

Complete Genome Sequence of *Vibrio anguillarum* M3, a Serotype O1 Strain Isolated from Japanese Flounder in China

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***Vibrio anguillarum* is an important bacterial pathogen that causes vibriosis in marine fish. We present the complete genome sequence of *V. anguillarum* M3, a serotype O1 clinical strain isolated from Japanese flounder (*Paralichthys olivaceus*) in Shandong, China.**

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Vibrio anguillarum causes vibriosis, a systemic disease of both wild and cultured marine fish characterized by hemorrhagic septicemia (1). There are 23 serotypes identified for this bacterium, and the O1 and O2 serotypes are the major causative agents of fish vibriosis (2). Recently, the genome sequences of three *V. anguillarum* strains, isolated from salmon (*Oncorhynchus kisutch*), striped bass (*Morone saxatilis*), and turbot (*Scophthalmus maximus*), were released (3). Here, we present the complete genome sequence of *V. anguillarum* M3, an O1 serotype clinical strain isolated from Japanese flounder (*Paralichthys olivaceus*) (4). This strain has been studied with respect to its *in vivo* antigen gene expression, metalloprotease and exopolysaccharide production, and biofilm formation (5–7).

The genome of *V. anguillarum* M3 was sequenced using the Roche 454 GS FLX Titanium system at SeqWrite, Inc. (Houston, TX). A total of 23,745 reads were obtained from the sequencing (~20-fold coverage of the genome). The reads were assembled using DataAnalysis version 2.6 (Roche/454 Life Sciences), generating 59 contigs. Using the genome of *V. anguillarum* strain 775 as a reference, all gaps were filled by local assembly using the CLC Genomics Workbench (64-bit) 6.0.5 and ABI 3730 sequencing of the PCR products of the gap region. The coding sequences (CDSs) were predicted by the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) and the Rapid Annotations using Subsystems Technology (RAST) server (8). Noncoding RNAs were identified using tRNAscan-SE 1.21 (9) and RNAmmer 1.2 (10) by searching against the Rfam database (11). Functional assignment of the CDSs was performed on the InterProScan (12) and the Swiss-Prot and trEMBL databases (13).

The complete genome of *V. anguillarum* M3 contains two circular chromosomes and a plasmid. Chromosome 1 has 3,063,587 bp containing 2,842 CDSs, chromosome 2 has 988,134 bp containing 918 CDSs, and the plasmid has 66,164 bp containing 64 CDSs. Overall, the M3 and 775 genomes share high levels of similarity, as >90% of the CDSs have the same annotation, length, and relative position. With respect to potential virulence traits, a majority of the

virulence genes are conserved in both strains, such as those for hemolysins, metalloproteases, repeat in toxin (RTX) toxins, and vibriolysin (14). Both strains present two type VI secretion system loci on chromosome 1 and chromosome 2, and the genes in the two loci are organized identically in M3 but differently in 775 (15). In addition, M3 has 74 specific genes, encoding a transposase and 73 hypothetical proteins; 775 has 168 specific genes, including genes encoding mobile element proteins (30 genes), molybdopterin biosynthesis proteins (MoeA-MoeB), dGTPase, methyl-accepting chemotaxis protein, tryptophanase, and ribonuclease E inhibitor RraB. Regarding the pathogenicity of M3, the complete genome sequence of this strain will increase the understanding of the evolution of *V. anguillarum* and will contribute new insights into virulence studies of this particular species.

Nucleotide sequence accession numbers. The sequence and annotation of the *V. anguillarum* M3 genome have been deposited in GenBank under accession no. CP006699 (M3 chromosome 1), CP006700 (M3 chromosome 2), and CP006701 (M3 plasmid).

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