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Publication date
2023

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

Citation (APA)
Sorokin, D. Y., & Merkel, A. Y. (2023). Thiohalobacterales ord. nov. In W. Whitman (Ed.), *Bergey's Manual of Systematics of Archaea and Bacteria* (pp. 1-4). John Wiley & Sons.

Order

Proteobacteria/Gammaproteobacteria/

Thiohalobacterales ord. nov.

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Thi.o.ha.lo.bac.ter.al'es N.L. masc. n. *Thiohalobacter*, the type genus of the order; L. fem. pl. n. suff. *-ales*, ending to denote an order; N.L. fem. pl. n. *Thiohalobacterales*, the order of the genus *Thiohalobacter*.

The order *Thiohalobacterales* accommodates obligately chemolithoautotrophic aerobic bacteria utilizing inorganic sulfur compounds as the energy source and assimilating CO_2 via the Calvin–Benson–Bassham cycle. The order is a deeply branching member of the *Gammaproteobacteria* and consists of two families *Thiohalobacteraceae* and *Thiogranaceae*, both of which include one genus. The order-level status was established by phylogenomic analysis based on the Genome Taxonomy DataBase classification.

Type genus: **Thiohalobacter** Sorokin et al. 2010^{VP}.

In the original paper of Sorokin et al. (2010), the genus *Thiohalobacter* was described as an unaffiliated genus within the *Gammaproteobacteria*, and the genus *Thiogranum* was classified in the order *Chromatiales* based on 16S rRNA sequence analyses (Mori et al., 2015). The use of phylogenomic approach based on the analysis of 120 single copy conserved bacterial marker proteins revealed that the genera *Thiohalobacter* and *Thiogranum* form a deeply branching lineage representing a separate order in the *Gammaproteobacteria* (Figure 1). The order *Thiohalobacterales* includes two families: *Thiohalobacteraceae* and *Thiogranaceae*, each of which comprises single monospecific genera, *Thiohalobacter* and *Thiogranum*.

The average amino acid identity (AAI) between the two *Thiohalobacterales* representative genomes and all available genomes of the species in the *Gammaproteobacteria* isolates were calculated using 39–59% of all genes (1,400 on average). The resulting AAI values (the top list is shown in Table 1) were in the range of 51.4–62.9% (mean value 56.1 ± 1.3%), which correlates well with the distribution of AAIs between different species of the same class (Konstantinidis and Tiedje, 2005). In such case, it is the phylogenetic reconstruction which should be used as decisive to define the taxonomy rank above the genus level. The AAI value between the two representative genera of this order, *Thiohalobacter* and *Thiogranum*, was 63.4%.

