

# Bathyarchaeum tardum gen. nov., sp. nov., a cultivated representative of the archaeal class Bathyarchaeia

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**Table 1:** Complete list of names proposed in the current register list.

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Class <i>Bathyarchaeia</i>	[Ba.thy.ar.chae'i.a] <b>N.L. neut. n.</b> <i>Bathyarchaeum</i> , type genus of the class; <i>-ia</i> , ending to denote a class; <b>N.L. neut. pl. n.</b> <i>Bathyarchaeia</i> , class of the genus <i>Bathyarchaeum</i>	GTDB 207 support delineation of the class <i>Bathyarchaeia</i> (c__Bathyarchaeia) with RED being equal to 0.514. The nomenclatural type of the class is the genus <i>Bathyarchaeum</i>	<i>Bathyarchaeota</i>	<i>Bathyarchaeum</i>	<a href="https://seqco.de/i:707">seqco.de/i:707</a>
Order <i>Bathyarchaeales</i>	[Ba.thy.ar.chae.a'les] <b>N.L. neut. n.</b> <i>Bathyarchaeum</i> , type genus of the order; <i>-ales</i> , ending denoting an order; <b>N.L. fem. pl. n.</b> <i>Bathyarchaeales</i> , order of the genus <i>Bathyarchaeum</i> , type genus of the order	Our phylogenomic reconstruction (Figure 1) as well as the phylogenomic reconstruction of GTDB 207 support delineation of the order <i>Bathyarchaeales</i> . RED in the phylogenomic reconstruction of GTDB 207 for the order <i>Bathyarchaeales</i> (o_B26-1) is 0.514. The nomenclatural type of the order is the genus <i>Bathyarchaeum</i>  <a href="#">SeqCode_Figure_1.pdf 39.7 KB</a>	<i>Bathyarchaeia</i>	<i>Bathyarchaeum</i>	<a href="https://seqco.de/i:31312">seqco.de/i:31312</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Family <i>Bathyarchaeaceae</i>	[Ba.thy.ar.chae.a.ce'ae] <b>N.L. neut. n.</b> <i>Bathyarchaeum</i> , type genus of the family; - <i>aceae</i> , ending to denote a family; <b>N.L. fem. pl. n.</b> <i>Bathyarchaeaceae</i> , family of the genus <i>Bathyarchaeum</i>	Our phylogenomic reconstruction (Figure 1) as well as the phylogenomic reconstruction of GTDB 207 support delineation of the family <i>Bathyarchaeaceae</i> . RED in the phylogenomic reconstruction of GTDB 207 for the family <i>Bathyarchaeaceae</i> (f__BA1) is 0.691. AAI values range between 59.6 and 70.8% among members of different genera of this family. The nomenclatural type of the family is the genus <i>Bathyarchaeum</i> .  <a href="#">SeqCode_Figure_1.pdf 39.7 KB</a>	<i>Bathyarchaeales</i>	<i>Bathyarchaeum</i>	<a href="https://seqco.de/i:31311">seqco.de/i:31311</a>
Genus <i>Bathyarchaeum</i>	[Ba.thy.ar.chae'um] <b>Gr. masc. adj. bathys</b> , deep as it locates deep phylogenetic branching within Archaea; <b>N.L. neut. n. archaeum</b> , ancient one, archaeon; from Gr. masc. adj. archaios, ancient; <b>N.L. neut. n. Bathyarchaeum</b> , deeply-branched archaeon	High-quality MAGs of this genus have been assembled from enrichment cultures with 3,4-dimethoxybenzoic acid inoculated from anaerobic sediment of a coastal lake at the Taman Peninsula, from enrichment cultures with lignin inoculated from coastal sediments of northern East China Sea, from deep sea sediments associated with petroleum seepage (Atlantic Ocean) and from sediment of high-sulfide freshwater Zodletone spring (Oklahoma, USA). Based on 16S rRNA gene sequence data microorganisms of this genus were often found in the marine sediments associated with the presence of terrigenous organic matter, e. g. terrigenous deposits, estuary (Li et al., 2012), sunken woods (Fagervold et al., 2012) and in ecotopes associated with methane seepages, e. g. hydrate-bearing sediments (Dang et al., 2009), cold seep sediment (Li et al., 1999), mud volcanoes (Cheng et al., 2012). AAI values among genomes representing separate species within the genus range between 71.87% and 83.83%. Our phylogenomic reconstruction (Figure 1) based on 122 archaeal single copy conserved marker genes (Parks et al., 2018) as well as phylogenomic reconstruction of GTDB 207 support delineation of the genus <i>Bathyarchaeum</i> . The Relative Evolutionary Divergence (RED) in the phylogenomic reconstruction of GTDB 207 for the genus <i>Bathyarchaeum</i> (g__BIN-L-1) is 0.931. The nomenclatural type of the genus is <i>Bathyarchaeum tardum</i>  <a href="#">SeqCode_Figure_1.pdf 39.7 KB</a>	<i>Bathyarchaeaceae</i>	<i>Bathyarchaeum tardum</i> <sup>Ts</sup>	<a href="https://seqco.de/i:31304">seqco.de/i:31304</a>
		According to our phylogenomic reconstruction based on 122 archaeal single copy conserved marker genes (Parks et al., 2018) <i>Bathyarchaeum tardum</i> is a part of BIN-L-1 genus-level lineage (Figure 1) which belongs to the BA1			

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Species <i>Bathyarchaeum tardum</i> <sup>Ts</sup>	[tar'dum] L. neut. adj. <i>tardum</i> , slow, referring to its slow growth	<p>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).</p> <p>The phylogenetic position of <i>Bathyarchaeum tardum</i> revealed by 16S rRNA gene-based phylogenetic reconstruction agrees well with the phylogenomic data (Figure 2).</p> <p><a href="#">SeqCode_Figure_2.pdf 40.9 KB</a></p> <p><a href="#">SeqCode_Figure_1.pdf 39.7 KB</a></p> <p><b>Description of <i>Bathyarchaeum tardum</i></b> 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<sup>-1</sup> (optimum 20 g l<sup>-1</sup>). 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, anthraquinone-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. <i>Bathyarchaeum tardum</i> 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 <i>Bathyarchaeum</i> genus, which were included in this genus based on our phylogenetic reconsideration (Figure 1), they have an ANI value no higher than 84.5%.</p>	<i>Bathyarchaeum</i>	INSDC Nucleotide: CP122380.1 <sup>Ts</sup>	<a href="https://seqco.de/i:31303">seqco.de/i:31303</a>