity of *Aeromonas* in multiple hosts.
- The genome data of *A. veronii* will be useful to the scientific community to enable investigation of functional and phylogenetic diversity of *Aeromonas* species.

1. Data

The overall data represents the genome sequencing, assembly, and annotation of multidrug-resistant *A. veronii* strain MS-18-37. The completed circularized genome of *A. veronii* strain MS-18-37 was found to be 4,683,931 bp and has a GC content of 58.60%. The genome contains 4329 genes, including 4083 coding sequences (CDS), 88 pseudogenes, and 158 RNAs (including 31 rRNAs [11, 10, and 10 for 5S, 16S, and 23 S, respectively], 122 tRNAs, and 4 ncRNAs). The complete genome of *A. veronii* strain MS-18-37 has 96.49% average nucleotide identity (ANI) with *A. veronii* strain B565 [3], 96.36% with *A. veronii* strain Ae52 (a multidrug-resistant isolate [4]), 96.41% with *A. veronii* strain TH0426 [5], and 96.37% with *A. veronii* strain AVNIH1 [6].

Comprehensive Antibiotic Resistance Database (CARD) analysis of the *A. veronii* strain MS-18-37 genomic data identified several antimicrobial resistance genes, including sulfonamide resistance (*sul1*), dihydrofolate reductase dfr (*dfrA12*) for trimethoprim resistance, EF-Tu for elfamycin resistance, CphA beta-lactamase (*cphA5*), resistance-nodulation-cell division (RND) antibiotic efflux pump (*adeF*), OXA

beta-lactamase (OXA-12), major facilitator superfamily (MFS) antibiotic efflux pump (*floR*), and resistance-nodulation-cell division (RND) antibiotic efflux pump (*tetE*). The resistance determinants were found to be associated with class 1 integron located in the *A. veronii* chromosome.

Analysis obtained from Rapid Annotation Subsystem Technology (RAST) server revealed that the *A. veronii* strain MS-18-37 genome contains 4307 coding sequence and 360 subsystems (Fig. 1). The most represented subsystem features are cofactors, vitamins, prosthetic croups, pigments (187 genes), membrane transport (113 genes), respiration (110 genes), stress response (70 genes), amino acids and derivatives (381 genes), carbohydrates (280 genes), virulence, disease and defense (58 genes), nucleosides and nucleotides (94 genes), and fatty acids, lipids, and isoprenoids (58 genes). RAST also identified a total of 43 genes associated with resistance to antibiotics and toxic compounds, including copper homeostasis (10 genes), cobalt-zinc-cadmium resistance (12 genes), mercuric reductase (1 gene), mercury resistance operon (1 gene), copper tolerance (8 genes), resistance to fluoroquinolones (4 genes), multidrug resistance efflux pumps (6 genes), and resistance to chromium compounds (1 gene).

2. Experimental design, materials and methods

A. veronii strain MS-18-37 was recovered from a diseased catfish in 2018 from the Aquatic Diagnostic Laboratory at the College of Veterinary Medicine, Mississippi State University. Strain MS-18-37 showed resistance to tetracycline, sulfamethoxazole-trimethoprim, florfenicol, and novobiocin. Genomic DNA of *A. veronii* strain MS-18-37 was extracted using the phenol-chloroform method. Long genomic DNA sequences were produced on a GridION instrument (Oxford Nanopore Technologies, Oxford, UK) using the RAD004 kit and v9.4.1 flow cells, and short genomic DNA sequences were produced on an Illumina MiSeq (Illumina Corp, LOCATION). The nanopore sequences were filtered to obtain 20,327 sequences with a minimum length of 30,000 bp and total yield of 876 Mb (37 × genome coverage). Corrected sequences were assembled into a single contig by Canu v1.7 [7].

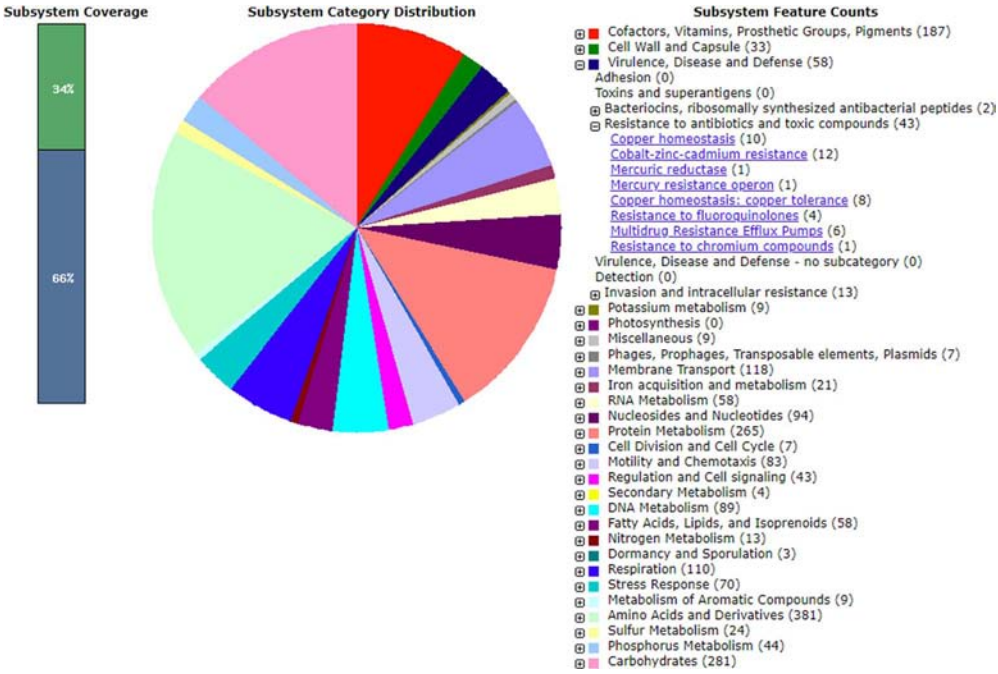

Fig. 1. The subsystem distribution of *A. veronii* strain MS-18-37 generated from RAST annotation server.

Paired Illumina sequences were aligned to the genomic contig at a depth of 233-fold using minimap2 [8]. Pilon v1.22 [9] was used to correct single nucleotide variants and insertions/deletions outside ribosomal DNA regions. Final Pilon operation corrected insertions/deletions along the entire contig. Average nucleotide identity (ANI) [10] was estimated using online calculators (http://enve-omics.ce.gatech.edu/ani/). Antibiotic resistance genes were predicted using Comprehensive Antibiotic Resistance Database (CARD) (https://card.mcmaster.ca/) [11]. Annotation of the genome was performed using the Rapid Annotation Subsystem Technology (RAST) sever (http://rast.nmpdr.org/) [12].

3. Nucleotide sequence accession numbers

The complete genome sequence of *A. veronii* strain MS-18-37 has been deposited in GenBank under accession number CP033604 (https://www.ncbi.nlm.nih.gov/nuccore/CP033604.1/).

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Transparency document. Supporting information

Transparency data associated with this article can be found in the online version at https://doi.org/10.1016/j.dib.2019.01.037.

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