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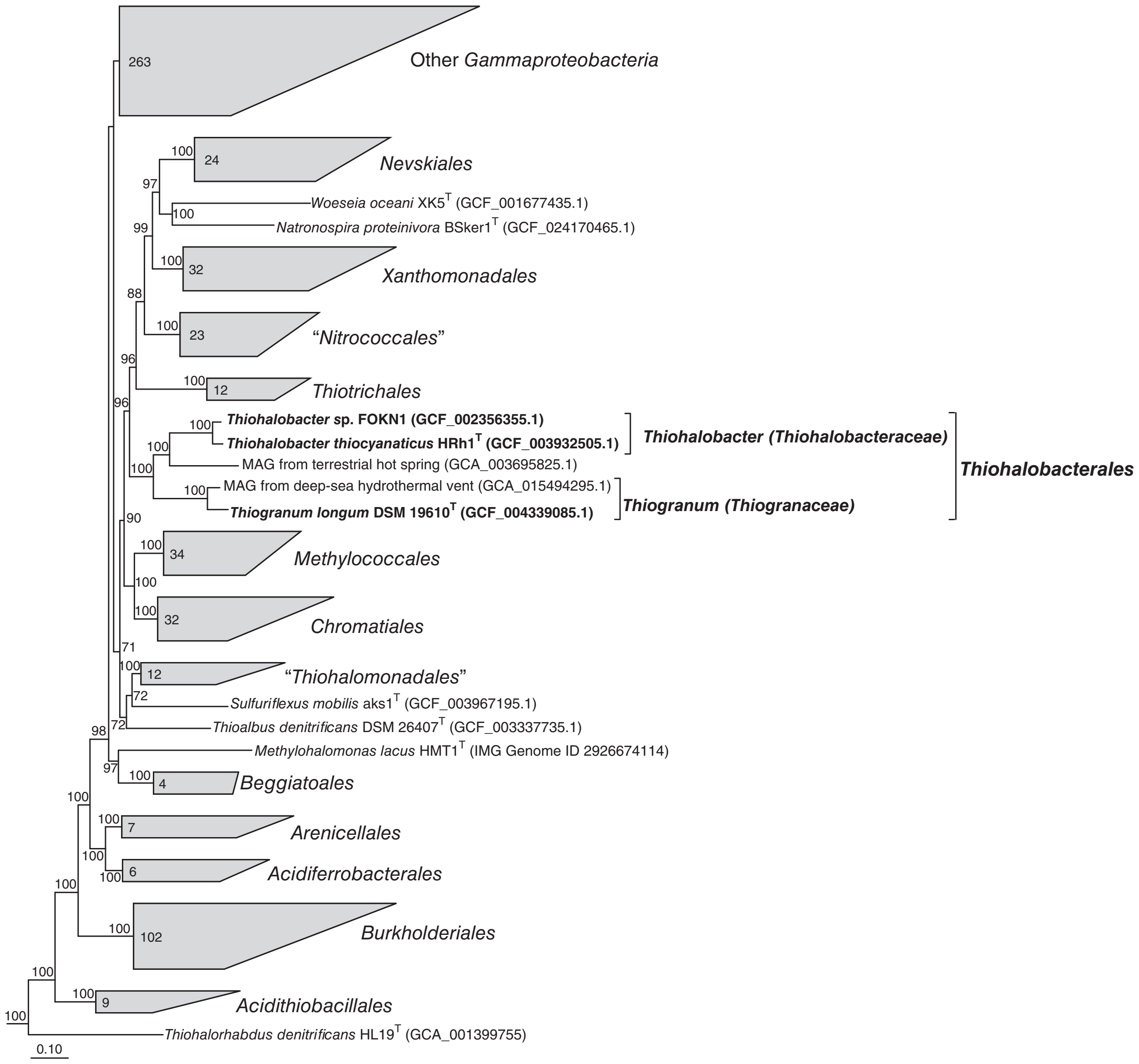
DOI: 10.1002/9781118960608.obm00184. Published by John Wiley & Sons, Inc., in association with Bergey's Manual Trust.

FIGURE 1. Phylogenetic position of the order *Thiohalobacterales* based on sequence analyses of concatenated alignment of 120 single copy conserved bacterial protein markers (Parks et al., 2018; taxonomic designations correspond to the Genome Taxonomy DataBase) within the *Gammaproteobacteria*. The trees were built using the IQ-TREEs 2 program (Minh et al., 2020) with approximate likelihood-ratio test for branches (Anisimova and Gascuel, 2006). Bootstrap consensus tree is shown with values above 70% placed at the nodes. Bar, 0.10 changes per position.



Both genera include obligately chemolithoautotrophic, sulfur-oxidizing bacteria (Sorokin et al., 2010; Mori et al., 2015) from saline habitats. The type genus of the *Thiohalobacterales* order is *Thiohalobacter*. It is a moderately halophilic bacterium with a unique capability to utilize thiocyanate as the energy and nitrogen source (Sorokin, 2008; Sorokin et al., 2006, 2010, 2020). The type strain of *Thiohalobacter thiocyanaticus* was enriched from hypersaline lakes with neutral pH in southwestern Siberia. *Thiogranum longum* is a low salt-tolerant, obligately aerobic, chemolithotrophic sulfur-oxidizing bacterium from a marine habitat able to utilize elemental sulfur, thiosulfate, and sulfide as electron donors (Mori et al., 2015).

Type genus: **Thiohalobacter** Sorokin et al. 2010^{VP}.

