

Taurinivorans muris gen. nov. sp. nov.

Submitted by Loy, Alexander

Genus *Taurinivorans*

Etymology

[Tau.ri.ni.vo'rans] N.L. neut. n. *taurinum*, taurine; L. part. adj. *vorans*, eating; N.L. masc. n. *Taurinivorans*, a taurine eater

Nomenclatural type

Species *Taurinivorans muris*^{Ts}

Description

Taurinivorans gen. nov. (Tau.ri.ni.vo'rans. N.L. n. *taurinum*, taurine; L. part. adj. *vorans*, eating; N.L. masc. n. *Taurinivorans*, a taurine eater). Comparative genome analyses suggest the common electron acceptor is taurine, which is degraded and reduced to sulfide via the Tpa-Xsc-DsrAB-DsrC pathway. Type species: *Taurinivorans muris* sp. nov., family: *Desulfovibrionaceae* VP, order: *Desulfovibrionales* VP (T) emend., class: *Desulfovibrionia* class. nov., phylum: *Desulfobacterota* phyl. nov.

Classification

Bacteria » *Desulfobacterota* » *Desulfovibrionia* » *Desulfovibrionales* » *Desulfovibrionaceae* » *Taurinivorans*

References

Effective publication: Ye et al., 2023 [1]

Registry URL

<https://seqco.de/i:32704>

Species *Taurinivorans muris*^{Ts}

Etymology

[mu'ris] L. gen. n. *muris*, of a mouse, referring to its origin from the mouse intestine

Nomenclatural type

[NCBI Assembly: GCA_025232395.1](#)^{Ts}

Reference Strain

LT0009 = [DSM 111569](#) = [JCM 34262](#)

Description

Taurinivorans muris sp. nov. (mu'ris. L. gen. n. *muris*, of a mouse, referring to its origin from the mouse intestine). The type strain is strain LT0009 (= DSM 111569 = JCM 34262), isolated from the mouse gut with taurine as the electron acceptor and lactate/pyruvate as electron donors. Formate was also used as an electron donor for taurine respiration. Cells are Gram-stain-negative, spirilloid in shape, and motile by means of lophotrichous polar flagella. The temperature range is 27–42°C and the optimum pH is 6.5 (range 6–8.5) for strictly anaerobic growth. The optimal taurine concentration for growth is 40 mmol/l, higher taurine concentrations inhibit growth. Sulfolactate and thiosulfate are additional electron acceptors for anaerobic respiration and are also reduced to hydrogen sulfide. Yeast extract and 1,4-naphthoquinone are required as growth supplements for laboratory cultivation of the isolate. Its genome size is 2.2 Mbp with a G+C content of 43.6%. The GenBank accession numbers for the genome and the 16S rRNA gene sequence of strain LT0009T are CP065938 and MW258658, respectively.

Classification

Bacteria » *Desulfobacterota* » *Desulfovibrionia* » *Desulfovibrionales* » *Desulfovibrionaceae* » *Taurinivorans* » *Taurinivorans muris*^{Ts}

References

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References

1. Ye et al. (2023). Ecophysiology and interactions of a taurine-respiring bacterium in the mouse gut. *Nature Communications*. [DOI:10.1038/s41467-023-41008-z](https://doi.org/10.1038/s41467-023-41008-z)

Register List Certificate of Validation

On behalf of the *Committee on the Systematics of Prokaryotes Described from Sequence Data* (SeqCode Committee), we hereby certify that the Register List seqco.de/r:pzblpla3 submitted by **Loy, Alexander** and including 2 new names has been successfully validated.

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