

Thiohalomonadaceae fam. nov.

Sorokin, Dimitry Y.; Merkel, Alexander Y.

Publication date
2023

Published in
Bergey's Manual of Systematics of Archaea and Bacteria

Citation (APA)
Sorokin, D. Y., & Merkel, A. Y. (2023). Thiohalomonadaceae fam. nov. In W. Whitman (Ed.), *Bergey's Manual of Systematics of Archaea and Bacteria* (pp. 1-2). John Wiley & Sons.

Important note
To cite this publication, please use the final published version (if applicable).
Please check the document version above.

Copyright
Other than for strictly personal use, it is not permitted to download, forward or distribute the text or part of it, without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license such as Creative Commons.

Takedown policy
Please contact us and provide details if you believe this document breaches copyrights.
We will remove access to the work immediately and investigate your claim.

Proteobacteria/Gammaproteobacteria/Thiohalomonadales/

Thiohalomonadaceae fam. nov.

Dimitry Y. Sorokin, *Winogradsky Institute of Microbiology, Research Centre of Biotechnology, Russian Academy of Sciences, Moscow, Russia and Department of Biotechnology, Delft University of Technology, Delft, The Netherlands*

Alexander Y. Merkel, *Winogradsky Institute of Microbiology, Research Centre of Biotechnology, Russian Academy of Sciences, Moscow, Russia*

Edited by: William Whitman, *University of Georgia, Athens, GA, USA*

Thi.o.ha.lo.mo.nad.a.ce'ae N.L. fem. n. *Thiohalomonas*, the type genus of the family, *-aceae* ending to denote a family; N.L. fem. pl. n. *Thiohalomonadaceae* the *Thiohalomonas* family.

The family *Thiohalomonadaceae* accommodates facultatively anaerobic, chemolithoautotrophic sulfur-oxidizing bacteria. They utilize reduced sulfur compounds as the energy source and either oxygen or NO_x as the electron acceptors. CO₂ is assimilated via the Calvin–Benson–Bassham cycle. The family is a member of the order *Thiohalomonadales* in the *Gammaproteobacteria* and consists of the genera *Thiohalomonas* and *Sulfurivermis*. The family-level status was established by phylogenomic analysis based on 120 single-copy conserved protein markers.

DNA G + C content (mol%): 58–65 (*T_m* of 3 species).

Type genus: **Thiohalomonas** Sorokin et al. 2007^{VP}.

The previously unaffiliated genus *Thiohalomonas* and the genus *Sulfurivermis*, originally classified as a member of the family *Thioprofundaceae*, are proposed to be (re)classified in a novel family *Thiohalomonadaceae* on the basis of phylogenomic analysis. This family, together with a novel family *Thiohalophilaceae*, form a deeply branching phylogenetic lineage in the *Gammaproteobacteria* that is proposed to be classified in a new order *Thiohalomonadales*. The

family *Thiohalomonadaceae* includes facultatively anaerobic, moderately halophilic (*Thiohalomonas*) and freshwater (*Sulfurivermis*), obligately autotrophic bacteria utilizing reduced sulfur compounds as the energy source and fixing CO₂ via the Calvin–Benson–Bassham cycle. They grow either aerobically or by sulfur-dependent denitrification. Cells are motile rods with the Gram-negative type of cell wall. Based on its genome sequence, ectoine serves as a compatible solute. The family includes two genera. The genus *Thiohalomonas* from hypersaline habitats consists of two species, the type species *Thiohalomonas denitrificans* with multiple isolates capable of complete denitrification of nitrate to N₂ and a single-strain species *Thiohalomonas nitratreducens* capable of partial anaerobic nitrate respiration to nitrite (Sorokin, 2008; Sorokin et al., 2006, 2007, 2020). The genus *Sulfurivermis* originated from a hot freshwater spring and currently includes a single species *Sulfurivermis fontis* (Kojima et al., 2017; Watanabe et al., 2019).

DNA G + C content (mol%): 58–65 (*T_m* of 3 species).

Type genus: **Thiohalomonas** Sorokin et al. 2007^{VP}.

References

- Kojima H, Watanabe M, & Fukui M (2017) *Sulfurivermis fontis* gen. nov., sp. nov., a sulfur-oxidizing autotroph, and proposal of *Thioprofundaceae* fam. nov. *Int J Syst Evol Microbiol* **67**: 3458–3461.

- Sorokin DY (2008) Diversity of halophilic sulfur-oxidizing bacteria in hypersaline habitats. In *Microbial Sulfur Metabolism*, C Dahl & CG Friedrich (eds). *Proc Intern Symp Microbial Sulfur Metabolism* 29.06.–02.07.2006. Münster, Germany. Springer, Berlin; pp 225–237.
- Sorokin DY, Tourova TP, Lysenko AM, & Muyzer G (2006) Culturable diversity of halophilic sulfur-oxidizing bacteria in hypersaline habitats. *Microbiology (SGM)* **152**: 3013–3023.
- Sorokin DY, Tourova TP, Bracker G, & Muyzer G (2007) *Thiohalomonas denitrificans* gen. nov. sp. nov, and *Thiohalomonas nitratireducens* sp. nov., novel obligately chemolithoautotrophic moderately halophilic thiodenitrifying *Gammaproteobacteria* from hypersaline habitats. *Int J Syst Evol Microbiol* **57**: 1582–1589.
- Sorokin DY, Merkel AY, & Muyzer G (2020) *Thiohalomonas*. In *Bergey's Manual of Systematics of Archaea and Bacteria*. John Wiley & Sons, Inc. DOI: 10.1002/9781118960608.gbm01695.
- Watanabe T, Kojima H, Umezawa K, Hori C, Takasuka TE, Kato Y et al. (2019) Genomes of neutrophilic sulfur-oxidizing chemolithoautotrophs representing 9 proteobacterial species from 8 genera. *Front Microbiol* **10**: 316. 