



Draft Genome Sequence of *Aeromonas popoffii* ID682, Isolated from a Natural Water Source in Idaho

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ABSTRACT A draft genome sequence of *Aeromonas popoffii* ID682, isolated from a natural water source in Idaho, is presented here. *A. popoffii* is a relatively understudied species within a diverse, expanding freshwater genus of bacteria. Here, we describe only the second genome published for this species to date.

Aeromonas is a genus of Gram-negative bacteria found ubiquitously in aquatic environments (1). Many *Aeromonas* species have been shown to be opportunistic pathogens of a number of animal species (1–3) and present a treatment challenge due to developed antimicrobial resistance profiles (4, 5). Simultaneously, *Aeromonas* species have also been shown to be important beneficial symbionts of a number of organisms (6, 7). The species *Aeromonas popoffii* was first isolated from drinking water (8) and has been identified as an opportunistic human pathogen as well (9, 10). Here, we present a draft genome sequence of the novel strain *Aeromonas popoffii* ID682, isolated from a natural water source in Idaho.

A. popoffii ID682 was isolated from a surface swab sample of a submerged stone within a spring-fed pond draining into the Snake River using R2A agar (11) and incubated at 19°C. A single colony was streaked for isolation two consecutive times onto R2A agar to obtain a pure culture before being stocked at –80°C in a glycerol solution. Genomic DNA was extracted using the MasterPure DNA and RNA purification kit (Lucigen, Middleton, WI). DNA for all steps was quantified using the Qubit 1X double-stranded DNA (dsDNA) high-sensitivity (HS) assay kit (Invitrogen, Waltham, MA). A genome library was constructed using a DNA prep kit (Illumina, San Diego, CA) followed by 2 × 250-bp paired-end sequencing on a MiSeq device using a MiSeq reagent kit V2 (500 cycles) (Illumina, San Diego, CA). Following sequencing, raw reads were demultiplexed on BaseSpace and then downloaded for further processing.

CLC Genomics Workbench version 12.0.2 (Qiagen, Hilden, Germany) was used for read trimming (maximum ambiguities = 2, minimum accuracy = 95%, minimum read length = 60 bp) and *de novo* genome assembly (minimum contig length = 200, word size = 21, bubble size = 241) with default parameters. The draft genome sequence of *A. popoffii* ID682 was 4.68 Mb in size and was assembled into 128 contigs with an N_{50} value of 112 kbp. The G+C content was 58.6%, and the average genome coverage was 85× (Table 1).

The genome was annotated using the NCBI Prokaryotic Genome Annotation Pipeline version 5.1 (12). A total of 4,648 coding sequences were identified. Secondary metabolite gene detection was performed using antiSMASH version 5.1.2 with relaxed detection strictness (13–17). Aryl polyene, bacteriocin, homoserine lactone, and nonribosomal peptide synthetase gene clusters were identified. Species-level identification was performed with digital DNA–DNA hybridization (dDDH) using TYGS version 267 (18). The closest genome to the subject strain was *Aeromonas popoffii* CIP 105493, with a dDDH of 84.3% when using the recommended d_4 formula.

Data availability. The genome of *A. popoffii* ID682 has been deposited in DDBJ/ENA/GenBank under accession number [JAGRZL000000000](https://www.ncbi.nlm.nih.gov/nuccore/JAGRZL000000000). The version described in this paper is

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TABLE 1 Genome summary and database accession information

Characteristic	Data for <i>Aeromonas popoffii</i> ID682
No. of raw reads	1,670,148
No. of reads in assembly	1,648,648
Genome size (Mbp)	4.68
Genome coverage (×)	85
No. of contigs	128
N_{50} (bp)	112,388
G+C content (%)	58.6
No. of coding sequences	4,472
No. of protein-coding sequences	4,180
No. of tRNAs	90
No. of rRNAs	8
Closest neighbor, whole genome (% dDDH)	<i>Aeromonas popoffii</i> CIP 105493 (84.3)
BioProject accession no.	PRJNA720925
BioSample accession no.	SAMN18685274
SRA accession no.	SRR14245844
GenBank accession no.	JAGRZL000000000

the first version, [JAGRZL010000000](https://doi.org/10.1101/2012.625023). The BioProject, BioSample, SRA, and GenBank accession numbers are provided in Table 1.

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