



# Draft Genome Sequence of *Vibrio parahaemolyticus* Strain PH1339, Which Causes Acute Hepatopancreatic Necrosis Disease in Shrimp in the Philippines

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**ABSTRACT** We report the first draft genome sequence of an acute hepatopancreatic necrosis disease (AHPND)-causing *Vibrio parahaemolyticus* strain isolated from a *Penaeus vannamei* sample from the Philippines. The strain carries the genes encoding the Pir-like toxin pair PirA<sup>VP</sup> and PirB<sup>VP</sup>.

Acute hepatopancreatic necrosis disease (AHPND), which affects multiple shrimp species, including the economically important *Penaeus monodon* and *Penaeus vannamei*, is characterized by massive sloughing of the epithelial cells of the hepatopancreas to the point of atrophy (1). *Vibrio parahaemolyticus* has been identified as the causative agent of AHPND. In order to mitigate further losses to the shrimp farming industry, it is imperative to identify and characterize the disease-causing strains of *V. parahaemolyticus*. In the present study, *V. parahaemolyticus* PH1339 was isolated from a *P. vannamei* sample displaying typical AHPND pathology in a farm in Negros Island, Philippines. Reinfection of *P. vannamei* with the strain replicated the original AHPND pathology.

The hepatopancreas of the AHPND-afflicted *P. vannamei* sample from a farm in Negros Island, Philippines, was dissected and homogenized in sterile seawater for plating in nutrient agar (Pronadisa) with 2% NaCl. The colony of *V. parahaemolyticus* PH1339 was isolated and grown in nutrient broth (Pronadisa) with 1.5% NaCl incubated overnight at 30°C. Genomic DNA of *V. parahaemolyticus* PH1339 was extracted from the overnight culture using the KingFisher cell and tissue DNA kit (Thermo Fisher Scientific). A paired-end library was generated from the genomic DNA using the Nextera XT DNA library prep kit (Illumina). The paired-end library was sequenced on the Illumina MiSeq (2 × 300-bp) platform (with the MiSeq reagent kit v. 3) at the DNA Sequencing Core Facility of the Philippine Genome Center at a sequencing coverage of 71×, resulting in a total of 2,784,132 paired-end reads.

The verification of the quality of the raw reads was performed using FastQC (2). The paired-end reads were assembled *de novo* into 57 contigs of sizes greater than 1,000 bp using SPAdes v. 3.13.0 (3) with error and mismatch correction using k-mer sizes of 21, 33, 55, 77, 99, and 127 ( $N_{50}$ , 294,559 bp). Assembly statistics were generated with QUAST v. 5.02 (4). The draft genome assembly of *V. parahaemolyticus* PH1339 has a length of 5,332,603 bp and a G+C content of 45.2%. PH1339 was assigned as *V. parahaemolyticus* after the average nucleotide identity (ANI) values between the draft genome of the strain and other publicly available strains of the species were established to be >95% using the aniM option calculate\_ani.py (5).

Annotation of the draft genome with Prokka v. 1.13.7 (6) identified 4,819 coding sequences (CDS), 106 tRNAs, 1 transfer-messenger RNA (tmRNA), and 6 rRNAs. The

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sequence type (ST) of *V. parahaemolyticus* PH1339 was determined to be ST1166 using the default parameters of SRST2 v. 0.20 (7). Moreover, the plasmid-borne *pirA<sup>VP</sup>* and *pirB<sup>VP</sup>* genes were detected in *V. parahaemolyticus* PH1339 using SRST2 v. 0.20 (7). The draft genome sequence of PH1339 serves to validate the presence of AHPND in *P. vannamei* farmed in the Philippines and is an additional genomic resource for comparative genomic studies of AHPND strains.

**Data availability.** This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession no. [VPFJ000000000](https://www.ncbi.nlm.nih.gov/nuccore/VPFJ000000000). The Illumina reads have been deposited under accession no. [SRR9937595](https://www.ncbi.nlm.nih.gov/nuccore/SRR9937595).

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