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Draft Genome Sequence of the Emerging Bivalve Pathogen *Vibrio tubiashii* subsp. *europaeus*

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**Vibrio tubiashii** subsp. *europaeus* is a bivalve pathogen isolated during episodes of mortality affecting larval cultures in different shellfish hatcheries. Here, we announce the draft genome sequence of the type strain PP-638 and describe potential virulence factors, which may provide insight into the mechanism of pathogenicity.

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*Vibrio tubiashii* subsp. *europaeus* is an emerging bivalve pathogen identified recently as the etiological agent responsible for larval and spat mortalities in clam, oyster, and abalone cultures detected in Spanish and French hatcheries (1, 2). This pathogen is a causative agent of vibriosis, inducing mass mortalities and important economic losses, representing the main bottleneck for the production process in shellfish aquaculture (1, 2).

*V. tubiashii* subsp. *europaeus* PP-638T (= CECT 8136T = DSM 27349T) was originally isolated from a culture tank of flat oyster (*Ostrea edulis*) during an episode of larval mortality in a shellfish hatchery (Galicia, Northwest Spain) (1). DNA was isolated from *V. tubiashii* subsp. *europaeus* PP-638T grown overnight in YP30 using the Wizard genomic DNA purification kit (Promega), according to the manufacturer’s instructions, except DNA was resuspended in 2 mM Tris-HCl buffer (Bio Basic). Genomic DNA was sequenced using an Illumina MiSeq at the Genomics and Sequencing Center at the University of Rhode Island, Kingston, RI. Reads were trimmed using CLC Genomics Workbench (version 8.5.1) for quality, ambiguous nucleotides, and adapters. A total of 5,157 open reading frames (5–7).

The genome encodes two secretion systems (type III secretion system [T3SS] and T6SS) that are used to deliver effector molecules directly into the host. The T3SS-secreted virulence factor has a domain similar to the GTPase-activating domain found on YopE from *Yersinia pestis* (12–16). While the T6SS structural components are encoded on the p251-like megaplasmid, the protein responsible for forming the puncturing tip of the T6SS secretion system, VgrG, appears to be encoded by two genes. One VgrG-encoding gene is on chromosome 1, and the second is on chromosome 2.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited in DDBJ/EMBL/GenBank under the accession no. LUAX0000000. The version described in this paper is the first version LUAX01000000.

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