

Register list for 8 new names including *Binatus soli* sp. nov.

Submitted by Chuvochina, Maria

Genus *Binatus*

Etymology

[Bi.na'tus] L. adv. num. *bis*, twice; L. part. adj. *natus*, born, made; N.L. masc. n. *Binatus*, born-twice, referring to the discovery of the organism from the reprocessing (second study) of the originally studied metagenomic data

Nomenclatural type

Species *Binatus soli*^{TS}

Description

The description is identical to the type species.

Classification

Bacteria » *Desulfobacterota* » *Binatia* » *Binatales* » *Binataceae* » *Binatus*

References

Effective publication: Chuvochina et al., 2019 [1]

Registry URL

<https://seqco.de/i:31410>

Genus *Hydrothermus*

Etymology

[Hy.dro.ther'mus] Gr. neut. n. *hydôr*, water; Gr. masc. adj. *thermos*, hot; N.L. masc. n. *Hydrothermus*, an organism living in hot water

Nomenclatural type

Species *Hydrothermus pacificus*^{TS}

Description

The description is identical to the type species.

Classification

Bacteria » "Hydrothermota" » *Hydrothermia* » *Hydrothermales* » *Hydrothermaceae* » *Hydrothermus*

References

Effective publication: Chuvochina et al., 2019 [1]

Registry URL

<https://seqco.de/i:31415>

Genus *Hydrothermarchaeum*

Etymology

[Hy.dro.therm.ar.chae'um] Gr. n. *hydôr*, water; Gr. masc. adj. *thermos*, hot; N.L. neut. n. *archaeum*, archaeon from Gr. adj. *archaios* -ê -on ancient; N.L. neut. n. *Hydrothermarchaeum*, n archaeon from a hydrothermal environment

Nomenclatural type

Species *Hydrothermarchaeum profundis*^{TS}

Description

Identical to the type species.

Classification

Archaea » "Hydrothermarchaeota" » *Hydrothermarchaeia* » *Hydrothermarchaeales* » *Hydrothermarchaeaceae* » *Hydrothermarchaeum*

References

Effective publication: Chuvochina et al., 2019 [1]

Registry URL

<https://seqco.de/i:31420>

Genus *Hadarchaeum*

Etymology

[Had.ar.chae'um] Gr. masc. n. *Haidēs*, Hades, the underworld; N.L. neut. n. *archaeum*, archaeon; N.L. neut. n. *Hadarchaeum*, archaeon from the subsurface

Nomenclatural type

Species *Hadarchaeum yellowstonense*^{Ts}

Description

Identical to the type species.

Classification

Archaea » *Hadarchaeota* » *Hadarchaeia* » *Hadarchaeales* » *Hadarchaeaceae* » *Hadarchaeum*

References

Effective publication: Chuvochina et al., 2019 [1]

Registry URL

<https://seqco.de/i:31424>

Species *Binatus soli*^{Ts}

Etymology

[so'li] L. gen. n. *soli*, of soil, referring to the isolation source of the organism

Nomenclatural type

[NCBI Assembly: GCA_002479255.1](https://ncbi.nlm.nih.gov/assembly/GCA_002479255.1)^{Ts}

Description

This species is the first genomic representative of candidate bacterial phylum UBP10. The MAG of this species was originally reconstructed from a soil metagenome by Parks et al. (2017).

Classification

Bacteria » *Desulfobacterota* » *Binatia* » *Binatales* » *Binataceae* » *Binatus* » *Binatus soli*^{Ts}

References

Effective publication: Chuvochina et al., 2019 [1]

Assigned taxonomically: Parks et al., 2017 [2]

Registry URL

<https://seqco.de/i:31409>

Species *Hadarchaeum yellowstonense*^{Ts}

Etymology

[yel.low.ston.en'se] N.L. **neut. adj.** *yellowstonense*, pertaining to the Yellowstone National Park, the place of sampling from where organism was found

Nomenclatural type

[NCBI Assembly: GCA_001515205.2](#)^{Ts}

Description

A detailed metabolic description of the proposed *Ca. H. yellowstonense*, formerly identified as YNP_45, is given in the original work by Baker *et al.* (2016) Nat. Microbiol. 1, 16002. doi: 10.1038/NMICROBIOL.2016.2. The organisms was found in hot spring in Yellowstone National Park, USA.

The reduced genome size and previously inferred gene content (821) suggests that the genome has undergone streamlining. The inferred metabolic capabilities indicates oxidation of carbon monoxide, which may be coupled to H₂O or nitrite reduction to ammonia. Also inferred to contain a variety of central carbon metabolic (C1 pathway) genes found in methanogens, which may be used for carbon fixation. The organism is inferred to be thermophilic.

Classification

Archaea » *Hadarchaeota* » *Hadarchaeia* » *Hadarchaeales* » *Hadarchaeaceae* » *Hadarchaeum* » *Hadarchaeum yellowstonense*^{Ts}

References

Effective publication: Chuvochina et al., 2019 [1]

Registry URL

<https://seqco.de/i:31423>

Species *Hydrothermarchaeum profundī*^{Ts}

Etymology

[pro.fun'di] L. **gen. n.** *profundi*, of/from the depth of the sea

Nomenclatural type

[NCBI Assembly: GCA_002011125.1](#)^{Ts}

Description

The organism was formerly identified as JdFR-18 in the hydrothermal fluid from Juan de Fuca Ridge by Jungbluth et al. (2017) Sci. Data 4, 170037. doi: 10.1038/sdata.2017.37. An annotation of the genome is provided in the same original study. Metabolic capabilities inferred from the genome reveal a thermophilic carboxidotroph capable of chemotaxis and motility. The organism appears to capable of anaerobic respiration with sulfate serving as a terminal electron acceptor.

Classification

Archaea » "Hydrothermarchaeota" » *Hydrothermarchaeia* » *Hydrothermarchaeales* » *Hydrothermarchaeaceae* » *Hydrothermarchaeum* » *Hydrothermarchaeum profundī*^{Ts}

References

Effective publication: Chuvochina et al., 2019 [1]

Registry URL

<https://seqco.de/i:31421>

Species *Hydrothermus pacificus*^{Ts}

Etymology

[pa.ci'fi.cus] L. **masc. adj.** *pacificus*, peaceful, pertaining to Pacific Ocean

Nomenclatural type

[NCBI Assembly: GCA_002011615.1](#)^{Ts}

Description

This is one of the first genomic representatives of the EM3 lineage, later known as Candidate bacterial phylum Hydrothermae as proposed by Jungbluth et al. (2017). The MAG of this species has been reconstructed from the deep subsurface biosphere - the Juan de Fuca Ridge seafloor.

Classification

Bacteria » "Hydrothermota" » *Hydrothermia* » *Hydrothermales* » *Hydrothermaceae* » *Hydrothermus* » *Hydrothermus pacificus*^{Ts}

References

Effective publication: Chuvochina et al., 2019 [1]

Registry URL

<https://seqco.de/i:31414>

References

1. Chuvochina et al. (2019). The importance of designating type material for uncultured taxa. *Systematic and Applied Microbiology*. DOI:10.1016/j.syapm.2018.07.003
2. Parks et al. (2017). Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life. *Nature Microbiology*. DOI:10.1038/s41564-017-0012-7

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:ivphtsqc submitted by **Chuvochina, Maria** and including 8 new names has been successfully validated.

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