

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](https://doi.org/10.1016/j.syapm.2025.126650)