Register list for 5 new names including Methylophilus medardensis sp. nov.

Submitted by Salcher, Michaela M

Genus *Methylosemipumilus*

Etymology

[Me.thy.lo.se.mi.pu.mi'lus] **N.L. neut. n.** *methyl*, pertaining to the methyl group; **L. pref.** *semi-*, half; **L. masc. n.** *pumilus*, dwarfish; **N.L. masc. n.** *Methylosemipumilus*, half-dwarfish methyl (group oxidizing) organism, pertaining to an intermediated genome size

Nomenclatural type

Species *Methylosemipumilus turicensis*$^{\mathrm{Ts}}$

Description

Consists of one species, *Methylosemipumilus turicensis* (GCF_000953015.1), that was initially proposed as '*Candidatus* Methylopumilus turicensis' in Salcher et. al. 2015 and later changed to *Methylosemipumilus turicensis* in Salcher et al. 2019. Also known as PRD01a001B from 16S rRNA gene based studies. *Methylosemipumilus* has a relatively small genome size (<1.8 Mb) but not as small as *Methylopumilus* (1.3-1.4 Mb), which – together with improved genomic analyses – led to the reclassification to *Methylosemipumilus*. The closest cultivated relatives are *Methylotenera* sp. L2L1 (GCF_000744605.1) with an average amino acid identity of 67.45% and average nucleotide identity of 70.55% and *Methylovorus* sp. MP688 (GCF_000183115.1) with an AAI of 69.37% and an ANI of 69.42%, while the genus Methylopumilus is more distantly related (AAI of 61.5-62.2% and ANI of 66.4-66.9%). *Methylosemipumilus* are aerobic methylotrophs containing pathways for methanol oxidation (Xox), the RuMP cycle and the tetrahydromethanopterin (H4MPT) pathway for formaldehyde oxidation. *Methylosemipumilus* are found in the plankton of lakes in relatively low abundances. The so far only strain was isolated via dilution-to extinction cultivation by using autoclaved lake water, no growth is observed in rich medium or on agar plates (Salcher et al. 2015). Therefore, the strain was not 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* » *Methylosemipumilus*

References

Effective publication: Salcher et al., 2019 [1]
Original (not valid) publication: Salcher et al., 2015 [2]
Corrigendum: Salcher et al., 2019 [1] (from "Candidatus Methylopumilus")
Assigned taxonomically: Salcher et al., 2019 [1]

Registry URL

https://seqco.de/i:49942

Species *Methylophilus medardensis*

Etymology

[me.dar.den'sis] **N.L. masc. adj.** *medardensis*, pertaining to Lake Medard (Czechia), the isolation source of the type strain.

Nomenclatural type

NCBI Assembly: GCF_006363915.1 Ts

Reference Strain

Strain sc|0038982: MMS-M-51

Description

Type genome is *Methylophilus medardensis* MMS-M-51 (GCF_006363915.1), that was isolated by dilution-to-extinction cultivation from the water column of Lake Medard, Czechia. MMS-M-51 has a genome size of 2.6 Mb with a genomic GC content of 49.8%, contains 6 rRNA genes and 42 tRNAs. The genome is complete, consisting of 1 circular chromosome. The closest cultivated relatives are *Methylophilus* sp. Q8 (GCF_000800115.1) with an average amino acid identity of 85.53% and average nucleotide identity of 78.73% and *Methylophilus* sp. OH31 (GCF_000576615.1) with an AAI of 85.28% and an ANI of 78.71%.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Nitrosomonadales* » *Methylophilaceae* » *Methylophilus* » *Methylophilus medardensis*

References

Effective publication: Salcher et al., 2019 [1]

Registry URL

https://seqco.de/i:39350

Species *Methylopumilus rimovensis*

Etymology

[ri.mo.ven'sis] **N.L. masc. adj.** *rimovensis*, pertaining to the Římov Reservoir, Czech Republic, the isolation source of the species.

