Archaea from terrestrial arthropods

Submitted by Protasov, Evgenii

Family *Bathycorpusculaceae*

Etymology

[Ba.thy.cor.pus.cu.la'ce.ae] **N.L. neut. n.** *Bathycorpusculum*, referring to the type genus Bathycorpusculum; *-aceae*, ending to denote a family; **N.L. fem. pl. n.** *Bathycorpusculaceae*, the Bathycorpusculum family

Nomenclatural type

Genus *Bathycorpusculum*

Description

The family is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group.

Classification

Archaea » “Bathyarchaeota” » *Bathyarchaeia* » *Bathyarchaeales* » *Bathycorpusculaceae*

References

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

Registry URL

https://seqco.de/i:32518

Genus *Methanorbis*

Etymology

[Me.than.or'bis] **N.L. neut. n.** *methanum*, methane; **L. masc. n.** *orbis*, a disk; **N.L. masc. n.** *Methanorbis*, a methane-producing disk

Nomenclatural type

Species *Methanorbis furvi*$^{\mathrm{Ts}}$

Description

The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group. Cells are ovoid cocci 1–3 µm. Non-motile. H2 and CO2 are the substrates for methanogenesis; formate can substitute H2. Acetate and formate are required for growth. The temperature range is 25-40 °C.

Classification

Archaea » *Methanobacteriota* » “Methanomicrobia” » *Methanomicrobiales* » *Methanocorpusculaceae* » *Methanorbis*

References

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

Registry URL

https://seqco.de/i:32539

Genus *Bathycorpusculum*

Etymology

[Ba.thy.cor.pus'cu.lum] **Gr. pref.** *bathy-*, deep, especially deep sea (from the Greek bathys, deep); **L. neut. n.** *corpusculum*, a little body, a particle; **N.L. neut. n.** *Bathycorpusculum*, a particle from the deep sea

Nomenclatural type

Species *Bathycorpusculum acetigenes*$^{\mathrm{Ts}}$

Description

The genus identified by metagenomic analyses. Putative mixotrophic CO2-reducing acetogens that use H2 and amino acids as electron donors.

Classification

Archaea » “Bathyarchaeota” » *Bathyarchaeia* » *Bathyarchaeales* » *Bathycorpusculaceae* » *Bathycorpusculum*

References

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

Registry URL

https://seqco.de/i:32517

Genus *Methanofilum*

Etymology

[Me.tha.no.fi'lum] **N.L. pref.** *methano-*, pertaining to methane; **L. neut. n.** *filum*, a thread or string; **N.L. neut. n.** *Methanofilum*, a methane-producing thread.

Nomenclatural type

Species *Methanofilum arcanum*$^{\mathrm{Ts}}$

Description

The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group.

Classification

Archaea » *Methanobacteriota* » “Methanomicrobia” » *Methanomicrobiales* » *Methanospirillaceae* » *Methanofilum*

References

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

Registry URL

https://seqco.de/i:32513

Genus *Methanofrustulum*

Etymology

[Me.tha.no.frus'tu.lum] **N.L. pref.** *methano-*, pertaining to methane; **L. neut. dim. n.** *frustulum*, morsel, crumb (of food); **N.L. neut. n.** *Methanofrustulum*, a methane-producing crumb

Nomenclatural type

Species *Methanofrustulum fimipullorum*$^{\mathrm{Ts}}$

Description

The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group.

Classification

Archaea » *Methanobacteriota* » “Methanomicrobia” » *Methanosarcinales* » *Methanosarcinaceae* » *Methanofrustulum*

References

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

Registry URL

https://seqco.de/i:32514

Genus *Methanacia*

Etymology

[Me.than.a'ci.a] **N.L. neut. n.** *methanum*, methane; **L. fem. n.** *acia*, thread, yarn; **N.L. fem. n.** *Methanacia*, a methane-producing thread

Nomenclatural type

Species *Methanacia filiformis*^{Ts}

Description

The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group. Filamentous rods with slightly tapered ends. Gram positive. Nonmotile. Strict anaerobe. Require yeast extract for growth. Optimum temperature is 30 °C. Use H2 + CO2 as substrates for methanogenesis.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanacia*

References

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

Registry URL

https://seqco.de/i:32450

Genus *Methanarmilla*

Etymology

[Me.than.ar.mil'la] **N.L. neut. n.** *methanum*, methane; **L. fem. n.** *armilla*, bracelet; **N.L. fem. n.** *Methanarmilla*, methane-producing bracelet, referring to the short chains of cells formed by the type species

Nomenclatural type

Species *Methanarmilla wolinii*^{Ts}

Description

The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group. Short oval rods or coccobacilli, 0.6 µm in width and 1–1.8 µm in length. Cells occur singly, in pairs or in short chains. Gram positive. Nonmotile. Require complex medium with acetate, yeast extract, trypticase, volatile fatty acids, coenzyme M. Optimum temperature is 37–40° C. Use H2 + CO2 or formate + CO2 as substrates for methanogenesis.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanarmilla*

