

Draft Genome Sequence of *Vibrio mimicus* Strain CAIM 602^T

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***Vibrio mimicus* is a Gram-negative bacterium associated with gastrointestinal diseases in humans around the world. We report the complete genome sequence of the *Vibrio mimicus* strain CAIM 602^T (CDC1721-77, LMG 7896^T, ATCC 33653^T).**

Received 5 February 2013 Accepted 14 February 2013 Published 14 March 2013

Citation Guardiola-Avila I, Acedo-Felix E, Noriega-Orozco L, Yepiz-Plascencia G, Sifuentes-Romero I, Gomez-Gil B. 2013. Draft genome sequence of *Vibrio mimicus* strain CAIM 602^T. Genome Announc. 1(2):e00084-13. doi:10.1128/genomeA.00084-13.

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Vibrio mimicus can cause gastrointestinal diseases in humans (1). It has been found to be associated with aquatic environments, such as fresh, brackish, and seawater (2). Studies around the world (in locations including Bangladesh, Japan, Costa Rica, Mexico, Thailand, the United States, Nigeria, Brazil, and Australia, among others) have demonstrated the presence of *V. mimicus* in foods, water samples, sediments, and aquatic plants (1–5).

Like other *Vibrio* species, *V. mimicus* has two chromosomes of different sizes, the larger of 3.0 Mb and a smaller of 1.5 Mb (6). The larger chromosome carries essential genes for growth and viability, as well as many virulence genes, while the smaller is where genes for adaptation to environmental change and a variant of *Vibrio* pathogenicity island 2 (VPI-2) are localized (7).

The type strain of *V. mimicus* was isolated from a 35-year-old female in North Carolina and was first designated a type strain in 1981 (5). It has been used as a control strain around the world and is partially sequenced (housekeeping genes).

CAIM 602^T was sequenced using a semiconductor NGS platform (Ion Torrent Personal Genome Machine sequencer; Life Technologies) with a 316 chip at CIAD Mazatlán. A total of 768,833 reads were obtained (mean length, 136 bp) for a total of 101 Mb and coverage of 23.5×; 611,888 reads were assembled with MIRA version 3.1.0 to obtain 120 contigs (N_{50} , 159,054 bp). A genome-wide assembly and contig synteny was constructed with Mauve genome alignment software version 2.3.1 using *V. cholerae* N16961 as a reference strain (8). The contigs were further reassembled with Geneious R6 version 6.0.3 (Biomatters Ltd.) and refined with Gap4 version 2.0.0b9 of the Staden package (9) to obtain 11 supercontigs in chromosome I (ChI) and 5 in chromosome II (ChII) and 37 contigs in ChII as part of the super-integron. Original contigs were annotated by RAST (10) (<http://rast.nmpdr.org/>), where 55% of the features found were classified within a subsystem.

The assembled genome of the type strain *V. mimicus* CAIM 602 is 4.30 Mb in size and has two chromosomes. Chromosome I is approximately 2.90 Mb, with six rRNA operons, 71 tRNAs, 2,639 coding sequences (CDS), and a G+C content of 46.6%. Chromosome II is approximately 1.40 Mb; it has six tRNAs, 1,383 CDS, no rRNAs, and a G+C content of 46.2%. No plasmids were detected.

The chromosome I sequence revealed various genes that encode virulence factors (e.g., hemolysins, proteases, mannose-sensitive hemagglutinin [MSHA] pili, type II and IV secretion systems, a putative RTX toxin, an aerobactin siderophore receptor, capsular polysaccharide biosynthesis protein, and an accessory colonization factor). Also revealed were several hypothetical proteins and genes with roles in DNA and RNA metabolism. Chromosome II contains genes encoding several membrane proteins and various hypothetical proteins, genes involved in cell signaling (genes for CdgA and GGDEF family proteins), genes encoding transcriptional regulator LysR family and AraC family proteins, multidrug resistance proteins, and type VI secretion proteins (VasI, VasL), and a lipoprotein ToxR-activated gene. A superintegron of at least 260 kb with approximately 402 CDS was found in ChII. One 13.2-kb prophage was also detected.

Nucleotide sequence accession numbers. *Vibrio mimicus* CAIM 602^T was obtained from the Collection of Aquatic Important Microorganisms (CAIM) (<http://www.ciad.mx/caim>). This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [AOMO00000000](https://www.ncbi.nlm.nih.gov/nuccore/AOMO00000000). The version described in this paper is the first version, [AOMO01000000](https://www.ncbi.nlm.nih.gov/nuccore/AOMO01000000).

ACKNOWLEDGMENTS

This work was supported partially by CONACYT grant Investigación, Innovación y Transferencia Tecnológica en Calidad e Inocuidad de los Alimentos and core funds of CIAD, A.C. “Integración del grupo Genómica Microbiana para la estandarización de técnicas en biología molecular y bioinformáticas.”

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