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Draft Genome Sequences of *Vibrio alginolyticus* Strains V1 and V2, Opportunistic Marine Pathogens

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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.