References

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

Registry URL

https://seqco.de/i:32439

Genus *Methanobinarius*

Etymology

[Me.tha.no.bi.na'ri.us] **N.L. pref.** *methano-*, pertaining to methane; **L. masc. adj.** *binarius*, consisting of two things; **N.L. masc. n.** *Methanobinarius*, methane-producing (organism) consisting of two things, referring to the pairs of cells formed by the type species

Nomenclatural type

Species *Methanobinarius arboriphilus*^{Ts}

Description

The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group. Short oval rods that occur singly, in pairs or in short chains. Gram positive. Nonmotile. Use H2 + CO2 as substrates for methanogenesis, might also grow poorly on formate. Grow poorly on mineral medium with vitamins; yeast extract, casamino acids, and rumen fluid strongly stimulate growth. Optimum temperature is 30–37 °C.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanobinarius*

References

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

Registry URL

https://seqco.de/i:32442

Genus *Methanobaculum*

Etymology

[Me.tha.no.ba'cu.lum] **N.L. pref.** *methano-*, pertaining to methane; **L. neut. n.** *baculum*, small rod; **N.L. neut. n.** *Methanobaculum*, a small methane-producing rod.

Nomenclatural type

Species *Methanobaculum cuticulare*^{Ts}

Description

The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group. Straight short rods with slightly tapered ends that occur singly, in pairs, or in short chains. Non-motile. Gram-positive. Strict anaerobe. Use H2 + CO2 as substrates for methanogenesis, growth on formate is poor. Grow poorly on mineral medium with vitamins. Yeast extract, casamino acids, and rumen fluid strongly stimulate growth. Optimum temperature is 30−37 °C.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanobaculum*

References

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

Registry URL

https://seqco.de/i:32445

Genus *Methanovirga*

Etymology

[Me.tha.no.vir'ga] **N.L. pref.** *methano-*, pertaining to methane; **L. fem. n.** *virga*, a rod; **N.L. fem. n.** *Methanovirga*, a methane-producing rod

Nomenclatural type

Species *Methanovirga basalitermitum*^{Ts}

Description

The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanovirga*

References

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

Registry URL
https://seqco.de/i:32454

Genus *Methanomicula*

Etymology
[Me.tha.no.mi'cu.la] **N.L. pref.** *methano-*, pertaining to methane; **L. fem. n.** *micula*, morsel, crumb (of salt); **N.L. fem. n.** *Methanomicula*, a methane-producing crumb

Nomenclatural type
Species *Methanomicula labiotermitis*$^{\mathrm{Ts}}$

Description
The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group.

Classification
Archaea » *Methanobacteriota* » *Thermoplasmata* » *Methanomassiliicoccales* » *Methanomethylophilaceae* » *Methanomicula*

References
Effective publication: Protasov et al., 2023 [1]

Registry URL
https://seqco.de/i:32531

Genus *Methanoflexus*

Etymology
[Me.tha.no.fle'xus] **N.L. pref.** *methano-*, pertaining to methane; **L. masc. n.** *flexus*, a bending, turning, winding; **N.L. masc. n.** *Methanoflexus*, methane-producing (organism) with a curved shape

Nomenclatural type
Species *Methanoflexus curvatus*$^{\mathrm{Ts}}$

Description
The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group. Curved rods that occur singly, in pairs, or in chains. Gram positive. Nonmotile. Strict anaerobe. Require yeast extract or rumen fluid for growth. Optimum temperature is 30 °C. Use H2 + CO2 as substrates for methanogenesis.

Classification
Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanoflexus*

References
Effective publication: Protasov et al., 2023 [1]

Registry URL
https://seqco.de/i:32447

Genus *Methanorudis*

Etymology
[Me.tha.no.ru'dis] **N.L. pref.** *methano-*, pertaining to methane; **L. fem. n.** *rudis*, a small stick; **N.L. fem. n.** *Methanorudis*, a small methane-producing stick

Nomenclatural type
Species *Methanorudis spinitermitis*$^{\mathrm{Ts}}$

Description

The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanorudis*

References

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

Registry URL

https://seqco.de/i:32452

Genus *Methanocatella*

Etymology

[Me.tha.no.ca.tel'la] **N.L. pref.** *methano-*, pertaining to methane; **L. fem. dim. n.** *catella*, a little chain; **N.L. fem. dim. n.** *Methanocatella*, a methane-producing chain, referring to the short chains of cells characteristic of this genus

