Pelagibacter ubiqueversans gen. nov. sp. nov.

Submitted by Rappe, Michael

Genus *Pelagibacter*

Etymology

[Pe.la.gi.bac'ter] **L. neut. n.** *pelagus*, the sea; **N.L. masc. n.** *bacter*, rod; **N.L. masc. n.** *Pelagibacter*, a rod from the sea

Nomenclatural type

Species *Pelagibacter ubiqueversans*^{Ts}

Description

Small, curved, rod-shaped and non-motile cells approximately 0.2 × 0.4 µm in size for newly divided cells. Aerobic chemoorganoheterotrophs that reside as plankton in seawater. Based on a phylogenetic reconstruction of 165 concatenated protein-coding marker genes, genomes of the genus Pelagibacter occupy a monophyletic node within the family Pelagibacteraceae that is known as SAR11 subclade Ia.1.I. Genomes share a minimum gANI of ~84.2% to the type genome. Using metagenomic read recruitment, members of the genus Pelagibacter preferentially occupy high-latitude, low diversity regions of the global ocean. The type species is Pelagibacter ubiqueversans.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Pelagibacterales* » *Pelagibacteraceae* » *Pelagibacter*

References

Effective publication: Rappé et al., 2002 [1]

Registry URL

https://seqco.de/i:175

Species *Pelagibacter ubiqueversans*^{Ts}

Etymology

[u.bi.que.ver'sans] **L. adv.** *ubique*, in any place whatever; **L. inf. v.** *versari*, to dwell, live, remain, stay, abide, be; **N.L. masc. part. adj.** *ubiqueversans*, one that dwells everywhere

Nomenclatural type

NCBI Assembly: GCA_000012345.1 ^{Ts}

Reference Strain

Strain sc|0039687: HTCC1062

Description

In addition to the properties given in the genus description, the species is described as follows. Growth can occur using pyruvate as a carbon and energy source, methionine as sole sulfur source, and glycine or serine to support one-carbon metabolism. Optimal growth occurs at 16 to 17 °C, with a maximum specific growth rate of approximately 0.5 per day. The complete genome is 1.31 Mbp, encodes approximately 1,354 protein-coding genes, and has a GC content of 29.7% calculated from the genome. The genome is highly streamlined, with minimal non-coding DNA and a high coding density (~91%), and few mobile elements or paralogous gene families. It lacks many biosynthetic pathways for amino acids and cofactors, reflecting extensive metabolic reliance on exogenous sources. The genome encodes a green-light absorbing proteorhodopsin, which functions as a light-driven proton pump. HTCC1062 exemplifies the ecological and physiological adaptations of SAR11 clade members to oligotrophic marine environments. Its minimal genome, slow growth, and specific substrate requirements reflect evolutionary pressures favoring replication efficiency, low resource demands, and close coupling to the ambient pool of labile dissolved organic matter.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Pelagibacterales* » *Pelagibacteraceae* » *Pelagibacter* » *Pelagibacter ubiqueversans*^{Ts}

References

Effective publication: Rappé et al., 2002 [1]

Registry URL

https://seqco.de/i:91

References

1. Rappé et al. (2002). Cultivation of the ubiquitous SAR11 marine bacterioplankton clade. *Nature*. DOI:10.1038/nature00917

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:i44xxws2** submitted by **Rappe, Michael** and including 2 new names has been successfully validated.

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