

Genome Sequence of *Vibrio cholerae* Strain O1 Ogawa El Tor, Isolated in Mexico, 2013

José Alberto Díaz-Quiñonez,^{a,b} Irma Hernández-Monroy,^a Irma López-Martínez,^a Joanna Ortiz-Alcántara,^a Elizabeth González-Durán,^a Cuitláhuac Ruiz-Matus,^c Pablo Kuri-Morales,^d José Ernesto Ramírez-González^a

Instituto de Diagnóstico y Referencia Epidemiológicos Manuel Martínez Báez, Mexico City, Mexico^a; Facultad de Medicina, UNAM, Mexico City, Mexico^b; Dirección General de Epidemiología, Mexico City, Mexico^c; Subsecretaría de Prevención y Promoción de la Salud, Mexico City, Mexico^d

We present the draft genome sequence of *Vibrio cholerae* InDRE 3140 recovered in 2013 during a cholera outbreak in Mexico. The genome showed the *Vibrio* 7th pandemic islands VSP1 and VSP2, the pathogenic islands VPI-1 and VPI-2, the integrative and conjugative element SXT/R391 (ICE-SXT), and both prophages CTX ϕ and RS1 ϕ .

Received 22 September 2014 Accepted 28 September 2014 Published 30 October 2014

Citation Díaz-Quiñonez JA, Hernández-Monroy I, López-Martínez I, Ortiz-Alcántara J, González-Durán E, Ruiz-Matus C, Kuri-Morales P, Ramírez-González JE. 2014. Genome sequence of *Vibrio cholerae* strain O1 Ogawa El Tor, isolated in Mexico, 2013. *Genome Announc*. 2(5):e01123-14. doi:10.1128/genomeA.01123-14.

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Address correspondence to José Alberto Díaz-Quiñonez, alberto.diaz@salud.gob.mx.

Cholera, caused by *Vibrio cholerae*, is a disease characterized by very severe diarrhea and dehydration, which can lead to death in less than 48 hours if left untreated (1). The principal virulence determinant is the potent cholera toxin, encoded by the *ctxAB* genes on the bacteriophage CTX ϕ found in toxigenic *V. cholerae* genomes. The toxin, together with other virulence factors encoded in clusters of genes called genomic islands, leads to the harmful effects of the *V. cholerae* infection (2).

We report the draft sequence of the genome of *Vibrio cholerae* InDRE 3140 that was collected in Mexico City in August 2013 as an imported cholera case from the Caribbean that later caused an outbreak in the La Huasteca region (3). The strain was isolated from a 46-year-old woman and identified as *V. cholerae* O1 serotype Ogawa, biotype El Tor, on the basis of standard biochemical and serologic testing. Pulsed-field gel electrophoresis and virulence gene amplification (*ctxA*, *ctxB*, *zot*, and *ace*) demonstrated that the strain was different than strains that had circulated in Mexico previously but indistinguishable from the strain that caused outbreaks in Haiti, the Dominican Republic, and Cuba (4, 5).

The *V. cholerae* InDRE 3140 genome was sequenced using the 454 FLX-Titanium platform (Roche, Brandford, CT). A single-end library was generated from genomic DNA and 205,226 reads were obtained. The draft genome was assembled using Newbler version 2.9, with the sequence of *Vibrio cholerae* O1 strain 2010EL-1786 as a mapping reference (CP003069.1 and CP003070.1). Ninety-two contigs were obtained with an N_{50} of 118,249 bp and an average coverage of 18.0 \times . The total sequence length was 4,017,985 bp. The contigs were annotated using the NCBI Prokaryotic Genome Annotation Pipeline with the best-placed reference protein set, GeneMarkS+ method, version 2.6 (revision 440435). The genome showed 3,676 genes, 2,875 coding sequences (CDS), 708 pseudogenes, 25 rRNAs, 67 tRNAs, and 1 noncoding RNA (ncRNA).

Preliminary analyses indicate that *V. cholerae* InDRE 3140 carries the *Vibrio* pathogenic islands VPI-1 and VPI-2, *Vibrio* 7th pandemic islands VSP1 and VSP2, as well as an SXT/R391 (ICE-

SXT) integrative and conjugative element, a cholera toxin (CTX ϕ), and RS1 ϕ prophages. The genomic core is similar to that of the *V. cholerae* O1 El Tor biotype strain 2010 EL-1786, a 2010 Haiti outbreak isolate (6).

A detailed case-control study from cholera case patients as well as the results of comparative and phylogenetic analyses of this genome and other available *V. cholerae* genomes in the La Huasteca region will be published elsewhere.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [JPHJ00000000](https://www.ncbi.nlm.nih.gov/nuccore/JPHJ00000000) and consists of sequences JPHJ01000001 to JPHJ01000092.

ACKNOWLEDGMENT

We thank all the staff of Molecular Biology and Bacteriology Departments, InDRE, for technical assistance.

For this work no external funding was received.

The findings and conclusions in this report are those of the authors and do not necessarily represent the official opinion of the Ministry of Health in Mexico.

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