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Draft Genome Sequence of the Pathogenic Bacterium *Vibrio vulnificus* V252 Biotype 1, Isolated in Israel

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We report the genome sequence of the pathogenic *Vibrio vulnificus* biotype 1 clade B, which is suggested to have a common ancestor with biotype 3. This draft genome of the clinical strain V252, isolated in Israel, represents the clonal clade B group that contains both clinical and environmental strains.

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Vibrio vulnificus is an aquatic bacterium and a highly invasive human pathogen (1–4). Strains of *V. vulnificus* are biochemically divided into three biotypes. Biotype 1 is responsible for the majority of human infections worldwide and is a highly varied pathogen (5, 6). Attempts to follow the evolutionary origin of the recently emerged biotype 3 indicate that biotype 3 and the newly identified subgroup clade B of biotype 1, both isolated in Israel, have a common ancestor (7, 8).

Here we describe the draft genome sequence of the clinical *V. vulnificus* biotype 1 clade B strain V252, isolated from a human wound infection in August 2004 at Western Galilee Hospital (collection of the Israeli Ministry of Health 7/04) and subjected to whole-genome shotgun sequencing.

Illumina MiSeq sequencing generated 1,181,041,212 bp (250-bp paired-end reads) with a coverage of 200×. Reads were *de novo* assembled with CLCbio Genomics Workbench version 7.0 (CLC Bio, Denmark) generating 220 contigs >200 bp, with an N_{50} of 205,385 bp and the longest contig size of 349,342 bp; 96% of the single reads were mapped to the assembly. There is evidence of the presence of a plasmid related to pYJ016 (contig_9 with high coverage of 620×).

The draft genome of V252 consists of 220 segments covering two chromosomes and one plasmid (5.05Mbp; 46.6% G+C content); 4,383 coding sequences, 68 pseudogenes, 3 rRNAs, 80 tRNAs, and 1 noncoding RNA (ncRNA) were predicted and annotated by the NCBI Prokaryotic Genome Annotation Pipeline (9), similar to the annotation predicted by RAST (10).

Genome alignment of V252 to published *V. vulnificus* genomes, using the NUCmer program of MUMmer version 3.23 (11, 12), revealed higher similarity (89.4%) to *V. vulnificus* VVyb1(BT3) (13) than to YJ016 (85.0%) (14). Comparison using the SEED viewer in RAST (10, 15) revealed that 91.5%, 84.1%, and 78.9% of the V252 genes are similar to VVyb1(BT3), CMCP6, and YJ016, respectively. These findings support the evolutionary relatedness of the V252 and VVyb1(BT3) strains.

Since clade B is highly clonal, the genome of the V252 strain provides representation of this phylogroup, contributing to the understanding of the evolution of this human pathogen.

Nucleotide sequence accession numbers. This project has been deposited in DDBJ/EMBL/GenBank under the accession number LIIO00000000. The version described here is the first version, LIIO01000000.

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