Register list for Patescibacterium danicum gen. nov. sp. nov. and their lineage

Submitted by Rinke, Chris

Phylum Patescibacteriota

Etymology

[Pa.tes.ci.bac.te.ri.o'ta] **N.L.** *Patescibacterium*, type genus of the phylum; *-ota*, ending to denote a phylum; **N.L. neut. pl. n.** *Patescibacteriota*, the Patescibacterium phylum

Nomenclatural type

Genus Patescibacterium

Description

The phylum represents a monophyletic lineage based on the concatenated phylogeny of 120 protein markers and contains the class *Patescibacteriia*. This phylum is characterized by members with a low genomic GC content (33.6 \pm 6.7%), reduced genome sizes (919.3 kbp \pm 256 kbp) and limited metabolic capabilities, that are likely to rely on symbiotic partners for survival. The type genus is *Patescibacterium*.

Classification

Bacteria » Patescibacteriota

References

Effective publication: Dutkiewicz et al., 2025 [1] Original (not valid) publication: Rinke et al., 2013 [2] Assigned taxonomically: Dutkiewicz et al., 2025 [1]

Registry URL

https://seqco.de/i:48240

Class Patescibacteriia

Etymology

[Pa.tes.ci.bac.te.ri'ia] **N.L. neut. n.** *Patescibacterium*, type genus of the class; *-ia*, ending to denote a class; **N.L. neut. pl. n.** *Patescibacteriia*, the Patescibacterium class

Nomenclatural type

Genus Patescibacterium

Description

The class represents a monophyletic lineage based on the concatenated phylogeny of 120 protein markers and contains the order Patescibacteriales. The description of the class is the same as for the order Patescibacteriales. The type genus is Patescibacterium.

Classification

Bacteria » Patescibacteriota » Patescibacteriia

References

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

Registry URL

https://seqco.de/i:49186

Order Patescibacteriales

Etymology

[Pa.tes.ci.bac.te.ri.a'les] **N.L. neut. n.** *Patescibacterium*, type genus of the order; *-ales*, ending to denote an order; **N.L. fem. pl. n.** *Patescibacteriales*, the Patescibacterium order

Nomenclatural type

Genus Patescibacterium

Description

The order represents a monophyletic lineage based on the concatenated phylogeny of 120 protein markers and contains the family Patescibacteriaceae. The description of the order is the same as for the family Patescibacteriaceae. The type genus is Patescibacterium.

Classification

Bacteria » Patescibacteriota » Patescibacteriia » Patescibacteriales

References

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

Registry URL

https://segco.de/i:49185

Family Patescibacteriaceae

Etymology

[Pa.tes.ci.bac.te.ri.a.ce'ae] **N.L. neut. n.** *Patescibacterium*, type genus of the family; *-aceae*, ending to denote a family; **N.L. fem. pl. n.** *Patescibacteriaceae*, the Patescibacterium family

Nomenclatural type

Genus Patescibacterium

Description

The family represents a monophyletic lineage based on the concatenated phylogeny of 120 protein markers and contains the genus Patescibacterium. The description of the family is the same as for its type genus Patescibacterium.

Classification

Bacteria » Patescibacteriota » Patescibacteria » Patescibacteriales » Patescibacteriaceae

References

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

Registry URL

https://seqco.de/i:49184

Genus Patescibacterium

Etymology

[Pa.tes.ci.bac.te'ri.um] **L. verb.** patesco, to become visible, bare; **N.L. neut. n.** bacterium, rod; **N.L. neut. n.** Patescibacterium, bare bacterium

Nomenclatural type

Species Patescibacterium danicum^{Ts}

Description

The description of the genus is based on the single species which is characterized by a small genome size below 1 Mbp and inferred to lack nucleotide and amino acid synthesis, which is compensated by encoded DNA uptake and peptide cleaving abilities. The lack of a pentose phosphate pathway (PPP) and a complete tricarboxylic acid (TCA) cycle leaves anaerobic glycolysis, albeit without the key enzyme phosphofructokinase-1 (PFK-1), as a means of energy conservation.

The type species of the genus is Patescibacterium danicum, obtained from the Mariagerfjord WWTP in Denmark.

Classification

Bacteria » Patescibacteriota » Patescibacteriia » Patescibacteriales » Patescibacteriaceae » Patescibacterium

References

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

Registry URL

https://seqco.de/i:48242

Species Patescibacterium danicum^{Ts}

Etymology

[da'ni.cum] **N.L. neut. adj.** danicum, Danish, named after Denmark, the country from which the type genome originates.

Nomenclatural type

NCBI Assembly: GCA 016699775.1 Ts

Description

The species is represented by the metagenome-assembled genome (MAG) sequence ABY1, available in GTDB as GCA_016699775.1, obtained from metagenomic sequences from Mariagerfjord WWTP; Denmark. ABY1 represents a complete, single-contig genome of 938,851 bp, with a GC content of 35.4%, a coding density of 88.17% and a protein count of 890. ABY1 encodes one 5S, 16S, and 23S ribosomal RNA gene and 41 tRNAs.

Classification

Bacteria » Patescibacteriota » Patescibacteriia » Patescibacteriales » Patescibacterium » Patescibacterium danicum^{Ts}

References

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

Registry URL

https://seqco.de/i:48241

References

- 1. Dutkiewicz et al. (2025). Proposal of *Patescibacterium danicum* gen. nov., sp. nov. in the ubiquitous bacterial phylum *Patescibacteriota* phyl. nov. *ISME Communications*. DOI:10.1093/ismeco/ycae147
- 2. Rinke et al. (2013). Insights into the phylogeny and coding potential of microbial dark matter. *Nature*. DOI:10.1038/nature12352

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:gs62mgo0** submitted by **Rinke, Chris** and including 6 new names has been successfully validated.

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