

Genus *Benthortus*

Etymology

[Benth'or.tus] Gr. n. *benthos*, deep water; L. masc. perf. part. *ortus*, risen; N.L. masc. n. *Benthortus*, risen from deep water

Nomenclatural type

Species *Benthortus lauensis*^{TS}

Description

The genome of the current sole member of this genus was recovered from metagenomic sequencing data of hydrothermal vent communities present in the Lau Basin in the Western Pacific ocean. AAI values among this genus and closely related genera range between 50 and 57 %. Ancestral state reconstruction analysis indicated likely acquisitions of multiple copies of genes encoding methylmalonyl-CoA mutase (McmA1/2), NO-forming nitrite reductase (NirK), and cytochrome C oxidase subunit III (CoxC), and one copy of genes encoding nitrous-oxide reductase (NosZ) and aerobic carbon-monoxide dehydrogenase large subunit (CoxL), each. The tungsten (Tup) transporter substrate-binding subunit A, is encoded by the genome representative of this genus, and the AOR- and FOR-like encoding genes conserved within the family are also present in this genus. The presence of several cytochrome C oxidase subunits and the aerobic carbon-monoxide dehydrogenase large subunit indicate likely capacity for aerobic respiration within the genus. A sulfide:quinone oxidoreductase (*sqr*) gene is present in the genome and also indicates likely sulfide-dependent respiration within the genus. This genus is supported as distinct and exclusive based on phylogenomics, AAI and RED, and is part of the family *Wolframiiaptoraceae*.

Classification

Incertae sedis (Archaea) » "Caldarchaeales" » *Wolframiiaptoraceae* » *Benthortus*

References

Effective publication: Buessecker et al., 2022 [1]

Registry URL

<https://seqco.de/i:22821>

References

1. Buessecker et al. (2022). An essential role for tungsten in the ecology and evolution of a previously uncultivated lineage of anaerobic, thermophilic Archaea. *Nature Communications*. DOI:10.1038/s41467-022-31452-8