

Magnetomonas plexicatena sp. nov. gen. nov.

Submitted by Grouzdev, Denis

Genus *Magnetomonas*

Etymology

[Mag.ne.to.mo'nas] Gr. masc. n. *magnes*, pertaining to a magnet; L. fem. n. *monas*, a unit, monad; N.L. fem. n. *Magnetomonas*, a magnetic monad

Nomenclatural type

Species *Magnetomonas plexicatena*^{Ts}

Description

Vibrioid-shaped, cell size 2.0 ± 0.4 μm long and 0.5 ± 0.1 μm wide, form magnetite magnetosomes organized in chains along the long axis of the bacterial cell body. Magnetosomes present a mean length of 108 ± 21.1 nm and a mean width of 45 ± 8.1 nm. Potentially capable of chemolithoautotrophy with the oxidation of sulfur compounds and carbon assimilation by Wood–Ljungdahl pathway. Potentially capable of heterotrophy by glycolysis. Not capable of nitrogen fixation.

Classification

Bacteria » *Nitrospirota* » *Thermodesulfovibrionia* » *Thermodesulfovibrionales* » *Magnetobacteriaceae* » *Magnetomonas*

References

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

Registry URL

<https://seqco.de/i:51020>

Species *Magnetomonas plexicatena*^{Ts}

Etymology

[ple.xi.ca.te'na] L. masc. adj. *plexus*, interwoven; L. fem. n. *catena*, chain; N.L. fem. n. *plexicatena*, an interwoven chain

Nomenclatural type

[NCBI Assembly: GCA_004376055.2](#)^{Ts}

Description

Vibrioid-shaped, cell size 2.0 ± 0.4 μm long and 0.5 ± 0.1 μm wide, form magnetite magnetosomes organized in chains along the long axis of the bacterial cell body. Magnetosomes present a mean length of 108 ± 21.1 nm and a mean width of 45 ± 8.1 nm. Potentially capable of chemolithoautotrophy with the oxidation of sulfur compounds and carbon assimilation by Wood–Ljungdahl pathway. Potentially capable of heterotrophy by glycolysis. Not capable of nitrogen fixation. The reference strain is LBB01. The genome reference sequence of LBB01 is CP049016. G + C content 42.0%.

Classification

Bacteria » *Nitrospirota* » *Thermodesulfovibrionia* » *Thermodesulfovibrionales* » *Magnetobacteriaceae* » *Magnetomonas* » *Magnetomonas plexicatena*^{Ts}

References

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

Assigned taxonomically: Uzun et al., 2022 [1]

Registry URL

<https://seqco.de/i:51019>

References

1. Uzun et al. (2022). Detection of interphylum transfers of the magnetosome gene cluster in magnetotactic bacteria. *Frontiers in Microbiology*. DOI:10.3389/fmicb.2022.945734

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:wl9gi9g9 submitted by **Grouzdev, Denis** and including 2 new names has been successfully validated.

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