Nomenclatural type

Species *Methanocatella smithii*^{Ts}

Description

The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group. Short oval rods or coccobacilli, 0.4–1 µm in width and 0.6–1.5 µm in length. Cells occur singly, in pairs or in chains of 4–6 cells. Gram positive. Nonmotile. Require complex medium with yeast extract, trypticase, rumen fluid, or fecal extract. Optimum temperature is 35–42 °C. Use H_2 + CO_2 as substrates for methanogenesis, some species grow poorly on formate.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanocatella*

References

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

Registry URL

https://seqco.de/i:32432

Genus *Methanolapillus*

Etymology

[Me.tha.no.la'pil.lus] **N.L. pref.** *methano-*, pertaining to methane; **L. masc. n.** *lapillus*, a pebble, gem, jewel; **N.L. masc. n.** *Methanolapillus*, a methane-producing jewel

Nomenclatural type

Species *Methanolapillus millepedarum*^{Ts}

Description

The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group. Cells are irregular cocci, 1-2 µm. Cells occur singly or sometimes in aggregates. Nonmotile. Require complex medium with yeast extract, peptone, and casamino acids. Grow between 25-42° C. H2 and methanol are the substrates for methanogenesis; methylamines can substitute methanol.

Classification

Archaea » *Methanobacteriota* » “Methanomicrobia” » *Methanosarcinales* » *Methanosarcinaceae* » *Methanolapillus*

References

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

Registry URL

https://seqco.de/i:32601

Species *Methanorbis rubei*

Etymology

[ru'be.i] **L. gen. masc. n.** *rubei*, of the red, referring to the color of the host.

Nomenclatural type

NCBI Assembly: GCA_032714495 Ts

Reference Strain

Cs1 = DSM 115765

Description

Ovoid cocci cells 1−3 µm. Non-motile. H2 and CO2 are the substrates for methanogenesis; formate can substitute H2. Yeast extract stimulates growth. The optimum temperature is 33 °C. The G+C content of the type genome is 50.2 mol%, and the genome size is 1.82 Mbp.

Classification

Archaea » *Methanobacteriota* » “Methanomicrobia” » *Methanomicrobiales* » *Methanocorpusculaceae* » *Methanorbis* » *Methanorbis rubei*

References

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

Registry URL

https://seqco.de/i:32573

Species *Bathycorpusculum fermentans*

Etymology

[fer.men'tans] **L. part. adj.** *fermentans*, fermenting

Nomenclatural type

NCBI Assembly: GCA_009787175 Ts

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 37.8 mol%, and the estimated genome size is 1.86 Mbp.

Classification

Archaea » “Bathyarchaeota” » *Bathyarchaeia* » *Bathyarchaeales* » *Bathycorpusculaceae* » *Bathycorpusculum* » *Bathycorpusculum fermentans*

References

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

Registry URL

https://seqco.de/i:32520

Species *Methanobinarius endosymbioticus*

Etymology

[en.do.sym.bi.o'ti.cus] **Gr. pref.** *endo-*, within; **N.L. masc. adj.** *symbioticus*, living together; **N.L. masc. adj.** *endosymbioticus*, living together within (another organism)

Nomenclatural type

NCBI Assembly: GCA_003315655 Ts

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 25.2 mol%, and the genome size is 1.91 Mbp.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanobinarius* » *Methanobinarius endosymbioticus*

References

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

Registry URL

https://seqco.de/i:32444

Species *Methanoflexus mossambicus*

Etymology

[mos.sam.bi'cus] **N.L. masc. adj.** *mossambicus*, of Mozambique

Nomenclatural type

NCBI Assembly: GCA_031261915 Ts

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 24.0 mol%, and the genome size is 3.25 Mbp.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanoflexus* » *Methanoflexus mossambicus*

References

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

Registry URL

https://seqco.de/i:32449

Species *Methanovirga aequatorialis*

Etymology

[ae.qua.to.ri.a'lis] **L. fem. adj.** *aequatorialis*, equatorial, denoting the origin of the host

Nomenclatural type

NCBI Assembly: GCA_031282205 Ts

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 29.3 mol%, and the genome size is 2.05 Mbp.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanovirga* » *Methanovirga aequatorialis*

References

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

Registry URL

https://seqco.de/i:32455

Species *Methanovirga australis*

Etymology

[aus.tra'lis] **L. fem. adj.** *australis*, southern, denoting the origin of the host from the southern hemisphere (Australia)

Nomenclatural type

NCBI Assembly: GCA_031272765 ^{Ts}

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 26.8 mol%, and the genome size is 2.50 Mbp.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanovirga* » *Methanovirga australis*

References

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

Registry URL

https://seqco.de/i:32456

Species *Methanovirga basalitermitum*^{Ts}

Etymology

[ba.sa.li.ter'mi.tum] **L. adj.** *basalis*, basal; **L. masc. n.** *termes*, a woodworm, a termite; **N.L. gen. pl. masc. n.** *basalitermitum*, of lower (basal) termites

Nomenclatural type

NCBI Assembly: GCA_031284445 ^{Ts}

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 27.8 mol%, and the genome size is 2.18 Mbp.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanovirga* » *Methanovirga basalitermitum*^{Ts}

References

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

Registry URL

https://seqco.de/i:32457

Species *Methanovirga meridionalis*

Etymology

[me.ri.di.o.na'lis] **L. fem. adj.** *meridionalis*, southern, denoting the origin of the host from the southern hemisphere (Chile).

