## Species *Tepidihabitans asiaticus*$^{Ts}$

**Etymology**

[a.si.a'ti.cus] **N.L. masc. adj.** *asiaticus*, pertaining to Asia

**Nomenclatural type**

INSDC Nucleotide: JBBFKS000000000.1 $^{Ts}$

**Description**

Tepidihabitans asiaticus U4-05 is presented by high-quality draft metagenome-assembled genome (MAG) of a member of the *Hydrothermota* (p__WOR-3) phylum, that was assembled from thermophilic microbial community from a hot stream formed by discharge of thermal artesian groundwater in Navoiy region (Republic of Uzbekistan). This microorganism represents 5% of the microbial community developing in the sediments under the ginger mat at a temperature of 54°C.

The results of the bac120-based phylogenomic analysis confirmed that the U4-05 is a part of candidate division WOR-3 ("Candidatus Hydrothermota" according to LPSN) and, along with many MAGs, forms a separate phylogenetic cluster at the class level, which is designated as c__WOR-3 according to GTDB (Fig). This cluster is sister to "Candidatus Hydrothermia", to which the recently described pure culture sy37 (Mori et al., 2025), “Candidatus Hydrothermus pacificus” (Chuvochina et al. 2019), "Candidatus Caldipriscus" and "Candidatus Thermoproauctor" (Colman et al., 2016) belong. Analysis of the distribution of U4-05-related phylotypes shows that they are found in hot springs and thermophilic bioreactors, can occupy a significant part of the community (6-8%) and prefer moderately thermophilic conditions, neutral pH and abundance of complex organic matter.

The MAG has genes for the complete Embden-Meyerhof-Parnas pathway, non-oxidative branch of the pentose-phosphate pathway and the fatty acids β-oxidation. Has only scant genes related to motility. Genes encoding most components of the tricarboxylic acid cycle are absent. Has no genes for CO2 fixation. Genes encoding components of the aerobic respiratory chain, and the $F_0F_1$-type $H^+$-transporting ATP synthase are absent. The genome encodes the Rnf electron-transporting complex and subunits of a V-type ATP synthase. On the basis of genome analysis, U4-05 is predicted to be an anaerobic heterotrophic bacterium with fermentative metabolism. The presence of the Rnf electron-transporting complex and subunits of a V-type ATP synthase may support ion gradient generation and ATP synthesis in the absence of a conventional electron transport chain.

Fig.pdf 46.7 KB

**Classification**

*Bacteria* » “Hydrothermota” » *Tepidihabitantia* » *Tepidihabitantales* » *Tepidihabitantaceae* » *Tepidihabitans* » *Tepidihabitans asiaticus*$^{Ts}$

**References**

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

**Registry URL**

https://seqco.de/i:51333

## 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