

Complete Genome Sequence for the Shellfish Pathogen *Vibrio coralliilyticus* RE98 Isolated from a Shellfish Hatchery

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***Vibrio coralliilyticus* is a pathogen of corals and larval shellfish. Publications on strain RE98 list it as a *Vibrio tubiashii*; however, whole genome sequencing confirms RE98 as *V. coralliilyticus* containing a total of 6,037,824 bp consisting of two chromosomes (3,420,228 and 1,917,482 bp) and two megaplasmids (380,714 and 319,400 bp).**

Received 6 November 2014 Accepted 10 November 2014 Published 18 December 2014

Citation Richards GP, Bono JL, Watson MA, Needleman DS. 2014. Complete genome sequence for the shellfish pathogen *Vibrio coralliilyticus* RE98 isolated from a shellfish hatchery. *Genome Announc.* 2(6):e01253-14. doi:10.1128/genomeA.01253-14.

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Vibrio coralliilyticus is a well-known coral pathogen responsible for coral bleaching and the associated losses to coral reefs worldwide (1, 2). It was also shown to infect a variety of shellfish larvae including Pacific oyster (*Crassostrea gigas*) larvae (3, 4). Another reported pathogen of Pacific as well as Eastern oyster (*C. virginica*) larvae is *Vibrio tubiashii*, which causes high mortalities in oyster and clam hatcheries and potentially in the wild (5–8). Some marine isolates thought to be *V. tubiashii*, like RE22 and the American Type Culture Collection strain ATCC 19105, have been identified by sequencing as *V. coralliilyticus* (9). Strain RE98, previously thought to be a *V. tubiashii* (8, 10), is particularly virulent toward larval oysters and clams and is identified in this paper by complete genome sequencing as *V. coralliilyticus*. A comparison of mortalities of Eastern and Pacific oyster larvae to RE98 indicate that this strain is most pathogenic among five strains of *V. coralliilyticus* tested (11). The misidentification of several *V. coralliilyticus* as *V. tubiashii* has complicated the discernment of the roles of these pathogens in larval shellfish mortalities and as potential etiological agents involved in coral bleaching.

The genome of *V. coralliilyticus* RE98 was sequenced using a PacBio RS II system (Pacific Biosciences, Menlo Park, CA) on single-molecule real-time (SMRT) cells using PacBio P5–C3 chemistry. Subread filtering was performed with the SMRT Analysis Software suite (12), error correction and assembly was conducted with Celera Assembler v8.1 (13), overlapping ends were trimmed using Geneious v7.1.5 (Biomatters, Auckland, New Zealand) and polished with Quiver (12). Coverage was 20×, and assemblies gave a consensus accuracy of 99.9996 to 100%. The fully assembled and closed genome contains 6,037,824 bp consisting of two chromosomes and two megaplasmids. Chromosome 1 is 3,420,228 bp, chromosome 2 is 1,917,482 bp, and the two megaplasmids (P381 and P319) are 380,714 and 319,400 bp, respectively. This is the first complete genome sequence for this species.

Genome annotation for *V. coralliilyticus* RE98 was acquired from the NCBI Prokaryotic Genome Annotation Pipeline (Bethesda, MD) and revealed 5,718 genes, 5,467 coding sequences, 98 pseudogenes, 34 rRNAs (5S, 16S, and 23S), 116

tRNAs, 3 noncoding RNA, and 11 frameshift genes. A Blast search of chromosomes 1 and 2 using the NCBI whole-genome shotgun (WGS) contig database, limited by organism (*Vibrionaceae*), showed >97% sequence similarity to other *V. coralliilyticus*.

Nucleotide sequence accession numbers. The complete genomic sequence of *V. coralliilyticus* RE98 (chromosomes 1 and 2 and its two megaplasmids) has been deposited in GenBank under accession no. CP009617, CP009618, CP009619, and CP009620.

ACKNOWLEDGMENTS

This work was supported in part by the USDA, Agricultural Research Service CRIS project no. 1935-42000-065-00D, “Pathogen Detection and Intervention Methods for Shellfish.”

We declare that we have no conflicts of interest.

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 United States Department of Agriculture (USDA).

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