

Thalassovivens spotae sp. nov.

Submitted by Thrash, Cameron

Genus *Thalassovivens*

Etymology

[Tha.las.so.vi'vens] **Gr. fem. n.** *thalassa*, the sea; **L. pres. part.** *vivens*, living; **N.L. fem. n.** *Thalassovivens*, an organism living in the sea, in reference to the marine habitat of these organisms

Nomenclatural type

Species *Thalassovivens spotae*^{Ts}

Description

Aerobic, with chemoorganoheterotrophic, chemolithotrophic, and anoxygenic phototrophic metabolisms. Encodes genes for glycolysis through the Entner-Doudoroff pathway and the TCA cycle. Genome sizes of ~3.6 Mbp, with GC content ~51% and a coding density ~89%. Prototrophy predicted for lysine, serine, threonine, glutamine, histidine, arginine, cysteine, glycine, valine, methionine, isoleucine, tryptophan, aspartate, and glutamate, with asparagine auxotrophy. Glycine betaine synthesis, glycine betaine/proline transport, and ecotine/hydroxyectoine transport genomically conserved. Genes for the PII nitrogen regulatory system, *ntrXY*, *amtB*, and urease conserved. Most genomes also encode genes for aerobic vitamin B12 synthesis. Genes for synthesis of bacteriochlorophyll a and/or b conserved. Motility via flagella is predicted.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Rhodobacterales* » *Roseobacteraceae* » *Thalassovivens*

References

Effective publication: Lanclos et al., 2025 [1]

Registry URL

<https://seqco.de/i:50985>

Species *Thalassovivens spotae*^{Ts}

Etymology

[spo'tae] **N.L. gen. n.** *spotae*, in reference to the San Pedro Ocean Time series (SPOT), from which the strain was isolated

Nomenclatural type

[NCBI Assembly: GCA_034423775.1](#)^{Ts}

Reference Strain

[Strain sc|0040320](#): US3C007 = [ATCC TSD-433](#) = [NCMA B160](#) = [DSM 119208](#)

Description

In addition to the characteristics of the genus, it has the following features. Cells are coccobacillus shaped, pleomorphic, with average dimensions of 0.23 µm radius, 1.65 µm length, and 0.44 µm³ volume. Halophilic, growing in salinities of 15–49 ppt, but not at 10 ppt or below. Mesophilic, growing between 16–25°C, but not at temperatures of 12°C or below, or at 28.5°C or above. Has a maximum growth rate of 1.55 ± 0.05 divisions day^{−1} at 20°C and salinity of 30 ppt.

The type strain, US3C007T (= ATCC TSD-433T = NCMA B160T), was isolated from surface water (2 m) collected at the San Pedro Ocean Time series (33°33' N, 118°24' W). The genome sequence is circularized at 3622411 bp with 50.7% GC content. The genome is available on NCBI at BioProject number PRJNA1044073.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Rhodobacterales* » *Roseobacteraceae* » *Thalassovivens* » *Thalassovivens spotae*^{Ts}

References

Effective publication: Lanclos et al., 2025 [1]
Assigned taxonomically: Lanclos et al., 2025 [1]

Registry URL

<https://seqco.de/i:50984>

References

1. Lanclos et al. (2025). New isolates refine the ecophysiology of the Roseobacter CHAB-I-5 lineage. *ISME Communications*. [DOI:10.1093/ismeco/ycaf068](https://doi.org/10.1093/ismeco/ycaf068)

Register List Certificate of Validation

On behalf of the *Committee on the Systematics of Prokaryotes Described from Sequence Data* (SeqCode Committee), we hereby certify that the Register List **seqco.de/r:cwvpuxq6** submitted by **Thrash, Cameron** and including 2 new names has been successfully validated.

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