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PROKARYOTES

Draft Genome Sequence of Fish Pathogen *Aeromonas bestiarum* GA97-22

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

[a]College of Veterinary Medicine, Mississippi State University, Mississippi State, Mississippi, USA

[b]Warmwater Aquaculture Research Unit, Agricultural Research Service, U.S. Department of Agriculture, Stoneville, Mississippi, USA

[c]Department of Biological Sciences, Auburn University, Auburn, Alabama, USA

[d]Recombinetics, St. Paul, Minnesota, USA

[e]Animal Genomics and Improvement Laboratory, Agricultural Research Service, U.S. Department of Agriculture, Beltsville, Maryland, USA

ABSTRACT *Aeromonas bestiarum* is a Gram-negative mesophilic motile bacterium causing acute hemorrhagic septicemia or chronic skin ulcers in fish. Here, we report the draft genome sequence of *A. bestiarum* strain GA97-22, which was isolated from rainbow trout in 1997. This genome sequence will improve our understanding of the complex taxonomy of motile aeromonads.

Aeromonas species are autochthonous to aquatic environments and cause disease in fish and mammals. *Aeromonas hydrophila*, *A. veronii*, *A. sobria*, *A. caviae*, and *A. bestiarum* species are causative agents of motile aeromonad septicemia (MAS) (1–3). *A. bestiarum* is a mesophilic motile aeromonad first described in 1996 (2), and it causes hemorrhagic septicemia and skin ulcers in fish (2, 4–6).

The genome sequencing of *A. bestiarum* strain GA97-22 was conducted with an Illumina Genome Analyzer IIx, and the draft genome sequence was obtained by adaptor trimming, quality control, and *de novo* assembly by using CLC Workbench 6.5.1 (CLC Bio) and Sequencher 5.4.5 (Gene Codes Corporation). Genome assembly included 6,380,282 reads (143× coverage of the genome), and the draft genome was annotated by using Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (7) and Rapid Annotations using Subsystems Technology (RAST) (8). The draft genome of *A. bestiarum* strain GA97-22 is 4,714,837 bp (26 contigs) and has a G+C content of 60.5%. It contains 4,349 predicted genes encoding 4,247 proteins, and no plasmid sequences were identified.

Average nucleotide identity (ANI) calculation (9) was used to differentiate *A. bestiarum* from other *Aeromonas* species using 95% ANI as the species cutoff (10). The calculated ANI between *A. bestiarum* strain GA97-22 and the reference *A. bestiarum* strain CECT 4227 (GenBank accession number NZ_CDDA00000000) was 97.1%. A lower ANI value (88.3%) was obtained between *A. bestiarum* strain GA97-22 and the catfish isolate *A. hydrophila* strain ML09-119 (11). Similarly, the ANI value between *A. bestiarum* strain GA97-22 and *A. salmonicida* subsp. *salmonicida* A449 (12) was below the species cutoff (89.7%).

A type 3 secretion system (T3SS), the chitobiose-specific regulators ChbF and ChbR, O polysaccharide, cold shock protein CspG, and cytoplasmic copper homeostasis protein CutC are unique to *A. bestiarum* strain GA97-22 compared to the reference *A. bestiarum* genome CECT 4227. Also, a type 6 secretion system and mannose-sensitive hemagglutinin type 4 pilus system are unique to *A. bestiarum* strain GA97-22 compared

Received 8 May 2018 **Accepted** 9 May 2018 **Published** 14 June 2018

Citation Kumru S, Tekedar HC, Griffin MJ, Waldbieser GC, Liles MR, Sonstegard T, Schroeder SG, Lawrence ML, Karsi A. 2018. Draft genome sequence of fish pathogen *Aeromonas bestiarum* GA97-22. Genome Announc 6:e00524-18. https://doi.org/10.1128/genomeA.00524-18.

Address correspondence to Attila Karsi, karsi@cvm.msstate.edu.

to *A. hydrophila* strain ML09-119 and *A. salmonicida* subsp. *salmonicida* A449, respectively.

Accession number(s). The draft genome sequence of *A. bestiarum* strain GA97-22 was submitted to GenBank under the accession number PPUX01000000.

ACKNOWLEDGMENTS

This work was funded by the U.S. Department of Agriculture (USDA), including the efforts of Attila Karsi, Mark R. Liles, Matt J. Griffin, and Mark L. Lawrence (NIFA grant 2013-67015–21313 to the Mississippi State University College of Veterinary Medicine) and the efforts of Geoffrey C. Waldbieser (USDA Agricultural Research Service CRIS project 6402-31000-009-00D).

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