

Family *Wolframiiaptoraceae*

Etymology

[Wolf.ra.mi.i.rap.to.ra.ce'ae] N.L. masc. n. *Wolframiiaptor*, type genus of the family; *-aceae*, ending to denote a family; N.L. fem. pl. n. *Wolframiiaptoraceae*, family of the genus *Wolframiiaptor*

Nomenclatural type

Genus *Wolframiiaptor*

Description

Members of this family are associated with thermal aquatic environments, and have been identified from geothermal springs in China, New Zealand and the USA, and a marine hydrothermal vent in the Western Pacific. Phylogenomic inference robustly recovers the genomes of these organisms as a well-supported monophyletic lineage within the order *Caldarchaeales*, and delineation of these taxa as a family is supported by Relative Evolutionary Divergence (RED) and Average Amino Acid Identity (AAI). AAI values among designated type genomes for species in this family range between 65 and 85 % within proposed genera, and between 49 and 57 % among members of different genera. The distribution of genes required for oxidative phosphorylation indicate that members of the family may either be strict or facultative anaerobes. Sulfide-dependent respiration may also occur in some members of the family, but this trait is not conserved for all genera. Several putative tungsten-dependent ferredoxin oxidoreductases, specifically aldehyde ferredoxin oxidoreductases (AORs), formaldehyde ferredoxin oxidoreductases (FORs) and glyceraldehyde-3-phosphate ferredoxin oxidoreductases (GAPORs) are encoded by genomes belonging to this family.

Classification

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

References

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

Registry URL

<https://seqco.de/i:22818>

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