TABLE 1. The average amino acid identity (AAI) between the *Thiohalobacterales* representative genomes and the most related genomes in the *Gammaproteobacteria* using the EzAAI program (Kim et al., 2021)

Thiohalobacterales representative	RefSeq assembly accession	Species	AAI (%)	Proteome coverage
Thiogranum longum DSM 19610 (GCF_004339085.1)	GCF_002000365.1	*Thioalkalivibrio denitrificans* ALJD	61.18	0.42
	GCF_900110965.1	*Ectothiorhodospira magna* B7-7	61.18	0.39
	GCF_000378965.1	*Thioalkalivibrio thiocyanodenitrificans* ARhD 1	61.20	0.41
	GCF_004366735.1	*Thiohalophilus thiocyanatoxydans* DSM 16326	61.25	0.50
	GCF_000021985.1	*Thioalkalivibrio sulfidiphilus* HL-EbGr7	61.36	0.45
	GCF_900102855.1	*Thiohalomonas denitrificans* HLD2	61.39	0.44
	GCF_000377945.1	*Thioalkalivibrio sulfidiphilus* ALJ17	61.69	0.46
	GCF_003337735.1	*Thioalbus denitrificans* DSM 26407	61.73	0.41
	GCF_004001245.1	*Sulfurivermis fontis* JG42	61.81	0.46
	GCF_003967195.1	*Sulfuriflexus mobilis* aks1	61.81	0.51
	GCF_003932505.1	*Thiohalobacter_thiocyanaticus*_HRh1	63.41	0.54
Thiohalobacter thiocyanaticus HRh1 (GCF_003932505.1)	GCF_900156225.1	*Ectothiorhodosinus mongolicus* M9	61.75	0.39
	GCF_900110965.1	*Ectothiorhodospira magna* B7-7	61.97	0.39
	GCF_002000365.1	*Thioalkalivibrio denitrificans* ALJD	61.97	0.45
	GCF_000378965.1	*Thioalkalivibrio thiocyanodenitrificans* ARhD 1	61.97	0.43
	GCF_000021985.1	*Thioalkalivibrio sulfidiphilus* HL-EbGr7	62.00	0.46
	GCF_900102855.1	*Thiohalomonas denitrificans* HLD2	62.05	0.46
	GCF_000377945.1	*Thioalkalivibrio sulfidiphilus* ALJ17	62.22	0.48
	GCF_013343005.1	*Thioalbus denitrificans* DSM 26407	62.57	0.42
	GCF_004001245.1	*Sulfurivermis fontis* JG42	62.81	0.46
	GCF_004366735.1	*Thiohalophilus thiocyanatoxydans* DSM 16326	62.92	0.55
	GCF_004339085.1	*Thiogranum longum* DSM 19610	63.41	0.54

References

Anisimova M & Gascuel O (2006) Approximate likelihood-ratio test for branches: a fast, accurate, and powerful alternative. *Syst Biol* **55**: 539–552.

Kim D, Park S, & Chun J (2021) Introducing EzAAI: a pipeline for high throughput calculations of prokaryotic average amino acid identity. *J Microbiol* **59**: 476–480.

Konstantinidis KT & Tiedje JM (2005) Towards a genome-based taxonomy for prokaryotes. *J Bacteriol* **187**: 6258–6264.

Minh BQ, Schmidt HA, Chernomor O, Schrempf D, Woodhams MD, von Haeseler A et al. (2020) IQ-TREE 2: new models and efficient methods for phylogenetic inference in the genomic era. *Mol Biol Evol* **37**: 1530–1534.

Mori K, Suzuki KI, Yamaguchi K, Urabe T, & Hanada S (2015) *Thiogranum longum* gen. nov., sp. nov., an obligately chemolithoautotrophic, sulfur-oxidizing bacterium of the family Ectothiorhodospiraceae isolated from a deep-sea hydrothermal field, and an emended description of the genus *Thiohalomonas*. International journal of systematic and evolutionary microbiology. *Int J Syst Evol Microbiol* **65**: 235–241.

Parks DH, Chuvochina M, Waite DW, Rinke C, Skarshewski A, Chaumeil P-A et al. (2018) A standardized bacterial taxonomy based on genome phylogeny substantially revises the tree of life. *Nat Biotechnol* **36**: 996–1004.

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, Kovaleva OL, Tourova TP, & Muyzer G (2010) *Thiohaloacter thiocyanaticus* gen. nov. sp. nov., a moderately halophilic, sulfur-oxidizing gammaproteobacterium from hypersaline lakes, that utilizes thiocyanate. *Int J Syst Evol Microbiol* **58**: 1685–1692.

Sorokin DY, Merkel AY, & Muyzer G (2020) *Thiohalobacter*. In *Bergey's Manual of Systematics of Archaea and Bacteria*. John Wiley & Sons, Inc. DOI: 10.1002/9781118960608.gbm01939. Ⓑ