Register list for Desulfocorpusculum asiaticum gen. nov. sp. nov. and their lineage

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Class *Desulfocorpusculia*

Etymology
[De.sul.fo.cor.pus.cu'li.a] **N.L. neut. n.** *Desulfocorpusculum*, type genus of the class; *-ia*, ending to denote a class; **N.L. neut. pl. n.** *Desulfocorpusculia*, the class of the genus Desulfocorpusculum

Nomenclatural type
Genus *Desulfocorpusculum*

Description
The class description is identical to that of the family *Desulfocorpusculaceae*.

Classification
Bacteria » *Desulfobacterota* » *Desulfocorpusculia*

References
Effective publication: Slobodkina et al., 2025 [1]

Registry URL
https://seqco.de/i:49949

Order *Desulfocorpusculales*

Etymology
[De.sul.fo.cor.pus.cu.la'les] **N.L. neut. n.** *Desulfocorpusculum*, type genus of the order; *-ales*, ending to denote an order; **N.L. fem. pl. n.** *Desulfocorpusculales*, the order of the genus Desulfocorpusculum

Nomenclatural type
Genus *Desulfocorpusculum*

Description
The order description is identical to that of the family *Desulfocorpusculaceae*.

Classification
Bacteria » *Desulfobacterota* » *Desulfocorpusculia* » *Desulfocorpusculales*

References
Effective publication: Slobodkina et al., 2025 [1]

Registry URL
https://seqco.de/i:49948

Family *Desulfocorpusculaceae*

Etymology

[De.sul.fo.cor.pus.cu.la'ce.ae] **N.L. neut. n.** *Desulfocorpusculum*, type genus of the family; -*aceae*, ending to denote a family; **N.L. fem. pl. n.** *Desulfocorpusculaceae*, the family of the genus Desulfocorpusculum

Nomenclatural type

Genus *Desulfocorpusculum*

Description

Desulfocorpusculaceae is a family of yet uncultured bacteria of the phylum *Desulfobacterota*. In addition to MAGs of the genus *Desulfocorpusculum*, this family also includes MAGs from hot springs of USA: Yellowstone (GCA_028275295.1), California (GCA_964514105.1); as well as from hot springs of Canada (GCA_964583655.1) and from Pacific Ocean hydrothermal fluid (GCA_002010915.1). This family is designated as f__JdFR-97 in GTDB R226.

Classification

Bacteria » *Desulfobacterota* » *Desulfocorpusculia* » *Desulfocorpusculales* » *Desulfocorpusculaceae*

References

Effective publication: Slobodkina et al., 2025 [1]

Registry URL

https://seqco.de/i:49947

Genus *Desulfocorpusculum*

Etymology

[De.sul.fo.cor.pus'cu.lum.] **N.L. pref.** *desulfo-*, desulfuricating; **L. neut. n.** *corpusculum*, a little body, a particle; **N.L. neut. n.** *Desulfocorpusculum*, a sulfate-reducing bacterium

Nomenclatural type

Species *Desulfocorpusculum asiaticum*$^{\mathrm{Ts}}$

Description

Desulfocorpusculum is a genus of yet uncultured bacteria of the phylum *Desulfobacterota*. In addition to *Desulfocorpusculum asiaticum* U4-17, this genus also includes MAGs from hot springs of Costa Rica (GCA_037443445.1) and Canada (GCA_964414345.1). This genus is designated as g__JBBFLE01 in GTDB R226.

Classification

Bacteria » *Desulfobacterota* » *Desulfocorpusculia* » *Desulfocorpusculales* » *Desulfocorpusculaceae* » *Desulfocorpusculum*

References

Effective publication: Slobodkina et al., 2025 [1]

Registry URL

https://seqco.de/i:49946

Species *Desulfocorpusculum asiaticum*^{Ts}

Etymology

[a.si.a'ti.cum] **N.L. neut. adj.** *asiaticum*, Asiatic, of Asia

Nomenclatural type

INSDC Nucleotide: JBNGEK000000000.1 ^{Ts}

Description

Desulfocorpusculum asiaticum U4-17 is presented by high-quality draft metagenome-assembled genome (MAG) of a member of the phylum *Desulfobacterota*, that was assembled from thermophilic microbial community from a hot stream formed by discharge of thermal artesian groundwater in Navoiy region (Republic of Uzbekistan).

The MAG has genes of the rod-shaped determining proteins, chemotaxis and the flagellar machinery required for motility. The genes essential for sporulation are absent. Encodes for the complete Embden-Meyerhof-Parnas and Wood-Ljungdahl pathways, non-oxidative branch of the pentose-phosphate pathway, pyruvate oxidation, the fatty acids β-oxidation and tricarboxylic acid cycle. Harbors genes involved in dissimilatory sulfate reduction (Sat-AprAB-DsrABC) including corresponding electron-transport complexes. Has only scant genes related to nitrogen metabolism. A complete electron transport chain is encoded including cytochromes oxidases as well as F-type H+/Na+- transporting ATPase.

The 16S rRNA-based analysis revealed that U4-17 is very distantly related to any of the known bacteria. The closest relative species were *Geobacter benzoatilyticus* Jerry-YXT (87.9% identity), *Syntrophus aciditrophicus* SBT (87.6%) and *Desulfococcus multivorans* 1be1T (87.4%), which belong to different classes of the phylum *Desulfobacterota*: *Desulfuromonadia*, *Syntrophia* and *Desulfobacteria*, respectively (Waite et al., 2020).

The results of phylogenomic reconstruction based on 120 single copy marker genes according to Parks et al., 2020 (bac120), but with much larger alignment length (20,331 aa), confirmed that the U4-17 with several MAGs form a phylogenetic cluster highly distant from other classes of *Desulfobacterota*.

120tree-U4-17.pdf 48.8 KB

Classification

Bacteria » *Desulfobacterota* » *Desulfocorpusculia* » *Desulfocorpusculales* » *Desulfocorpusculaceae* » *Desulfocorpusculum* » *Desulfocorpusculum asiaticum*^{Ts}

References

Effective publication: Slobodkina et al., 2025 [1]

Registry URL

https://seqco.de/i:49945

References

1. Slobodkina et al. (2025). Taxonomic and metabolic diversity of microbial communities in a thermal water stream in Uzbekistan and proposal of two new classes of uncultivated bacteria, Desulfocorpusculia class. nov. and Tepidihabitantia class. nov., named following the rules of SeqCode. *Systematic and Applied Microbiology*. DOI:10.1016/j.syapm.2025.126650

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:mfkhvkkb** submitted by **Merkel, Alexander** and including 5 new names has been successfully validated.

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