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Draft Genome Sequence of *Vibrio parahaemolyticus* VH3, Isolated from an Aquaculture Environment in Greece

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***Vibrio parahaemolyticus* is an important foodborne pathogen responsible for gastroenteritis outbreaks globally. It has also been identified as an important pathogen in aquatic organisms. Here, we report a draft genome sequence of *V. parahaemolyticus*, strain VH3, isolated from farmed juvenile greater amberjack, *Seriola dumerili*, in Greece.**

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Vibrio parahaemolyticus is one of the most important foodborne pathogens globally. Infections are almost exclusively associated with the consumption of raw or improperly cooked contaminated seafood (1, 2). Clinical characteristics include watery diarrhea, abdominal cramps, nausea, and fever (3, 4). However, *V. parahaemolyticus* infections are not exclusive to humans and have recently been demonstrated to be a major source of disease in aquaculture production (5, 6). Therefore, monitoring of this pathogenic *Vibrio* species in aquaculture environments is important for both the aquaculture industry and human health. In the present study, *V. parahaemolyticus* VH3 was isolated from the aquaculture facility of the Institute of Aquaculture of the Hellenic Centre for Marine Research (HCMR) at the port of Heraklion, Greece, during a vibriosis outbreak in juvenile greater amberjack.

Genomic DNA of *V. parahaemolyticus* VH3 was extracted using the QIAamp DNA minikit (Qiagen) according to the manufacturer's protocol. The genome was sequenced by standard shotgun sequencing methods using a 454 GS-FLX Titanium sequencing system (Roche). The sequence data consisted of 5,600,000 reads (average length, 79 bp), providing 89-fold coverage. *De novo* assembly of the whole sequencing reads was performed with a GS De Novo Assembler. A total of 67 contigs, with a minimum length of 943 bp and a maximum length of 592,284 bp (N_{50}, 187.7 kbp), were obtained. Annotation was performed by the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP) (7). Additionally, the genome was screened for presence of specific genetic markers for *V. parahaemolyticus* (*tlh, tdh, trh*, *orf8*, and *toxRSnew*) (8), prophages (9), virulence factors (10), and antibiotic resistance genes (11).

The draft genome of *V. parahaemolyticus* VH3 was 4,955,051 bp in length, with a G+C composition of 45.3%. Genome annotation resulted in 4,338 coding sequences (CDS), 39 tRNAs, 37 pseudogenes, and 4 rRNAs. One phage-related sequence of 12.5 kb was found. Virulence factors related to adhesion (arylsulfatases and colonization factor Acfa), hemolysin, metalloproteases, and *Mycobacterium* virulence operon and multidrug resistance efflux pumps were found. Antibiotic resistant genes were detected for fluoroquinolones and tetracycline.

To the best of our knowledge, this is the first genome report of a *V. parahaemolyticus* strain isolated in an aquaculture system in Greece. The current sequence data generated here will contribute to the understanding of genome variability of *V. parahaemolyticus* isolates in future genomic studies.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at GenBank under the accession number LCVL00000000. The version described in this paper is version LCVL01000000.

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