

Genus *Bathyarchaeum*

Etymology

[Ba.thy.ar.chae'um] Gr. masc. adj. *bathys*, deep as it locates deep phylogenetic branching within Archaea; N.L. neut. n. *archaeum*, ancient one, archaeon; from Gr. masc. adj. *archaios*, ancient; N.L. neut. n. *Bathyarchaeum*, deeply-branched archaeon

Nomenclatural type

Species *Bathyarchaeum tardum*^{Ts}

Description

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 *Bathyarchaeum*. The Relative Evolutionary Divergence (RED) in the phylogenomic reconstruction of GTDB 207 for the genus *Bathyarchaeum* (g_BIN-L-1) is 0.931.

The nomenclatural type of the genus is *Bathyarchaeum tardum*

[SeqCode_Figure_1.pdf 39.7 KB](#)

Classification

Archaea » "Bathyarchaeota" » *Bathyarchaeia* » *Bathyarchaeales* » *Bathyarchaeaceae* » *Bathyarchaeum*

References

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

Registry URL

<https://seqco.de/i:31304>

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)