




Complete Genome Sequence of Acute Hepatopancreatic Necrosis Disease-Causing *Vibrio campbellii* LA16-V1, Isolated from *Penaeus vannamei* Cultured in a Latin American Country

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ABSTRACT We report here the complete genome sequence of *Vibrio campbellii*, isolated from *Penaeus vannamei* cultured in a Latin American country. The Tn3-like transposon and *pirAB* genes were encoded on the plasmid pLA16-2. These data support the geographical variations in the virulence plasmid found among acute hepatopancreatic necrosis disease (AHPND)-causing *Vibrio* isolates from Latin America and Asia.

Acute hepatopancreatic necrosis disease (AHPND), which is caused by *Vibrio* spp. carrying a virulence plasmid encoding the *pirAB* gene, has caused significant economic losses in the shrimp-farming industry (1). Initially, *V. parahaemolyticus* was the only species known to cause this disease; later, other AHPND-causing *Vibrio* spp., such as *V. owensii* and *V. campbellii*, were also reported (2–5). Recent studies have also shown that there are geographical variations in the virulence plasmid among AHPND isolates (6). There is limited information for other AHPND-causing *Vibrio* spp., and so we present here the complete genome of *V. campbellii* LA16-V1, isolated from *Penaeus vannamei* cultured in a Latin American country.

Genomic DNA was isolated using a DNeasy blood and tissue kit (Qiagen). Sequencing was performed by Macrogen, Inc., using a hybrid approach with the PacBio RS II (Pacific Biosciences) (20-kb SMRTbell template library) and Illumina HiSeq 2000 (paired-end short-read data) platforms. The PacBio long-read data (1,787,793,760 bp, 255,476 reads) were *de novo* assembled by FALCON version 0.2.1, and the Illumina paired-end reads (1,053,525,915 bp, 10,439,662 reads) were mapped to the assembled contigs to improve the accuracy of the genome. Annotation was carried out using the NCBI's Prokaryotic Genome Annotation Pipeline (<http://www.ncbi.nlm.nih.gov/books/NBK174280>).

The fully assembled genome contained 6,124,368 bp consisting of two chromosomes, designated Chr I (3,579,637 bp) and Chr II (2,230,177 bp), and a total of four plasmids, designated pLA16-1 (109,793 bp), pLA16-2 (73,461 bp), pLA16-3 (67,308 bp), and pLA16-4 (63,992 bp). The two chromosomes showed similar G+C contents (45.6% and 45.4%) and percentages of coding regions (87.1% and 86.8%). Moreover, most of the predicted tRNAs ($n = 133$), rRNA ($n = 37$), and noncoding RNAs ($n = 4$) were encoded on Chr I, except 15 tRNAs and 3 rRNAs on Chr II and one tRNA on pLA16-1. Overall genome similarities among LA16-V1 and other completely sequenced *V. campbellii* strains were assessed using the orthologous average nucleotide identity algorithm

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(7), and the results indicated 96.7% and 97.9% genome similarities to those of *V. campbellii* ATCC BAA-1116 (8) and *V. campbellii* 20130629003S01 (9), respectively.

The *pirAB*-containing region that comprises the homologue counterparts of the *pirAB* and *pirAB*-Tn903 composite transposons was encoded on the plasmid pLA16-2. The *pirAB*-containing region was almost identical (>99%) to those from the AHPND-related plasmids pVPE61a (10), pVA1 (11), and pVPA3-1 (1) identified in *V. parahaemolyticus*, plasmid pVHvo (12) in *V. owensii*, and plasmid pVCGX1 (8) in *V. campbellii*. Similar to the previous report (6), the pLA16-2 contained a 3-kb Tn3-like transposon that is absent in pVCGX1 in *V. campbellii* 20130629003S01 isolated from China, as well as other plasmids in *V. parahaemolyticus* from southeast Asia, thus supporting the geographical variations in the virulence plasmid found among AHPND-related *Vibrio* isolates from Latin America and Asia. The genome of *V. campbellii* LA16-V1 provides important insights for the study of virulence plasmids to facilitate AHPND control in shrimp aquaculture.

Accession number(s). The genome of *V. campbellii* strain LA16-V1 has been deposited at DDBJ/ENA/GenBank under the accession numbers CP021145 (Chr I), CP021146 (Chr II), CP021147 (pLA16-1), CP021148 (pLA16-2), CP021149 (pLA16-3), and CP021150 (pLA16-4).

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