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Draft Genome Sequence of the Type Strain *Aeromonas salmonicida* subsp. *salmonicida* ATCC 33658

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ABSTRACT Here, we report the draft genome sequence of the type strain *Aeromonas salmonicida* subsp. *salmonicida* ATCC 33658 isolated from *Salmo salar*. The size of the genome is 4,728,143 bp with a G+C content of 58.5%. The *A. salmonicida* subsp. *salmonicida* ATCC 33658 genome lacks essential virulence genes that were likely lost during genomic rearrangements.

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First described in the 19th century, *Aeromonas salmonicida* subsp. *salmonicida* is one of the oldest known fish pathogens. *A. salmonicida* subsp. *salmonicida* is an important pathogen due to its nearly worldwide distribution, broad host range, and potentially devastating impacts on wild and farm fish. *A. salmonicida* subsp. *salmonicida*, a Gram-negative, nonmotile gammaproteobacteria, is the etiological agent of the so-called "typical" furunculosis. *A. salmonicida* subsp. *salmonicida* ATCC 33658 (1), isolated from Atlantic salmon (*Salmo salar*), has been utilized as the type strain for phylogenetic (2), detection (3, 4), and pathogenesis studies (5, 6). Additionally, *A. salmonicida* subsp. *salmonicida* ATCC 33658 is the type strain for antimicrobial susceptibility testing of aquatic bacteria (7). Although it has been recognized that this strain has lost several virulence genes (6, 8), its genome remains uncharacterized. Here, we report the draft genome sequence of *A. salmonicida* subsp. *salmonicida* ATCC 33658, a nonvirulent strain that lacks the A-layer and type III secretion-related genes.

A. salmonicida subsp. *salmonicida* ATCC 33658 was routinely grown in Trypticase soy broth (TSA) (Difco) with aeration (180 rpm) at 15°C. The genomic DNA was extracted according to Wilson (9) and purified using silica (10). Sequencing was performed using the Illumina MiSeq next-generation sequencing platform (Universidad Mayor, Center for Genomics and Bioinformatics, Huechuraba, Chile) and paired-end libraries. Low-quality sequences were examined by FastQC version 0.10.1 (11). The sequences were trimmed and assembled using the CLC Genomics Workbench version 10.1.1 (Qiagen) *de novo* tool, which resulted in 119 contigs over 1 kb with an N_{50} of 89,474 bp. The total length of the draft genome of *A. salmonicida* subsp. *salmonicida* ATCC 33658 strain J208 was 4,728,143 bp with a G+C content of 58.5%.

The assembled sequences were annotated by the NCBI Prokaryotic Genome Annotation Pipeline (https://www.ncbi.nlm.nih.gov/genome/annotation_prok). The tRNAs were detected by tRNA scan-SE version 1.3 (12) and the rRNAs with RNAmmer (13). A total of 4,273 coding sequences, 208 pseudogenes, 5 complete rRNA operons (5S-16S-23S), 81 tRNAs, and 4 noncoding RNAs were predicted by the pipeline.

The S-layer of *A. salmonicida* subsp. *salmonicida* is an essential virulence factor that allows *A. salmonicida* subsp. *salmonicida* to resist the complement and ultimately infects and kills the fish host. (14–16). The S-layer is an array formed by the VapA protein (17), whose encoding gene is susceptible to inactivation by thermal inducible insertion elements (IS) (18, 19). We found that the *vapA* gene is truncated, likely by an IS during previous culture and passages. As a consequence, *A. salmonicida* subsp.

salmonicida ATCC 33658 shows an A$^-$ phenotype and no expression of the VapA protein (20). Also, as described previously (8), *A. salmonicida* subsp. *salmonicida* ATCC 33658 lacks type III secretion-related genes, like *acsV* and *ascR*.

The resistome was identified using the Comprehensive Antibiotic Resistance Database (21). MCR-3 related to polymyxin resistance (contig 119, 224 to 1,849 bp) and carbapenem-hydrolyzing metallo-beta-lactamase (*cphA5*) related to beta-lactam resistance (contig 83, 10,993 to 11,754 bp) genes were identified. *A. salmonicida* subsp. *salmonicida* ATCC 33658 is susceptible to ampicillin and polymyxin, suggesting that these genes are inactive or require activation.

Accession number(s). This whole-genome shotgun project (BioProject PRJNA310296) has been deposited at DDBJ/EMBL/GenBank under accession number LSGW00000000. The version described here is the first version, LSGW01000000.

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