

Draft Genome Sequence of the Fish Pathogen *Vibrio harveyi* Strain ZJ0603

Yucong Huang,^{a,b} Jichang Jian,^{a,b} Yishan Lu,^{a,b} Shuanghu Cai,^{a,b} Bei Wang,^{a,b} Jufen Tang,^{a,b} Huanying Pang,^{a,b} Yu Ding,^{a,b} and Zaohe Wu^{b,c}

Fisheries College, Guangdong Ocean University, Zhanjiang, China^a; Guangdong Provincial Key Laboratory of Pathogenic Biology and Epidemiology for Aquatic Economic Animals, Zhanjiang, China^b; and Zhongkai University of Agriculture and Engineering, Guangzhou, China^c

***Vibrio harveyi* is an important pathogen that causes vibriosis in various aquatic organisms. Here, we announce the draft genome sequence of *V. harveyi* strain ZJ0603, which was isolated from diseased Orange-spotted grouper (*Epinephelus coioides*) in Guangdong, China.**

Vibrio harveyi has been identified as an opportunistic pathogen that causes serious production losses in marine fish farms, with mortality up to 100%, particularly in juvenile populations (9). In addition to marine fish, *V. harveyi* is also an important agent capable of infecting a wide range of aquatic animals, including shrimp, seahorse, bivalves, cephalopods, and elasmobranchs (1). *V. harveyi* has caused recurrent outbreaks of the form of vibriosis known as “skin ulcer disease” in Orange-spotted grouper (*Epinephelus coioides*) in Guangdong Province of China since 2008 (8). To date, although a number of virulence-related genes have been identified in *V. harveyi*, the pathogenic mechanism of *V. harveyi* remains unclear (7). It is known that quorum-sensing systems, lipopolysaccharide, and extracellular products, including alkaline proteases, metalloproteases, and hemolysins, are involved in *V. harveyi* infection (5). It is generally believed that genome sequence information could greatly strengthen our understanding of the molecular pathogenic mechanisms of *V. harveyi*. Here, we report the complete genome sequence of *V. harveyi* strain ZJ0603, which was isolated from diseased Orange-spotted grouper after a vibriosis outbreak in Guangdong Province, China.

Genomic DNA was isolated from overnight cultures by using a Wizard genomic DNA purification kit (Fermentas MBI, Hanover, MD). The genomes were sequenced by Beijing Genomics Institute (BGI; Shenzhen, China) by using high-throughput paired-end Illumina sequencing technology, according to the manufacturer’s instructions, with 98-fold coverage. Sequencing libraries were constructed according to the manufacturer’s instructions. The GAI paired-end reads were assembled into genomic sequences using the SOAP *de novo* program, an in-house assembler based on de Bruijn graph-based sequence assembly methods, and gaps were filled by mapping information (6). Gene prediction and annotation were carried out using Glimmer3 (4), the RAST annotation server (2), and the NCBI COG database. A total of 65 scaffolds containing 206 contigs were obtained, with a total length of 6,697,981 bp. A total of 6,326 genes were discovered, with an average GC content of 44.63%. The number of ribosomal genes was 97, including 94 tRNAs and 3 rRNAs.

A variety of genes related to iron acquisition, virulence, and environmental adaptation were identified in this genome, such as hemolysins, proteases, chitinases, collagenases, RTX toxins, and vibriolysin, as well as some iron transport genes. The genome sequence analysis also revealed several protein secretion systems, including type I, II, III, IV, and VI secretion systems

and a Flp-type pilus system. The latter has been proposed to represent a new subtype of type II secretion systems and is essential for motility, biofilm formation, and colonization (3). The presence of these genes is involved in the organism’s pathogenicity and confers a fitness advantage to marine bacteria, increasing long-term survival in the marine environment. The content of the genome also revealed genes associated with stress responses, including osmotic and oxidative stress, cold and heat shock, and detoxification.

Nucleotide sequence accession numbers. The whole-genome shotgun sequence of *V. harveyi* strain ZJ0603 has been deposited in the GenBank database under accession number [AKIH00000000](https://www.ncbi.nlm.nih.gov/nuccore/AKIH00000000). The version described in this study is the first version, with accession number [AKIH01000000](https://www.ncbi.nlm.nih.gov/nuccore/AKIH01000000).

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Address correspondence to Zaohe Wu, Wuzaohe@163.com.

Y.H. and J.J. contributed equally to this work.

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