

Register list for 6 new names including *Sacchlamyda saccharinae* sp. nov.

Submitted by Davison, Helen Rebecca

Genus *Sacchariniichlamydia*

Etymology

[Sac.cha.ri.ni.i.chla.my'di.a] **N.L. fem. n.** *Saccharina*, the putative algal host of the bacterium, *Saccharina japonica*; **N.L. fem. n.** *Chlamydia*, the bacterial genus *Chlamydia*; **N.L. fem. n.** *Sacchariniichlamydia*, *Chlamydia* related bacteria from *Saccharina* algae

Nomenclatural type

Species *Sacchariniichlamydia saccharinae*^{Ts}

Description

A genus of Rhabdochlamydiaceae bacteria. The type species was extracted through a metagenomic assembly pipeline from the seaweed *Saccharina japonica*. Genus status was established on the basis of sharing <65% Average Amino-acid Identity (AAI) with any other Rhabdochlamydiaceae bacteria, as well as phylogenetic analysis of single copy core amino acids from 112 *Chlamydiae* bacteria. Analysis using the GTDB-tk pipeline assigned the type genome to an unnamed Rhabdochlamydiaceae genus.

Classification

Bacteria » *Chlamydiota* » *Chlamydiia* » *Parachlamydiales* » "Rhabdochlamydiaceae" » *Sacchariniichlamydia*

References

Proposed: Davison, Hurst, 2023

Registry URL

<https://seqco.de/i:31325>

Genus *Amphritriteisimkania*

Etymology

[Am.phri.tri.te.i.sim.ka'ni.a] **N.L. fem. n.** *Amphritrite*, from Gr. Amphritrite, wife of Poseidon; **N.L. fem. n.** *Simkania*, the bacterial genus *Simkania*; **N.L. fem. n.** *Amphritriteisimkania*, the "Simkania" of Amphritrite

Nomenclatural type

Species *Amphritriteisimkania amoebophyrae*^{Ts}

Description

A genus of Simkaniaceae bacteria. The type species was extracted through a metagenomic assembly pipeline from the syndinian parasite *Amoebophrya* sp. AT5.2. Genus status was established on the basis of sharing <65% Average Amino-acid Identity (AAI) with any other Simkaniaceae bacteria, as well as phylogenetic analysis of single copy core amino acids from 112 *Chlamydiae* bacteria. Analysis using the GTDB-tk pipeline assigned the type genome to an unnamed Simkaniaceae genus.

Classification

Bacteria » *Chlamydiota* » *Chlamydiia* » *Chlamydiales* » *Simkaniaceae* » *Amphritriteisimkania*

References

Proposed: Davison, Hurst, 2023

Registry URL

<https://seqco.de/i:31322>

Genus *Acherontichlamydia*

Etymology

[A.che.ron.ti.chla.my'di.a] L. **masc. n.** *Acheron*, the Greek mythological river that flows above and below ground through swamps and caverns; **N.L. fem. fem. n.** *Chlamydia*, the bacterial genus Chlamydia; **N.L. fem. n.** *Acherontichlamydia*, the Chlamydia from Acheron

Nomenclatural type

Species *Acherontichlamydia pituitae*^{Ts}

Description

A genus of Rhabdochlamydiaceae bacteria. The type species was identified through the NCBI nr database with bait sequences from other Rhabdochlamydiaceae. Genus status was established on the basis of sharing <65% Average Amino-acid Identity (AAI) with any other Rhabdochlamydiaceae bacteria, as well as phylogenetic analysis of single copy core amino acids from 112 Chlamydiae bacteria. Analysis using the GTDB-tk pipeline assigned the type genome to an unnamed Rhabdochlamydiaceae genus.

Classification

Bacteria » *Chlamydiota* » *Chlamydiia* » *Parachlamydiales* » "Rhabdochlamydiaceae" » *Acherontichlamydia*

References

Proposed: Davison, Hurst, 2023

Registry URL

<https://seqco.de/i:31374>

Species *Sacchariniichlamydia saccharinae*^{Ts}

Etymology

[sac.cha.ri'nae] **N.L. gen. n.** *saccharinae*, of *Saccharina* seaweed

Nomenclatural type

[NCBI Assembly: GCA_030408505.1](#)^{Ts}

Description

A species of Rhabdochlamydiaceae bacteria. The type species was extracted through a metagenomic assembly pipeline applied to the seaweed *Saccharina japonica* (accession SRR2043156). Species status was established based on sharing <95% Average Nucleotide Identity (ANI) with any other Rhabdochlamydiaceae.

Classification

Bacteria » *Chlamydiota* » *Chlamydiia* » *Parachlamydiales* » "Rhabdochlamydiaceae" » *Sacchariniichlamydia* » *Sacchariniichlamydia saccharinae*^{Ts}

References

Proposed: Davison, Hurst, 2023

Registry URL

<https://seqco.de/i:31324>

Species *Amphritriteisimkania amoebophyrae*^{Ts}

Etymology

[a.moe.bo.phy'rae] **N.L. gen. n.** *amoebophyrae*, of amoebophyra

Nomenclatural type

[NCBI Assembly: GCA_030408475.1](#)^{Ts}

Description

A species of Simkaniaceae bacteria. The type species was extracted through a metagenomic assembly pipeline applied to the syndinian parasite *Amoebophrya* sp. AT5.2 (accession SRR3080743). Species status was established based on sharing <95% Average Nucleotide Identity (ANI) with any other Simkaniaceae.

Classification

Bacteria » *Chlamydiota* » *Chlamydiia* » *Chlamydiales* » *Simkaniaceae* » *Amphritriteisimkania* » *Amphritriteisimkania amoebophyrae*^{Ts}

References

Proposed: Davison, Hurst, 2023

Registry URL

<https://seqco.de/i:31321>

Species *Acherontichlamydia pituitae*^{Ts}

Etymology

[pi.tu.i'tae] L. gen. n. *pituitae*, sludge

Nomenclatural type

[NCBI Assembly: GCA_019634675.1](#)^{Ts}

Description

A species of Rhabdochlamydiaceae bacteria. The type species was identified through the NCBI nr database with bait sequences from other Rhabdochlamydiaceae. Species status was established based on sharing <95% Average Nucleotide Identity (AAI) with any other Rhabdochlamydiaceae.

Classification

Bacteria » *Chlamydiota* » *Chlamydiia* » *Parachlamydiales* » "Rhabdochlamydiaceae" » *Acherontichlamydia* » *Acherontichlamydia pituitae*^{Ts}

References

Proposed: Davison, Hurst, 2023

Registry URL

<https://seqco.de/i:31373>

References

1. Davison, Hurst (2023). Hidden from plain sight: Novel Simkaniaceae and Rhabdochlamydiaceae diversity emerging from screening genomic and metagenomic data. *Systematic and Applied Microbiology*. [DOI:10.1016/j.syapm.2023.126468](https://doi.org/10.1016/j.syapm.2023.126468)

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:bsk8pkm4 submitted by **Davison, Helen Rebecca** and including 6 new names has been successfully validated.

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