Draft genome sequences of Vibrio alginolyticus strains V1 and V2, opportunistic marine pathogens

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Vibrio alginolyticus is a Gram-negative bacterium and an important opportunistic pathogen for marine organisms (1). This bacterium is associated with epidemic vibriosis, which results in high mortality for cultured marine animals, including fish (2), shellfish (3) and shrimp (4). In addition, V. alginolyticus can be pathogenic in humans and can lead to otitis and wound infections after contact with V. alginolyticus-containing seawater (5). We report the draft genome sequences of V. alginolyticus strains V1 and V2, which were isolated from farmed juvenile Sparus aurata and Dentex dentex, respectively, during two separate vibriosis incidences in Crete, Greece.

V. alginolyticus strains V1 and V2 were grown in Luria broth (Mo Bio, 12106-05) supplemented with NaCl 1.7% overnight at 22°C with agitation. Genomic DNA was extracted using the QIAamp DNA minikit (Qiagen) according to manufacturer's protocol. A sequencing library was prepared using an Illumina HiSeq platform (BGI, China) with pair-end read sizes of 100 bp. A total of 9,374,944 paired-end reads for strain V1 and 10,880,660 paired-end reads for strain V2, respectively, during outbreaks of vibriosis. The genome sequences are 5,257,950 bp with a G+C content of 44.5% for V. alginolyticus V1 and 5,068,299 bp with a G+C content of 44.8% for strain V2. These genomes provide further insights into the putative virulence factors, prophage carriage, and evolution of this opportunistic marine pathogen.