Nomenclatural type

NCBI Assembly: GCA_031289325 ^{Ts}

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 23.7 mol%, and the genome size is 2.39 Mbp.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanovirga* » *Methanovirga meridionalis*

References

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

Registry URL

https://seqco.de/i:32458

Species *Methanovirga procula*

Etymology

[pro.cu'la] **L. fem. adj.** *procula*, from far away, denoting the origin from a remote island (Réunion)

Nomenclatural type

NCBI Assembly: GCA_031280375 Ts

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 26.7 mol%, and the genome size is 2.38 Mbp.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanovirga* » *Methanovirga procula*

References

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

Registry URL

https://seqco.de/i:32459

Species *Methanorudis spinitermitis*Ts

Etymology

[spi.ni.ter'mi.tis] **N.L. gen. masc. n.** *spinitermitis*, of Spinitermes (the host genus)

Nomenclatural type

NCBI Assembly: GCA_031286225 Ts

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 25.8 mol%, and the genome size is 1.96 Mbp.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanorudis* » *Methanorudis spinitermitis*Ts

References

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

Registry URL

https://seqco.de/i:32453

Species *Bathycorpusculum hydrogenotrophicum*

Etymology

[hyd.ro.ge.no.tro.phi'cum] **N.L. pref.** *hydrogeno-*, pertaining to hydrogen; **Gr. masc. adj.** *trophikos*, pertaining to food; **N.L. neut. adj.** *hydrogenotrophicum*, feeding on hydrogen

Nomenclatural type

NCBI Assembly: GCA_009783705 ^{Ts}

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 43.2 mol%, and the estimated genome size is 2.24 Mbp.

Classification

Archaea » “Bathyarchaeota” » *Bathyarchaeia* » *Bathyarchaeales* » *Bathycorpusculaceae* » *Bathycorpusculum* » *Bathycorpusculum hydrogenotrophicum*

References

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

Registry URL

https://seqco.de/i:32521

Species *Methanofilum arcanum*^{Ts}

Etymology

[ar.ca'num] **L. neut. adj.** *arcanum*, hidden mysterious

Nomenclatural type

NCBI Assembly: GCA_031285085 ^{Ts}

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 29.3 mol%, and the genome size is 2.05 Mbp.

Classification

Archaea » *Methanobacteriota* » “Methanomicrobia” » *Methanomicrobiales* » *Methanospirillaceae* » *Methanofilum* » *Methanofilum arcanum*^{Ts}

References

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

Registry URL

https://seqco.de/i:32512

Species *Methanocatella smithii*^{Ts}

Etymology

[smith'i.i] **N.L. gen. masc. n.** *smithii*, of Smith, named after P.H. Smith, who isolated the type strain

Nomenclatural type

NCBI Assembly: GCF_000016525 ^{Ts}

Reference Strain

ATCC 35061 = PS = DSM 861

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 31.0 mol%, and the genome size is 1.85 Mbp. Cells are short oval rods or coccobacilli with tapered ends, 0.6–0.7 µm in width and ~1.0 µm in length. Cells occur most frequently in pairs or in chains of 4–6 cells. Gram positive. Nonmotile. H2 and CO2 are the preferred energy sources. Growth on formate is poor. Cells grow optimally at 37 to 39 °C. (as in Balch et al., 1979; Miller, 2015).

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanocatella* » *Methanocatella smithii*^{Ts}

References

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

Registry URL

https://seqco.de/i:32433

Species *Bathycorpusculum soli*

Etymology

[so'li] **L. gen. n.** *soli*, of soil

Nomenclatural type

NCBI Assembly: GCA_031277345 ^{Ts}

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 37.5 mol%, and the estimated genome size is 1.88 Mbp.

Classification

Archaea » “Bathyarchaeota” » *Bathyarchaeia* » *Bathyarchaeales* » *Bathycorpusculaceae* » *Bathycorpusculum* » *Bathycorpusculum soli*

References

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

Registry URL

https://seqco.de/i:32522

Species *Methanorbis basalitermitum*

Etymology

[ba.sa.li.ter'mi.tum] **L. adj.** *basalis*, basal; **L. masc. n.** *termes*, a woodworm, a termite; **N.L. gen. pl. masc. n.** *basalitermitum*, of lower (basal) termites

Nomenclatural type

NCBI Assembly: GCA_031287415 ^{Ts}

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 50.9 mol%, and the genome size is 1.27 Mbp.

