

# Draft Genome Sequence of Hawaiian Sea Slug Symbiont *Vibrio* sp. Strain ER1A

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**Bacteria belonging to the genus *Vibrio* are prevalent in the marine environment and are known for forming symbiotic relationships with hosts. *Vibrio* sp. strain ER1A is a dominant symbiont of the Hawaiian sea slug, *Elysia rufescens*. Here we report the draft genome sequence of *Vibrio* sp. ER1A.**

Received 22 July 2014 Accepted 28 July 2014 Published 21 August 2014

**Citation** Davis J, Hill RT. 2014. Draft genome sequence of Hawaiian sea slug symbiont *Vibrio* sp. strain ER1A. *Genome Announc.* 2(4):00820-14. doi:10.1128/genomeA.00820-14.

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**V**ibrios are a diverse group of bacteria that are widely distributed in the marine environment and form both mutualistic and parasitic relationships with a variety of hosts (1). Many of the well-studied vibrios, *V. cholerae*, *V. vulnificus*, and *V. parahaemolyticus* are responsible for human diseases, including gastroenteritis and wound sepsis (1, 2). With the exception of the mutualistic symbiont *V. fischeri* of the Hawaiian bobtail squid, there is little known about symbiotic *Vibrio* spp., that are not parasitic to their marine host. Consequently there is a need to characterize symbiotic vibrios to understand their ecological importance in relation to host function and health.

In this study we examine the genome of a symbiotic *Vibrio* sp. strain ER1A that has been continuously cultured over several years and is a major component of the bacterial community associated with Hawaiian sea slug, *Elysia rufescens* (3).

*Vibrio* sp. strain ER1A was isolated from *E. rufescens* and was grown overnight in MB2216 at 30°C with shaking. Genomic DNA from the bacterial cells was extracted using the Mo Bio Ultra-Clean Microbial DNA isolation kit (Mo Bio Laboratories Inc., Carlsbad, CA) following the manufacturer's instructions.

*Vibrio* sp. strain ER1A was sequenced at the Institute of Marine and Environmental Technology (IMET) in Baltimore, Maryland using the Nextera XT kit with 250-bp paired-end read sequencing on an Illumina MiSeq. The 3,959,866 raw reads had an average length of 210 bps and represented 833,381,541 total bases. One hundred eight contigs (>1,000 bps) with a total size of 6,092,013 were assembled from the raw reads using CLC Main Workbench Genome Finishing Module version 7.0 (CLC Inc, Aarhus, Denmark), which resulted in about 140× coverage. The minimum contig length is 1,224 bps and the maximum contigs length is 1,593,462 bps. The overall G+C content of *Vibrio* sp. strain ER1A is 44%. The genome sequence was annotated using the NCBI Prokaryotic Genomes Annotation Pipeline (PGAP) (4) version 2.0 ([http://www.ncbi.nlm.nih.gov/genome/annotation\\_prok/](http://www.ncbi.nlm.nih.gov/genome/annotation_prok/)) A total of 5,202 coding sequences were predicted and 8 rRNA and 70 tRNAs were annotated. The biosynthetic gene cluster potential of *Vibrio* sp. ER1A was accessed using antiSMASH 2.0 (5) and resulted in the identification of two biosynthetic gene clusters: a putative nonribosomal peptide synthetase independent sidero-

phore biosynthetic gene cluster and a putative homoserine lactone biosynthetic gene cluster. The presence of these types of clusters sheds light on the lifestyle within a marine invertebrate host, where both the acquisition of iron, and the coordination of community behaviors (quorum sensing) are important (6).

We have obtained a draft-genome sequence of a symbiotic *Vibrio* sp. strain ER1A, associated with the Hawaiian sea slug, *E. rufescens*. The genome sequence provides a basis for studying the potential ecological roles of non-parasitic *Vibrio* spp. associated with marine hosts, as additional genome sequences become available from these symbiotic bacteria.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has deposited in DDBJ/EMBL/GenBank under accession no. [JPJA00000000](https://ncbi.nlm.nih.gov/nucl/JPJA00000000). The version described in this paper is the first version, JPJA01000000.

## ACKNOWLEDGMENTS

This research was funded by U.S. National Science Foundation grant IOS-0919728.

We thank the Institute of Marine and Environmental Technology Bio-analytical Service Laboratory for performing the sequencing. We are grateful to Mohamed Donia for performing the antiSMASH analysis. We thank Tsvetan Bachvaroff for his bioinformatics guidance and Mark Hamann for advice on collection of *E. rufescens*. J.D. thanks Tamara Hamilton, National Science Foundation, Louis Stokes Alliance for Minority Participation (LSAMP)-Bridge to the Doctorate Graduate Fellowship for support. Rosemary Jagus and the National Oceanic & Atmospheric Administration, Living Marine Resource Cooperative Science Center (LM-RCS) Graduate Fellowship are thanked for scholarship funding for J.D.

This is IMET contribution no. 14-129 and UMCES contribution no. 4940.

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