# Complete Genome Sequence of *Vibrio vulnificus* 93U204, a Bacterium Isolated from Diseased Tilapia in Taiwan

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*Vibrio vulnificus* 93U204 is a bacterium isolated from a moribund tilapia collected in Kaohsiung, Taiwan. Here, we report the complete genome sequence of this bacterium to facilitate the investigation of its pathogenicity and for comparative analyses with human-pathogenic strains within the same species.

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*V*ibrio vulnificus* is a Gram-negative bacterium commonly found in coastal marine environments throughout the world. While biotype 1 strains within this species are opportunistic pathogens of humans by infection through wounds or contaminated seafood (1), biotype 2 strains are pathogens of eel (2) and tilapia (3) in aquaculture. The biotype 1 strain *V. vulnificus* 93U204 was isolated from a moribund tilapia collected in Kaohsiung, Taiwan (4). To facilitate future characterization of this strain, we determined its complete genome sequence.

The procedure for genome sequencing, assembly, and annotation is based on that described in our previous studies (5–8). Briefly, the Illumina MiSeq platform was used to generate 251-bp reads from one paired-end library (~315-bp insert, 6,818,142 reads), and the Illumina HiSeq 2000 platform was used to generate 126-bp reads from one mate-pair library (~4.1-kb insert, 6,962,414 reads). The *de novo* assembly was performed using AllPaths-LG release 42781 (9). The initial assembly was iteratively improved by mapping the raw reads to the contigs using Burrows-Wheeler Aligner (BWA) version 0.6.2 (10), programmatically checked using the mpileup program in SAMTools package version 0.1.18 (11), and visually inspected using Integrative Genomics Viewer (IGV) version 2.1.24 (12). All gaps were filled by using reads overhanging at the contig margins, and the scaffolding across repetitive regions were confirmed by PCR. The programs RNAmmer (13), tRNAscan-SE (14), and Prodigal (15) were used for gene prediction. For each protein-coding gene, the gene name and product description were initially annotated based on the homologous genes in *V. vulnificus* YJ016 (16), as identified by OrthoMCL (17). Subsequently, BLASTp (18) searches against the NCBI nonredundant (nr) protein database (19) and the Kyoto Encyclopedia of Genes and Genomes (KEGG) database (20) were used to assist manual curation of the annotation.

The complete genome of *V. vulnificus* 93U204 contains three replicons, including two circular chromosomes (chromosome I: 3,315,989 bp, 46.5% G+C content; chromosome II: 1,805,637 bp, 47.1% G+C content) and a circular plasmid p93U204 (5,719 bp, 40.3% G+C content). The first version of annotation includes eight sets of 16S-23S-5S rRNA genes (seven on chromosome I and one on chromosome II), 107 tRNA genes (covering all 20 amino acids), and 4,512 protein-coding genes.

**Nucleotide sequence accession numbers.** The complete genome sequences of *V. vulnificus* 93U204 have been deposited at DDBJ/EMBL/GenBank under the accession numbers CP009261 to CP009263.

## ACKNOWLEDGMENTS

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