Classification

Archaea » *Methanobacteriota* » “Methanomicrobia” » *Methanomicrobiales* » *Methanocorpusculaceae* » *Methanorbis* » *Methanorbis basalitermitum*

References

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

Registry URL

https://seqco.de/i:32538

Species *Bathycorpusculum termitum*

Etymology

[ter'mi.tum] **N.L. gen. pl. n.** *termitum*, of termites, referring to the host

Nomenclatural type

NCBI Assembly: GCA_031254875 ^{Ts}

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 43.8 mol%, and the estimated genome size is 2.30 Mbp.

Classification

Archaea » “Bathyarchaeota” » *Bathyarchaeia* » *Bathyarchaeales* » *Bathycorpusculaceae* » *Bathycorpusculum* » *Bathycorpusculum termitum*

References

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

Registry URL

https://seqco.de/i:32524

Species *Methanoplasma glyptotermitis*

Etymology

[gly.pto.ter'mi.tis] **N.L. gen. n.** *glyptotermitis*, referring to Glyptotermes, the host genus

Nomenclatural type

NCBI Assembly: GCA_031267895 ^{Ts}

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 49.7%, and the estimated genome size is 1.84 Mbp.

Classification

Archaea » *Methanobacteriota* » *Thermoplasmata* » *Methanomassiliicoccales* » *Methanomethylophilaceae* » *Methanoplasma* » *Methanoplasma glyptotermitis*

References

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

Registry URL

https://seqco.de/i:32527

Species *Methanoplasma porotermitis*

Etymology

[po.ro.ter'mi.tis] **N.L. gen. n.** *porotermitis*, referring to Porotermes, the host genus

Nomenclatural type

NCBI Assembly: GCA_031290095 ^{Ts}

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 57.3%, and the estimated genome size is 1.69 Mbp.

Classification

Archaea » *Methanobacteriota* » *Thermoplasmata* » *Methanomassiliicoccales* » *Methanomethylophilaceae* » *Methanoplasma* » *Methanoplasma porotermitis*

References

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

Registry URL

https://seqco.de/i:32528

Species *Methanoplasma reticulitermitis*

Etymology

[re.ti.cu.li.ter'mi.tis] **N.L. gen. n.** *reticulitermitis*, referring to Reticulitermes, the host genus

Nomenclatural type

NCBI Assembly: GCA_031287135 Ts

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 53.4%, and the estimated genome size is 1.34 Mbp.

Classification

Archaea » *Methanobacteriota* » *Thermoplasmata* » *Methanomassiliicoccales* » *Methanomethylophilaceae* » *Methanoplasma* » *Methanoplasma reticulitermitis*

References

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

Registry URL

https://seqco.de/i:32529

Species *Methanimicrococcus odontotermitis*

Etymology

[o.don.to.ter'mi.tis] **N.L. gen. masc. n.** *odontotermitis*, referring to Odontotermes, the host genus

Nomenclatural type

NCBI Assembly: GCA_031286065 Ts

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 43.8%, and the estimated genome size is 1.88 Mbp.

Classification

Archaea » *Methanobacteriota* » “Methanomicrobia” » *Methanosarcinales* » *Methanosarcinaceae* » *Methanimicrococcus* » *Methanimicrococcus odontotermitis*

References

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

Registry URL

https://seqco.de/i:32598

Species *Bathycorpusculum terrae*

Etymology

[ter'rae] **L. gen. n.** *terrae*, of the earth

Nomenclatural type

NCBI Assembly: GCA_009784175 Ts

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 38.1 mol%, and the estimated genome size is 1.27 Mbp.

Classification

Archaea » “Bathyarchaeota” » *Bathyarchaeia* » *Bathyarchaeales* » *Bathycorpusculaceae* » *Bathycorpusculum* » *Bathycorpusculum terrae*

References

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

Registry URL

https://seqco.de/i:32523

Species *Bathycorpusculum grumuli*

Etymology

[gru'mu.li] **L. gen. n.** *grumuli*, of a little hill

Nomenclatural type

NCBI Assembly: GCA_009776805 Ts

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 35.5 mol%, and the estimated genome size is 2.30 Mbp.

Classification

Archaea » “Bathyarchaeota” » *Bathyarchaeia* » *Bathyarchaeales* » *Bathycorpusculaceae* » *Bathycorpusculum* » *Bathycorpusculum grumuli*

References

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

Registry URL

https://seqco.de/i:32525

Species *Bathycorpusculum acidaminoxidans*

Etymology

[a.cid.am.in.ox'i.dans] **N.L. neut. n.** *acidum aminum*, amino acid; **N.L. pres. part.** *oxydans*, to oxidize; **N.L. part. adj.** *acidaminoxidans*, amino acid-oxidizing

Nomenclatural type

NCBI Assembly: GCA_009786255 Ts

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 37.9 mol%, and the estimated genome size is 1.99 Mbp.