Nomenclatural type

NCBI Assembly: GCF_006364615.1 Ts

Reference Strain

Strain sc|0038980: MMS-RI-1

Description

Type genome is *Methylopumilus rimovensis* MMS-RI-1 (GCF_006364615.1), an axenic bacterial strain isolated by dilution-to-extinction cultivation from the water column of the Římov Reservoir (Czechia). MMS-RI-1 has a genome size of 1.28 Mb with a genomic GC content of 36.7%, contains 3 rRNA genes and 37 tRNAs. The genome is complete, consisting of 1 circular chromosome. *Methylopumilus rimovensis* are very small, 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 rimovensis* are highly abundant only in their isolation source (the Římov Reservoir in Czechia) and recorded in very low abundances in other freshwater lakes, which contrasts with members of other species of the genus that have a global distribution (*Methylopumilus planktonicus* and *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 rimovensis*

References

Effective publication: Salcher et al., 2019 [1]

Registry URL

https://seqco.de/i:42658

Species *Methylopumilus universalis*

Etymology

[u.ni.ver.sa'lis] **L. adj. masc.** *universalis*, universal, pertaining to the widespread distribution of the species

Nomenclatural type

NCBI Assembly: GCF_006363895.1 Ts

Reference Strain

Strain sc|0038979: MMS-RVI-51

Description

Type genome is *Methylopumilus universalis* MMS-RVI-51 (GCF_006363895.1), an axenic bacterial strain isolated by dilution-to-extinction cultivation from the water column of the Římov Reservoir (Czechia). MMS-RVI-51 has a genome size of 1.27 Mb with a genomic GC content of 37.2%, contains 3 rRNA genes and 36 tRNAs. The genome is complete, consisting of 1 circular chromosome. *Methylopumilus universalis* are very small, 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 universalis* are abundant in the plankton of freshwater lakes with a world-wide distribution and a preference for lakes with a higher nutrient level than members of another species, *Methylopumilus planktonicus*. 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 universalis*

References

Effective publication: Salcher et al., 2019 [1]

Registry URL

https://seqco.de/i:41611

Species *Methylosemipumilus turicensis*^{Ts}

Etymology

[tu.ri.cen'sis] **N.L. masc. adj.** *turicensis*, referring to Turicum, the latin name of Zurich, pertaining to Lake Zurich, the isolation source of the type strain

Nomenclatural type

NCBI Assembly: GCF_000953015.1 Ts

Reference Strain

Strain sc|0038981: MMS-10A-171

Description

Type genome is *Methylosemipumilus turicensis* MMS-10A-171 (GCF_000953015.1)*,* that was initially proposed as '*Candidatus* Methylopumilus turicensis' in Salcher et. al. 2015 and later changed to *Methylosemipumilus turicensis* in Salcher et al. 2019. The strain was isolated by dilution-to-extinction cultivation from the water column of Lake Zurich, Switzerland. MMS-10A-171 has a genome size of 1.76 Mb with a genomic GC content of 44.52%, contains 6 rRNA genes and 40 tRNAs. The genome is complete, consisting of 1 circular chromosome. *Methylosemipumilus turicensis* MMS-10A-171 has a relatively small genome size (1.76 Mb) but not as small as *Methylopumilus* (1.3-1.4 Mb), which – together with improved genomic analyses – led to the reclassification to *Methylosemipumilus*. The genome contains genes encoding proteorhodopsins and the biosynthetic pathway for retinal biosynthesis. Pathways for methanol oxidation (Xox), the ribulose monophosphate (RuMP) cycle and the tetrahydromethanopterin (H4MPT) pathway for formaldehyde oxidation were predicted. The closest cultivated relatives are *Methylotenera* sp. L2L1 (GCF_000744605.1) with an average amino acid identity of 67.45% and average nucleotide identity of 70.55% and *Methylovorus* sp. MP688 (GCF_000183115.1) with an AAI of 69.37% and an ANI of 69.42%, while the genus *Methylopumilus* is more distantly related (AAI of 61.5-62.2% and ANI of 66.4-66.9%).

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Nitrosomonadales* » *Methylophilaceae* » *Methylosemipumilus* » *Methylosemipumilus turicensis*^{Ts}

References

Effective publication: Salcher et al., 2019 [1]
Original (not valid) publication: Salcher et al., 2015 [2]
Corrigendum: Salcher et al., 2019 [1] (from "Candidatus Methylopumilus turicensis")
Assigned taxonomically: Salcher et al., 2019 [1]

Registry URL

https://seqco.de/i:44148

References

1. 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
2. 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

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:y_q1qhwb** submitted by **Salcher, Michaela M** and including 5 new names has been successfully validated.

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