Methylopumilus planktonicus gen. nov. sp. nov.

Submitted by Salcher, Michaela M

Genus *Methylopumilus*

Etymology

[Me.thy.lo.pu.mi'lus] **N.L. neut. n.** *methyl*, pertaining to the methyl group; **L. masc. adj.** *pumilus*, dwarfish; **N.L. masc. n.** *Methylopumilus*, dwarfish methyl (group oxidizing) organism

Nomenclatural type

Species *Methylopumilus planktonicus*$^{\mathrm{Ts}}$

Description

Consists of three species, *Methylopumilus planktonicus* (GCF_000981505.1), *Methylopumilus universalis* (GCF_006363895.1), and *Methylopumilus rimovensis* (GCF_006364615.1), that were initially proposed as *Candidatus* taxa in Salcher et. al. 2015 and Salcher et al. 2019. Type species is *Methylopumilus planktonicus* MMS-2-53 (GCF_000981505.1). Also known as LD28 or betIV from 16S rRNA gene based studies. *Methylopumilus* are generally very small in cell size (<0.1 µm3) and genome size (<1.5 Mb), i.e., they are genome-streamlined. They are aerobic methylotrophs containing pathways for methanol oxidation (Xox) and the RuMP (ribulose monophosphate) cycle for formaldehyde assimilation/oxidation. The genomes contain genes encoding two rhodopsins (proteorhodopsin and xantho-like rhodopsin) and the biosynthetic pathway for retinal biosynthesis. No genes for flagellar or pilus assembly and chemotaxis were annotated in any so far sequenced genomes. *Methylopumilus* are abundant in the plankton of lakes with a global distribution. Most strains were so far isolated via dilution-to extinction cultivation by using either autoclaved lake water or a defined medium containing methanol and methylamine as sole carbon sources, no growth is observed in rich medium or on agar plates (Salcher et al. 2015, Salcher et al. 2019, Layoun et al. 2024). None of the isolated strains were yet submitted to a culture collection because these bacteria are hard to maintain, i.e., they are very slowly growing, reach low densities in liquid culture, and do not grow on agar plates.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Nitrosomonadales* » *Methylophilaceae* » *Methylopumilus*

References

Effective publication: Salcher et al., 2015 [1]
Emendavit: Salcher et al., 2019 [2]
Assigned taxonomically: Salcher et al., 2015 [1]

Registry URL

https://seqco.de/i:37730

Species *Methylopumilus planktonicus*^{Ts}

Etymology

[plan.kto'ni.cus] **N.L. masc. adj.** *planktonicus*, living in the plankton, planktonic; from Gr. masc. adj. planktos, wandering

Nomenclatural type

NCBI Assembly: GCF_000981505.1 ^{Ts}

Reference Strain

Strain scj0040319: MMS-2-53

Description

Type genome is *Methylopumilus planktonicus* MMS-2-53 (GCF_000981505.1), an axenic bacterial strain isolated by dilution-to-extinction cultivation from the water column of Lake Zurich, Switzerland. MMS-2-53 has a genome size of 1.35 Mb with a genomic GC content of 36.97%, contains 3 rRNA genes and 36 tRNAs. The genome is complete, consisting of 1 circular chromosome. *Methylopumilus planktonicus* are very tiny (0.041 µm3 during stationary growth phase and 0.075 µm3 during during exponential growth phase), aerobic, non-motile and methylotrophic. The genome contains genes encoding two rhodopsins (proteorhodopsin and xantho-like rhodopsin) and the biosynthetic pathway for retinal biosynthesis. No genes for flagellar or pilus assembly and chemotaxis were annotated. Pathways for methanol oxidation (Xox) and the RuMP cycle for methylotrophy and the biosynthesis of all amino acids were predicted. *Methylopumilus planktonicus* are abundant in the plankton of freshwater lakes with a world-wide distribution and a preference for lakes with a lower nutrient level than members of another species, *Methylopumilus universalis*. None of the isolated strains were yet submitted to a culture collection because these bacteria are hard to maintain, i.e., they are very slowly growing, reach low densities in liquid culture, and do not grow on agar plates.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Nitrosomonadales* » *Methylophilaceae* » *Methylopumilus* » *Methylopumilus planktonicus*^{Ts}

References

Effective publication: Salcher et al., 2015 [1]

Registry URL

https://seqco.de/i:41787

References

1. Salcher et al. (2015). The ecology of pelagic freshwater methylotrophs assessed by a high-resolution monitoring and isolation campaign. *The ISME Journal*. DOI:10.1038/ismej.2015.55
2. Salcher et al. (2019). Evolution in action: habitat transition from sediment to the pelagial leads to genome streamlining in Methylophilaceae. *The ISME Journal*. DOI:10.1038/s41396-019-0471-3

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:vc1ok6m8** submitted by **Salcher, Michaela M** and including 2 new names has been successfully validated.

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