Classification

Archaea » “Bathyarchaeota” » *Bathyarchaeia* » *Bathyarchaeales* » *Bathycorpusculaceae* » *Bathycorpusculum* » *Bathycorpusculum acidaminoxidans*

References

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

Registry URL

https://seqco.de/i:32516

Species *Bathycorpusculum acetigenes*Ts

Etymology

[a.ce.ti'ge.nes] **L. neut. n.** *acetum*, vinegar; **Gr. suff.** *-genes*, to produce; **N.L. part. adj.** *acetigenes*, vinegar- or acetic acid producing

Nomenclatural type

NCBI Assembly: GCA_009781675 ^{Ts}

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 43.4mol%, and the estimated genome size is 2.15Mbp.

Classification

Archaea » “Bathyarchaeota” » *Bathyarchaeia* » *Bathyarchaeales* » *Bathycorpusculaceae* » *Bathycorpusculum* » *Bathycorpusculum acetigenes*^{Ts}

References

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

Registry URL

https://seqco.de/i:32519

Species *Methanomicula labiotermitis*^{Ts}

Etymology

[la.bi.o.ter'mi.tis] **N.L. gen. n.** *labiotermitis*, of or pertaining to Labiotermes, the genus name of the host

Nomenclatural type

NCBI Assembly: GCA_009780575 ^{Ts}

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 49.7%, and the estimated genome size is 1.44 Mbp.

Classification

Archaea » *Methanobacteriota* » *Thermoplasmata* » *Methanomassiliicoccales* » *Methanomethylophilaceae* » *Methanomicula* » *Methanomicula labiotermitis*^{Ts}

References

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

Registry URL

https://seqco.de/i:32530

Species *Methanofrustulum fimipullorum*^{Ts}

Etymology

[fi.mi.pul.lo'rum] **L. neut. n.** *fimus*, dung, excrement; **L. masc. n.** *pullus*, chicken; **N.L. gen. pl. masc. n.** *fimipullorum*, of chicken dung; denoting the putative origin from chicken manure

Nomenclatural type

NCBI Assembly: GCA_012518265 ^{Ts}

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 42.9%, and the estimated genome size is 1.93 Mbp.

Classification

Archaea » *Methanobacteriota* » “Methanomicrobia” » *Methanosarcinales* » *Methanosarcinaceae* » *Methanofrustulum* » *Methanofrustulum fimipullorum*^{Ts}

References

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

Registry URL

https://seqco.de/i:32515

Species *Methanoplasma cognatum*

Etymology

[cog.na'tum] **L. neut. adj.** *cognatum*, related by blood, sibling, referring to the Methanoplasma termitum as relative

Nomenclatural type

NCBI Assembly: GCA_009777615 Ts

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 52.2%, and the estimated genome size is 1.61 Mbp.

Classification

Archaea » *Methanobacteriota* » *Thermoplasmata* » *Methanomassiliicoccales* » *Methanomethylophilaceae* » *Methanoplasma* » *Methanoplasma cognatum*

References

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

Registry URL

https://seqco.de/i:32526

Species *Methanimicrococcus labiotermitis*

Etymology

[la.bi.o.ter'mi.tis] **N.L. gen. n.** *labiotermitis*, referring to Labiotermes, the host genus

Nomenclatural type

NCBI Assembly: GCA_009784005 Ts

Description

The species identified by metagenomic analyses. The G+C content of the type genome is 45.5%, and the estimated genome size is 1.83 Mbp.

Classification

Archaea » *Methanobacteriota* » “Methanomicrobia” » *Methanosarcinales* » *Methanosarcinaceae* » *Methanimicrococcus* » *Methanimicrococcus labiotermitis*

References

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

Registry URL

https://seqco.de/i:32597

Species *Methanocatella gottschalkii*

Etymology

[gott.schalk'i.i] **N.L. gen. masc. n.** *gottschalkii*, of Gottschalk, named in honor of Gerhard Gottschalk for his notable contributions to the understanding of the biochemistry of methanogenesis

Nomenclatural type

NCBI Assembly: GCF_003814835 Ts

Reference Strain

HO = ATCC BAA-1169 = DSM 11977

Description

Coccobacillus with rounded ends, about 0.7 µm in width and 0.9 µm in length, occurring in pairs or short chains. Gram-positive reaction. Cell walls are composed of pseudomurein. Cells are resistant to lysis by SDS. Optimum temperature 37 °C. Optimum pH 7 (as in Miller, Lin, 2002). The G+C content of the type genome is 30.0 mol%, and the genome size is 1.87 Mbp.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanocatella* » *Methanocatella gottschalkii*

