

Pelagibacter ubiqueversans gen. nov. sp. nov.

Submitted by Rappe, Michael

Table 1: Complete list of names proposed in the current register list.

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Genus <i>Pelagibacter</i>	[Pe.la.gi.bac'ter] L. neut. n. <i>pelagus</i> , the sea; N.L. masc. n. <i>bacter</i> , rod; N.L. masc. n. <i>Pelagibacter</i> , a rod from the sea	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 <i>Pelagibacter</i> occupy a monophyletic node within the family Pelagibacteraceae that is known as SAR11 subclade Ia.1.1. Genomes share a minimum gANI of ~84.2% to the type genome. Using metagenomic read recruitment, members of the genus <i>Pelagibacter</i> preferentially occupy high-latitude, low diversity regions of the global ocean. The type species is <i>Pelagibacter ubiqueversans</i> .	<i>Pelagibacteraceae</i>	<i>Pelagibacter ubiqueversans</i> ^{Ts}	seqco.de/i:175
Species <i>Pelagibacter ubiqueversans</i> ^{Ts}	[u.bi.que.ver'sans] L. adv. <i>ubique</i> , in any place whatever; L. inf. v. <i>versari</i> , to dwell, live, remain, stay, abide, be; N.L. masc. part. adj. <i>ubiqueversans</i> , one that dwells everywhere	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	<i>Pelagibacter</i>	NCBI Assembly: GCA_000012345.1 ^{Ts}	seqco.de/i:91

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		coupling to the ambient pool of labile dissolved organic matter.			