Draft Genome Sequences of Shewanella sp. Strain UCD-FRSP16_17 and Nine Vibrio Strains Isolated from Abalone Feces

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We present here the draft genome sequences for nine strains of Vibrio (V. cyclitrophicus, V. splendidus, V. tasmaniensis, and three unidentifed) and one Shewanella strain. Strains were isolated from red (Haliotis rufescens) and white (Haliotis sorenseni) abalone, with and without exposure to "Candidatus Xenohaliotis californiensis," the causative agent of abalone withering syndrome.

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Withering abalone syndrome ("Candidatus Xenohaliotis californiensis" infection) has caused a large decline in the population of abalone in coastal California in recent years (1). In this study, we isolated bacteria from the feces of both red abalone (Haliotis rufescens) and white abalone (Haliotis sorenseni) with and without exposure to "Ca. Xenohaliotis californiensis." All of the resulting strains for which we obtained genome sequence data were either Vibrio or Shewanella species. Vibrio is a genus of Gram-negative marine bacteria that can cause illness (e.g., cholera and vibriosis) in humans and animals. Shewanella species are normal flora of shellfish and are not known to cause disease.

Abalone feces were streaked onto seawater agar (15.0 g of agar, 5.0 g of peptone, 2.0 g of beef extract, 0.5 g of KNO3, and 1.0 liter of InstantOcean), Columbia blood agar, lysogeny broth (LB), and Difco seawater medium. Liquid cultures were prepared from single colonies and grown at room temperature for four days. DNA was isolated using a Qiagen DNeasy blood and tissue kit. A 16S rRNA gene product was amplified using the 1391R (5'-GACGGGC GGTGTTGTRCA-3') and 27F (5'-AGAGTTTGATCMTGGCTCAG-3') universal primers. Isolates were identified by Sanger sequencing of the PCR product. Sequencing libraries were constructed using a Kapa HyperPlus kit, and libraries were size selected to 600 to 900 bp using a BluePippin platform (Sage Science). Paired-end (PE) 300-bp sequencing was performed on an Illumina MiSeq platform.

An average of 682,098 reads were generated for each of the Vibrio strains, and 534,102 reads were generated for the Shewanella strain (Table 1). All sequence processing and assembly was performed using the A5-miseq assembly pipeline (version 20150522). This pipeline automates the processes of data cleaning, error correction, contig assembly, and quality control (2, 3).

The final Vibrio assemblies had an average of 66 contigs, with an average genome size of 4.85 Mbp and an assembly N50 of 510,207 bp (Table 1). The assembly for Shewanella sp. strain UCD-FRSP16_17 contained 51 contigs, a genome size of 5 Mbp,

### TABLE 1 Genome assembly information

| Strain | Accession no. | Host species | WS exposure | Contigs | Genome size (bp) | N50 (bp) | No. of raw reads (×) | Coverage of RNAs | No. of genes | No. of RNAs |
|--------|---------------|--------------|-------------|---------|------------------|----------|---------------------|-----------------|--------------|-------------|
| Vibrio cyclitrophicus UCD-FRSP16_1 | LZFR000000000 | H. rufescens | Exposed | 66 | 5,051,153 | 373,940 | 821,306 | 49 | 4,362 | 198 |
| Vibrio cyclitrophicus UCD-FRSP16_8 | LZFZ000000000 | H. rufescens | Exposed | 64 | 5,018,558 | 550,710 | 722,502 | 43 | 4,351 | 199 |
| Vibrio sp. UCD-FRSP16_10 | LZFX000000000 | H. rufescens | Exposed | 81 | 3,599,647 | 147,192 | 717,028 | 60 | 3,168 | 155 |
| Vibrio splendidus UCD-FRSP16_15 | LZGA000000000 | H. rufescens | Unexposed | 44 | 5,379,662 | 819,026 | 577,438 | 32 | 4,658 | 179 |
| Vibrio cyclitrophicus UCD-FRSP16_18 | LZTF000000000 | H. rufescens | Unexposed | 50 | 5,046,131 | 354,326 | 710,666 | 42 | 4,394 | 184 |
| Vibrio tasmaniensis UCD-FRSP16_25 | LZE000000000 | Unknown | Unknown | 39 | 5,556,487 | 968,710 | 643,116 | 35 | 4,827 | 175 |
| Vibrio sp. UCD-FRSP16_30 | LZFW000000000 | H. rufescens | Exposed | 85 | 3,606,693 | 175,784 | 667,338 | 56 | 3,167 | 151 |
| Vibrio cyclitrophicus UCD-FRSP16_31 | LZFU000000000 | Unknown | Unexposed | 94 | 4,963,458 | 495,080 | 640,182 | 39 | 4,330 | 192 |
| Vibrio tasmaniensis UCD-FRSP16_35 | LZFY000000000 | H. rufescens | Exposed | 73 | 5,660,313 | 390,830 | 778,512 | 41 | 4,963 | 180 |
| Shewanella sp. UCD-FRSP16_17 | LZFV000000000 | H. sorenseni | Unexposed | 66 | 4,853,869 | 510,207 | 682,098 | 44 | 4,232 | 177 |

WS, Withering Syndrome.
and an N50 of 603,668 bp. Completeness of the genomes was assessed using the PhyloSift software (4), which searches for a list of 37 highly conserved single-copy marker genes (5), of which all 37 were found in all assemblies.

Automated annotation was performed using the RAST annotation server (6). Shewanella sp. UCD-FRSSP16_17 contains an estimated 4,319 protein-coding sequences and 125 noncoding RNA sequences. The Vibrio isolates contain an estimated average 4,232 protein-coding sequences and 177 noncoding RNA sequences (Table 1).

Taxonomy was determined for Shewanella sp. UCD-FRSSP16_17 by taking the full-length 16S rRNA sequence from RAST, adding to an alignment of Shewanella strains at the Ribosomal Database Project (RDP) (7), and inferring a maximum-likelihood tree with FastTree (8). Because the resulting tree contained polyphyletic clades and significant ambiguity, we did not assign a species name to this isolate. For all Vibrio strains, we generated a whole-genome concatenated marker tree. This tree was inferred from an alignment of 441 Vibrio genomes and contained mostly well-supported monophyletic clades that allowed us to assign species names to the V. cyclitrophicus, V. splendidus, and V. tasmaniensis isolates.

Accession number(s). All 10 assemblies described in this paper have been deposited as whole-genome shotgun projects in DDBJ/EMBL/GenBank under the accession numbers provided in Table 1.

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