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Published in:
Genome Announcements

DOI:
10.1128/genomeA.00729-15

Publication date:
2015

Document Version
Publisher's PDF, also known as Version of record

Citation for published version (APA):
Draft Genome Sequences of *Vibrio alginolyticus* Strains V1 and V2, Opportunistic Marine Pathogens

Daniel Castillo, a Paul D’Alvise, b Panos G. Kalatzis, c Constantina Kokkari, c Mathias Middelboe, a Lone Gram, b Siyang Liu, d Pantelis Katharios a

Marine Biological Section, University of Copenhagen, Helsingør, Denmark; bDepartment of Systems Biology, Technical University of Denmark, Kongens Lyngby, Denmark; cInstitute of Marine Biology, Biotechnology and Aquaculture, Hellenic Centre for Marine Research, Former American Base of Gournes, Crete, Greece; dBGI Europe A/S, Copenhagen, Denmark

We announce the draft genome sequences of *Vibrio alginolyticus* strains V1 and V2, isolated from juvenile *Sparus aurata* and *Dentex dentex*, respectively, during outbreaks of vibriosis. The genome sequences are 5,257,950 bp with a G+C content of 44.5% for strain 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.


