

Species *Bathyarchaeum tardum*^{Ts}

Etymology

[tar'dum] L. neut. adj. *tardum*, slow, referring to its slow growth

Nomenclatural type

[INSDC Nucleotide: CP122380.1](#)^{Ts}

Description

According to our phylogenomic reconstruction based on 122 archaeal single copy conserved marker genes (Parks et al., 2018) *Bathyarchaeum tardum* is a part of BIN-L-1 genus-level lineage (Figure 1) which belongs to the BA1 family-level lineage and B26-1 order-level lineage according to GTDB (Parks et al., 2018). B26-1 group is formerly referred to as Bathy-8 (Yu et al., 2017). The phylogenetic position of *Bathyarchaeum tardum* revealed by 16S rRNA gene-based phylogenetic reconstruction agrees well with the phylogenomic data (Figure 2).

[SeqCode_Figure_2.pdf](#) 40.9 KB

[SeqCode_Figure_1.pdf](#) 39.7 KB

Description of *Bathyarchaeum tardum*

Cells are small, non-motile cocci, with a diameter of 0.4-0.7 µm. Occasionally forms chains of 3-5 cells covered by a common sheath. The cytoplasmic membrane is surrounded by an S-layer. Strictly anaerobic. Mesophilic. Grows at 10–45°C (optimum 37°C), at pH 6.0–10.0 (optimum 8.0) and at NaCl concentrations of 0–60 g l⁻¹ (optimum 20 g l⁻¹). Grows on 3,4-dimethoxybenzoic acid, vanillate in the presence of yeast extract, casamino acids or soytone. Does not utilize glucose, fructose, sucrose, lactate, pyruvate, lignin, chitin, peptone, tryptone, casein, cellulose, formate, methanol, benzoate, 3,4-dihydroxybenzoate, 2-methoxyphenol, 2-methoxybenzoate, molecular hydrogen and carbon monoxide. Dimethyl sulfoxide and nitrate stimulate growth, while oxygen, elemental sulfur, carbon monoxide and molecular hydrogen inhibit growth. Does not reduce sulfate, thiosulfate, antraquinone-2,6-disulfonate, selenate, selenite, arsenate, Fe(III)-citrate elemental sulfur, sulfite, nitrite or oxygen. Growth depends on addition of sterile natural sediment. The complete genome of strain M17C, available under the GenBank assembly accession number (CP122380Ts) is the designated nomenclatural type for the species and was recovered from an enrichment culture, cultivated on 3,4-dimethoxybenzoic acid and established from the anaerobic sediment of a coastal lake at the Taman Peninsula, Russian Federation. The genome has the size of 2.15 Mb and a G + C content of 38.1%. Completeness is estimated by CheckM at 98.28% with 0.934% contamination. *Bathyarchaeum tardum* is also presented by high-quality MAG M17C-73-01 (GCA_029762755.1; Genome size – 2139529bp, # of contigs – 12, completeness - 97.82%, contamination - 0.934%). Both MAGs have identical full-length 16S rRNA genes and ANI value between MAGs is 99.31%. With the other MAGs of the *Bathyarchaeum* genus, which were included in this genus based on our phylogenetic reconsideration (Figure 1), they have an ANI value no higher than 84.5%.

Classification

Archaea » “Bathyarchaeota” » *Bathyarchaeia* » *Bathyarchaeales* » *Bathyarchaeaceae* » *Bathyarchaeum* » *Bathyarchaeum tardum*^{Ts}

References

Effective publication: Khomyakova et al., 2023 [1]

Registry URL

<https://seqco.de/i:31303>

References

1. Khomyakova et al. (2023). Phenotypic and genomic characterization of *Bathyarchaeum tardum* gen. nov., sp. nov., a cultivated representative of the archaeal class Bathyarchaeia. *Frontiers in Microbiology*.
[DOI:10.3389/fmicb.2023.1214631](https://doi.org/10.3389/fmicb.2023.1214631)