



# Genome Sequence of a Canadian *Vibrio parahaemolyticus* Isolate with Unique Mobilizing Capacity

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**ABSTRACT** *Vibrio parahaemolyticus* is a clinically significant marine bacterium implicated in gastroenteritis among consumers of raw or undercooked seafood. This report presents the whole-genome sequence of a unique strain of *V. parahaemolyticus* isolated from oysters harvested in Canada.

*Vibrio parahaemolyticus* is autochthonous in estuarine environments around the world and is detected in seafood from contaminated harvest sites. Since the 1950s, *V. parahaemolyticus* has been frequently implicated in cases of seafood-borne gastroenteritis and other related illnesses (1, 2). Most of the clinical isolates are known to express thermostable direct hemolysin (TDH) and/or TDH-related hemolysin (TRH), encoded by *tdh* and *trh*, respectively (1, 3, 4). However, clinical isolates lacking both *tdh* and *trh*, as confirmed by PCR, have been detected from several regions, including in recent years from Canada (5) and from the United States (6). The diversity and dynamics of *V. parahaemolyticus* strains testify to the adaptability of the species to a wide range of habitat and/or environmental challenges by virtue of its genome plasticity and resultant evolution (7). Changes can also occur via the processes of integration and/or conjugation of genetic material through horizontal transfer (8). These events can lead to the emergence of new pathogenic strains as well as evolution of the existing pathogens (7, 9).

Knowledge of the global distribution and epidemiology of *V. parahaemolyticus*, including its genomic profile, will help understand its impact on the human host and the marine environment. Here, we report the genomic sequence of an environmental *V. parahaemolyticus* isolate from oysters harvested in Canada in the summer of 2005 and sourced to Ladysmith Harbor, British Columbia, Canada.

*V. parahaemolyticus* strain S107-1 was isolated and characterized at the Health Canada laboratory by an in-house procedure, the details of which have been published elsewhere (10). An antimicrobial resistance profile (AMR) of the isolate was determined by Kirby-Bauer's disk diffusion method (11, 12). Whole-genome sequencing of *V. parahaemolyticus* S107-1 containing ICEVpaCan1 was carried out from genomic DNA extracted from 2 ml of exponential-phase culture using the Genra Puregene kit (Qiagen). PacBio RS II single-molecule real-time sequencing (PacBio SMRTcell) and *de novo* genome assembly were performed at the McGill University and Génome Québec Innovation Centre with the HGAP version 3 method. Annotation data for *V. parahaemolyticus* S107-1 were provided by the NCBI Prokaryotic Genome Annotation Pipeline (13).

Biochemical analysis using API20E diagnostic strips confirmed the isolate (S107-1) to be *V. parahaemolyticus*, which also tested positive by PCR for the presence of the species-specific marker, thermolabile hemolysin gene (*tlh*), while the known virulence markers (*tdh* and *trh*) for *V. parahaemolyticus* tested negative by PCR. This isolate was resistant to three antibiotics, ampicillin, streptomycin, and cephalothin, and showed intermediate resistance to piperacillin and kanamycin. Whole-genome sequencing

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analysis identified and assembled the two chromosomes of sizes 3,445,421 bp and 1,757,905 bp for chromosomes I and II, respectively.

The presence of an integrative and conjugative element (ICE), consequently named ICEVpaCan1, was detected at the 5' end of the *prfC* gene on chromosome I of the *V. parahaemolyticus* isolate S107-1. This element of the SXT/R391 family has a size of 81,255 bp and does not carry any predicted resistance genes.

**Accession number(s).** The complete genome sequences of the two chromosomes of *V. parahaemolyticus* strain S107-1 were deposited at GenBank under accession numbers [CP028481](#) (chromosome I) and [CP028482](#) (chromosome II).

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