

Omnitrophus fodinae sp. nov. and Omnitrophus gen. nov.

Submitted by Rinke, Chris

Genus *Omnitrophus*

Etymology

[Om.ni.tro'phus] L. masc. adj. *omnis*, all; Gr. n. *trophos*, feeder; N.L. masc. n. *Omnitrophus*, eating all

Nomenclatural type

Species *Omnitrophus fodinae*^{Ts}

Description

This monotypic genus belongs to the family *Omnitrophaceae*, order *Omnitrophales*, class *Omnitrophia*, in the phylum *Omnitrophota*. Although only a single medium-quality genome is available for this genus currently, the historical name for the lineage represented by this phylum is based on the name of this genus. The description for this genus is the same as for the species *Omnitrophus fodinae*, the type species of the genus.

Classification

Bacteria » *Omnitrophota* » “Omnitrophia” » “Omnitrophales” » “Omnitrophaceae” » *Omnitrophus*

References

Effective publication: Rinke et al., 2013 [1]

Registry URL

<https://seqco.de/i:23568>

Species *Omnitrophus fodinae*^{Ts}

Etymology

[fo.di'nae] L. gen. n. *fodinae*, of a mine, coal mine

Nomenclatural type

[NCBI Assembly: GCA_000405945.1](https://ncbi.nlm.nih.gov/assembly/GCA_000405945.1)^{Ts}

Description

This species is the type of the genus *Omnitrophus*. No data on cell size in the species is available. This species is represented by only one medium-quality genome, however, for historical significance, this genome serves as the nomenclatural type for the species. The %GC content of the genome is 49.56%. The estimated genome size is 2.9 Mb, with the available genome estimated to be 65 % complete. The genome available for this species encodes 2 very large ORFs with domains typically implicated in eukaryotic cell adhesion. This organism originated from groundwater sampled at Homestake Mine (Sanford Lab Homestake), South Dakota. The nomenclatural type for the species is the genome GCA_000405945.1.

Classification

Bacteria » *Omnitrophota* » “Omnitrophia” » “Omnitrophales” » “Omnitrophaceae” » *Omnitrophus* » *Omnitrophus fodinae*^{Ts}

References

Effective publication: Rinke et al., 2013 [1]

Registry URL

<https://seqco.de/i:23567>

References

1. Rinke et al. (2013). Insights into the phylogeny and coding potential of microbial dark matter. *Nature*.
[DOI:10.1038/nature12352](https://doi.org/10.1038/nature12352)

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:d841ck02 submitted by **Rinke, Chris** and including 2 new names has been successfully validated.

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