



Three Draft Genome Sequences of *Vibrio coralliilyticus* Strains Isolated from Bivalve Hatcheries

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ABSTRACT Reported here are the genome sequences of three *Vibrio coralliilyticus* isolates RE87, AIC-7, and 080116A. Each strain was isolated in association with oyster larvae in commercial aquaculture systems. These draft genomes will be useful for further studies in understanding the genomic features contributing to *V. coralliilyticus* pathogenicity.

Vibrio coralliilyticus is a known pathogen of corals (1) and shellfish, including Pacific oyster (*Crassostrea gigas*) larvae (2–5). In order to further the understanding of the genomic repertoire of *V. coralliilyticus*, particularly isolates pathogenic to oyster larvae, we sequenced three strains isolated from oyster aquaculture facilities. Strain RE87 was isolated in 2000 from dying *C. gigas* seed at a Hawaii nursery. Strain AIC-7 was isolated from a vibriosis outbreak among Eastern oysters (*Crassostrea virginica*) in 2015 at a hatchery in New Jersey. Strain 080116A was isolated in 2016 from *C. gigas* larvae tanks at an Oregon hatchery. All three strains demonstrated a degree in pathogenicity in preliminary pathogenicity challenges with *C. gigas* larvae (80 to 100% larval mortalities after 48 h [our unpublished data]).

DNA from overnight cultures was isolated and the Nextera XT kit (Illumina) was used to prepare libraries for sequencing on a MiSeq Illumina platform at the Center for Genome Research and Biocomputing at Oregon State University. Each genome library was sequenced with 250-bp paired-end reads at an estimated minimum coverage of 65-fold. The resulting reads were trimmed and quality filtered ($Q > 28$, minimum read length 150 bp) using Sickle (6) and randomly subsampled to an estimated coverage of 50-fold. Reads were subsequently *de novo* assembled using IDBA-UD (7). The assembly for strain RE87 had a genome size of 5.59 Mbp (45.8% GC), 49 contigs ($N_{50} = 335,391$ bp), and a maximum contig size of 1,074,445 bp; the assembly for strain AIC-7 resulted in a genome size of 5.95 Mbp (45.3% GC), 65 contigs ($N_{50} = 274,060$ bp), and a maximum contig size of 1,201,114 bp; and the assembly for strain 080116A had a genome size of 5.63 Mb (45.7% GC), 107 contigs ($N_{50} = 275,484$ bp), and a maximum contig size of 1,249,611 bp.

Gene predictions for the draft assemblies were performed using Prokka version 1.11 (8) and Rapid Annotation using Subsystem Technology (RAST) (9). There were 5,145, 5,542, and 5,205 coding sequences detected for strains RE87, AIC-7, and 080116A, respectively. Proteinortho (10) detected 1,813 orthologous clusters that were shared among the three isolates, representing 57 to 62% of the predicted proteome of each genome. Strain RE87 has 266 unique genes, AIC-7 has 504, and 080116A has 287. To compare genome similarities with other *V. coralliilyticus* strains, average nucleotide identities (ANI) were calculated using Enviomics (11). ANI values for each strain with *V. coralliilyticus* strains ATCC BAA-450 (12), RE98 (13), OCN014 (14), and 58 (15) were >96%, corresponding to grouping at the species level (16, 17). All three strains had

Received 14 September 2017 **Accepted** 18 September 2017 **Published** 12 October 2017

Citation Kehlet-Delgado H, Richards GP, Häse C, Mueller RS. 2017. Three draft genome sequences of *Vibrio coralliilyticus* strains isolated from bivalve hatcheries. Genome Announc 5:e01162-17. <https://doi.org/10.1128/genomeA.01162-17>.

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open reading frames displaying 99% homology to the *VtpA* extracellular zinc metalloprotease of *V. coralliilyticus* RE98, a known virulence factor for *C. gigas* (18). A more in-depth genomic analysis of these and other *V. coralliilyticus* strains will be conducted for a future publication.

Accession number(s). This whole-genome shotgun project has been deposited in GenBank under the accession numbers [NRHY00000000](#) (RE87), [NRQO00000000](#) (AIC-7), and [NRHV00000000](#) (080116A). The versions described in this paper are the first versions.

ACKNOWLEDGMENTS

This study was funded by Agriculture and Food Research Initiative grant 2015-08632 of the USDA National Institute of Food and Agriculture.

The use of trade names or commercial products in this publication is solely for the purpose of providing specific information and does not imply recommendation or endorsement by the USDA.

We thank Mark Dasenko at the Center for Genome Research Biocomputing at Oregon State University for help with library preparation and sequencing and David Madison for advice regarding pathogenicity tests.

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