References

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

Registry URL

https://seqco.de/i:32434

Species *Methanacia filiformis* Ts

Etymology

[fi.li.for'mis.] **L. neut. n.** *filum*, a thread; **L. fem. adj. suff.** *-formis*, like, in the shape of; **N.L. fem. adj.** *filiformis*, thread-shaped

Nomenclatural type

NCBI Assembly: GCF_001639265 Ts

Reference Strain

RFM-3 = DSM 11501

Description

Filament-forming rods with slightly tapered ends, 0.23–0.28 µm in width by up to several hundred µmin length. Rarely occurs as single 4-µm-long cells. Nonmotile. trict anaerobe. Catalase positive. Metabolizes H2 and CO2 to CH4. Optimum temperature is 30 °C (range 10–33.5 °C). Optimum pH is 7.0–7.2 (range 6.0–7.5). Yeast extract (>0.01%) is required for growth (as in Miller, 2015). The G+C content of the type genome is 26.9 mol%, and the genome size is 2.60 Mbp.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanacia* » *Methanacia filiformis* Ts

References

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

Registry URL

https://seqco.de/i:32451

Species *Methanocatella millerae*

Etymology

[mil'ler.ae] **N.L. gen. fem. n.** *millerae*, of Miller, named after Terry L. Miller for her contributions to the taxonomy of methanogens, in particular the genus Methanobrevibacter

Nomenclatural type

NCBI Assembly: GCF_900103415 Ts

Reference Strain

ZA-10 = DSM 16643

Description

Cells occur singly or in pairs or chains and are coccobacilli (0.5−1.2 µm) with rounded ends. Cells stain Gram-positive, are non-motile and are resistant to lysis by 10% SDS. Grows and produces methane from H2/CO2 and from formate plus CO2. The optimum temperature range for growth is 36−42 °C. pH range for growth is 5.5−10.0; optimum pH is 7.0−8.0. The maximum salt tolerance for growth is 2.6 % (as in Rea et al., 2007). The G+C content of the type genome is 36.5 mol%, and the genome size is 2.72 Mbp.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanocatella* » *Methanocatella millerae*

References

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

Registry URL

https://seqco.de/i:32435

Species *Methanocatella oralis*

Etymology

[o.ra'lis] **L. fem. adj.** *oralis*, pertaining to the mouth

Nomenclatural type

NCBI Assembly: GCF_001639275 ^{Ts}

Reference Strain

ZR = DSM 7256 = JCM 30027

Description

Cells are short, oval rods with tapered ends, 0.4−0.5 µm in width and 0.7−1.2 µm in length, occurring most frequently in pairs or short chains. Cells give a Gram-positive reaction when less than 4 d old. Ultrathin sections show a tristratified cell wall that is highly invaginated. Nonmotile (as in Miller, 2015). The G+C content of the type genome is 27.7 mol%, and the genome size is 2.14 Mbp.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanocatella* » *Methanocatella oralis*

References

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

Registry URL

https://seqco.de/i:32436

Species *Methanocatella thaueri*

Etymology

[thau'er.i] **N.L. gen. masc. n.** *thaueri*, of Thauer, named in honor of Rudolf K. Thauer for his fundamental contributions to the delineation of the biochemistry of methanogenesis

Nomenclatural type

NCBI Assembly: GCF_003111625 ^{Ts}

Reference Strain

DSM 11995

Description

Coccobacillus, with slightly tapered ends, about 0.5 µm in width and 0.6−1.2 µm in length, occurring in pairs and short chains. Some chains may have elongat- ed cells. Gram-positive reaction. Cell walls are composed of pseudomurein. Cells are resistant to lysis by SDS. Optimum temperature 37 °C. Optimum pH 7 (as in Miller, Lin, 2002). The G+C content of the type genome is 36.9 mol%, and the genome size is 2.24 Mbp.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanocatella* » *Methanocatella thaueri*

References

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

Registry URL

https://seqco.de/i:32437

Species *Methanocatella woesei*

Etymology

[woe'se.i] **N.L. gen. masc. n.** *woesei*, of Woese, named in honor of Carl R. Woese for his pioneering contributions to the understanding of the phylogeny of methanogens and other microorganisms

Nomenclatural type

NCBI Assembly: GCF_003111605 Ts

Reference Strain

DSM 11979

Description

Coccobacillus with slightly tapered or rounded ends, about 0.6 µm in width and 1.0 µm in length, occurring in pairs or short chains. Gram-positive reaction. Cell walls are composed of pseudomurein. Cells are resistant to lysis by SDS. Optimum temperature 37 °C. Optimum pH 7 (as in Miller, Lin, 2002). The G+C content of the type genome is 29.9 mol%, and the genome size is 1.54 Mbp.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanocatella* » *Methanocatella woesei*

References

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

Registry URL

https://seqco.de/i:32438

Species *Methanarmilla wolinii* Ts

Etymology

[wo.lin'i.i.] **N.L. gen. masc. n.** *wolinii*, of Wolin, named in honor of Meyer J. Wolin for his singular contributions to the physiological understanding of the role of methanogens and interspecies hydrogen transfer in anaerobic habitats

