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Draft Genome Sequences of the Fish Pathogen Vibrio harveyi Strains VH2 and VH5

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Vibrio harveyi is an important marine pathogen that is responsible for vibriosis outbreaks in cultured fish and invertebrates worldwide. Here, we announce the draft genome sequences of V. harveyi strains VH2 and VH5, isolated from farmed juvenile Seriola dumerili during outbreaks of vibriosis in Crete, Greece.

V. harveyi is a marine bacterium that can be pathogenic to a wide range of organisms, especially fish and invertebrates (1, 2). The bacterium can cause mass mortalities in aquaculture species with significant economic impact for the industry. Several fish species can be infected by V. harveyi, including gilthead sea bream, European sea bass, common dentex, and Senegalese sole (3, 4). The virulence determinants of the pathogen have not been fully elucidated, however, and it has been suggested that they include biofilm formation, extracellular products, and quorum-sensing mechanisms (1). Here, we report the draft genomes sequences of Vibrio harveyi strains VH2 and VH5, which were isolated from juvenile Seriola dumerili during a vibriosis outbreak in Crete, Greece.

V. harveyi strains VH2 and VH5 were grown overnight at 22°C with agitation in Luria broth (MO BIO, no. 12106-05) supplemented with 1.7% NaCl. Genomic DNA was extracted using the QIAamp DNA miniKit (QIAGEN) according to the manufacturer’s protocol. A sequencing library was prepared using the Illumina HiSeq platform (BGI, China) with paired-end read sizes of 100 bp. A total of 10,356,788 paired-end reads for strain VH2 and 9,876,345 paired-end reads for strain VH5 were used for de novo assembly in Geneious version 7.1.7 (5). Short and low-coverage contigs were filtered out, resulting in a set of 107 contigs with an average coverage of 99× (N50 110 Kbp), and 121 contigs with coverage of 105× (N50 101 Kbp) for V. harveyi strains VH2 and VH5, respectively. Annotation was performed by the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP) (6). Additionally, the genomes were analyzed on the Rapid Annotation using Subsystems Technology (RAST) server (7). Genome comparison was achieved using Mauve version 2.4.0 (8). Acquired antibiotic resistance genes were identified using ResFinder version 2.1 (9), virulence factors by VirulenceFinder version 1.2 (10), and prophage-related sequences using PHAST (11).

The final assembly for V. harveyi strain VH2 had a total length of 5,685,755 bp and a G + C content of 45%. Genome annotation resulted in 5,079 coding sequences (CDSs), 33 tRNAs, 38 pseudogenes, and 3 rRNAs. V. harveyi strain VH5 had a total length of 5,916,358 bp, and a G + C content of 44.9%. Genome annotation resulted in 5,254 CDSs, 93 tRNAs, 56 pseudogenes, and 3 rRNA sequences.

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