

# Draft Genome Sequences of *Vibrio renopiscarius* Strains CECT 8603<sup>T</sup> and CECT 8604, Two Marine *Gammaproteobacteria* Isolated from Cultured Gilthead Sea Bream (*Sparus aurata*)

David R. Arahal, Lidia Rodrigo-Torres, Teresa Lucena, María J. Pujalte

Departamento de Microbiología y Ecología and Colección Española de Cultivos Tipo (CECT), Universitat de València, Valencia, Spain

*Vibrio renopiscarius* DCR 1-4-2<sup>T</sup> (CECT 8603<sup>T</sup>) and DCR 1-4-12 (CECT 8604) were isolated from healthy gilthead sea bream (*Sparus aurata*) from Mediterranean fish farms (Castellón, Spain). Their draft genome sequences (30 and 44 contigs, respectively) have 4.3 Mbp and a G+C content of 45.2 mol% and contain almost 3,700 protein-encoding genes.

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Address correspondence to David R. Arahal, arahal@uv.es.

The genus *Vibrio*, with more than one hundred species (<http://www.bacterio.net/vibrio.html>), contains the majority of facultative anaerobic bacteria that can be recovered by cultural methods from the marine environment. *Vibrio* species have a worldwide distribution, having been isolated from seawater and sediments, marine invertebrates, and fish.

Strains DCR 1-4-2<sup>T</sup> (CECT 8603<sup>T</sup>) and DCR 1-4-12 (CECT 8304) were isolated from healthy cultured gilthead sea bream (*Sparus aurata*) from the Mediterranean Spanish coast using marine agar and tryptone soy agar plus 2% NaCl (cultured at 26°C for 48 h). They were presumptively identified as *Vibrio ichthyenteri*-like (1), but subsequent characterization permitted us to propose them as a novel species, *Vibrio renopiscarius* (E. Tarazona, M. A. Ruvira, T. Lucena, M. C. Macián, D. R. Arahal, and M. J. Pujalte, submitted for publication).

*V. renopiscarius* is a facultative anaerobe; it ferments glucose without gas production and reduces nitrate to nitrite. Cells are coccoid to rod shaped and motile. Oxidase and catalase are positive. This organism grows from 4°C to 28°C and from 2% to 6% NaCl. C<sub>16:1</sub> ω7c/ω6c is the major fatty acid. It grows on defined medium with several carbohydrates, organic acids, and amino acids as sole carbon and energy sources.

Genome sequencing of strains CECT 8603<sup>T</sup> and CECT 8304 was done using the Illumina MiSeq system by the Central Service of Support to Experimental Research (SCSIE) of the University of Valencia (Spain). Strain CECT 8603<sup>T</sup> yielded a total of 3,196,666 reads that were assembled using SeqMan NGen 12.0.1, available as free application in BaseSpace, and a draft genome of 30 contigs more than 500 bp in size was obtained. With the same sequencing strategy, strain CECT 8604 yielded fewer reads (2,666,946) and a few more contigs (44). The draft genome sequences of both strains were quite similar in length (4,339,718 bp and 4,347,351 bp, respectively), with average coverage (109) and G+C content (45.2 mol%).

Automatic gene annotation was carried out by the NCBI Prokaryotic Genomes Annotation Pipeline (PGAP) (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>) (2). The genome of strain CECT 8603<sup>T</sup> contained 3,684 protein-coding genes, 102 pseudogenes, 25 rRNAs, 103 tRNAs, and 1 noncoding RNA (ncRNA), whereas strain CECT 8604 had 3,690 protein-coding genes, 103 pseudogenes, 28 rRNAs, 108 tRNAs, and 1 ncRNA.

Genome annotation and analysis were also done using the RAST server (<http://rast.nmpdr.org/>) (3). According to this annotation tool, complete glycolysis/gluconeogenesis, pentose phosphate, Entner-Doudoroff, and glyoxylate pathways, as well as the tricarboxylic acid (TCA) cycle and mixed-acid fermentation, were present in both genomes. Also, a type I restriction-modification system, type IV fimbria apparatus, and several multidrug efflux pumps were detected. The absence of a complete arginine deiminase (ADI) system or acetoin-butanediol synthetizing genes justify the negative response of these strains to arginine dihydrolase (ADH) and Voges-Proskauer (VP) tests.

The coding densities of strains CECT 8603<sup>T</sup> and CECT 8304 are 85.4% and 85.7%, respectively.

**Nucleotide sequence accession numbers.** These whole-genome shotgun projects have been deposited at DDBJ/ENA/GenBank under the accession numbers [JTKH000000000](https://www.ncbi.nlm.nih.gov/nuccore/JTKH000000000) (strain CECT 8603<sup>T</sup>) and [JTKI000000000](https://www.ncbi.nlm.nih.gov/nuccore/JTKI000000000) (strain CECT 8604). The versions described in this paper are the first version of each.

## ACKNOWLEDGMENTS

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