Nomenclatural type

NCBI Assembly: GCF_000621965 Ts

Reference Strain

SH = ATCC BAA-1170 = DSM 11976

Description

Coccobacillus with slightly tapered or rounded ends, about 0.6 µm in width and 1.0−1.4 µm in length, occurring in pairs or short chains. Gram-positive. Cell walls are composed of pseudomurein. Cells are resistant to lysis by SDS. Optimum temperature 37 °C. Optimum pH 7 (as in Miller, Lin, 2002). The G+C content of the type genome is 24.2 mol%, and the genome size is 2.04 Mbp.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanarmilla* » *Methanarmilla wolinii*^{Ts}

References

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

Registry URL

https://seqco.de/i:32440

Species *Methanarmilla boviskoreani*

Etymology

[bo.vis.ko.re.a'ni] **L. gen. n.** *bovis*, cattle; **N.L. masc. adj.** *koreanus*, Korean; **N.L. gen. masc. / fem. n.** *boviskoreani*, of Korean cattle

Nomenclatural type

NCBI Assembly: GCF_000320505 ^{Ts}

Reference Strain

JH1 = DSM 25824 = JCM 18376 = KCTC 4102

Description

Cells stain Gram-positive, occur singly or in pairs or chains and are rod-shaped (1.5−1.8 µm). Cells are non-motile. The optimum pH and temperature for growth are pH 6.5−7.0 and 37−40 °C. The maximum salt (NaCl) tolerance for growth is 0.5 M (as in Lee et al., 2013). The G+C content of the type genome is 28.9 mol%, and the genome size is 2.04 Mbp.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanarmilla* » *Methanarmilla boviskoreani*

References

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

Registry URL

https://seqco.de/i:32441

Species *Methanobinarius arboriphilus*^{Ts}

Etymology

[ar.bo.ri'phi.lus] **L. fem. n.** *arboris*, tree; **N.L. masc. adj.** *philus*, friend, loving; **N.L. masc. adj.** *arboriphilus*, tree-loving

Nomenclatural type

NCBI Assembly: GCF_002072215 ^{Ts}

Reference Strain

JCM 13429 = DSM 1125 = DH1

Description

Cells are short rods with rounded ends, 0.5 µm in width and 1.2−1.4 µminlength. Some cells may have a slighdy truncated end. They occur singly or in pairs. Growth is stimulated by trypticase peptones, yeast extract, and rumen fluid. H2 and CO2 may be the sole or preferred energy sources. The optimal temperature for growth was 30 to 37 °C. (as in Zeikus and Henning, 1975; Miller, 2015). The G+C content of the type genome is 25.4 mol%, and the genome size is 2.44 Mbp.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanobinarius* » *Methanobinarius arboriphilus*Ts

References

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

Registry URL

https://seqco.de/i:32443

Species *Methanobaculum cuticulare*Ts

Etymology

[cu.ti.cu.la're] **N.L. neut. adj.** *cuticulare*, referring to the cuticular surface of the termite hindgut epithelium, which is colonized by this organism

Nomenclatural type

NCBI Assembly: GCA_001639285 Ts

Reference Strain

DSM 11139

Description

The species description remains the same as in Miller (2015). The G+C content of the type genome is 26.7 mol%, and the genome size is 2.60 Mbp.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanobaculum* » *Methanobaculum cuticulare*Ts

References

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

Registry URL

https://seqco.de/i:32446

Species *Methanoflexus curvatus*Ts

Etymology

[cur.va'tus] **L. masc. adj.** *curvatus*, bent, curved; referring to the shape of the cell

Nomenclatural type

NCBI Assembly: GCF_001639295 Ts

Reference Strain

DSM 11111

Description

Curved rods with slightly tapered ends, 0.34 by 1.6 µm in size, occurring singly or in pairs. Nonmotile. Metabolizes H2 and CO2, yielding CH4 as the sole product. Optimum temperature is 30 °C (range10−30 °C). Optimum pH is 7.1−7.2 (range 6.5−8.5). Complex nutritional supplements, e.g., 40% (v/v) clarified rumen fluid and nutrient broth (Difco) are required for growth (as in Miller, 2015). The G+C content of the type genome is 25.7 mol%, and the genome size is 2.41 Mbp.

Classification

Archaea » *Methanobacteriota* » *Methanobacteria* » *Methanobacteriales* » *Methanobacteriaceae* » *Methanoflexus* » *Methanoflexus curvatus*^{Ts}

References

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

Registry URL

https://seqco.de/i:32448

Species *Methanimicrococcus hacksteinii*

Etymology

[hack.stein'i.i.] **N.L. gen. masc. n.** *hacksteinii*, of Hackstein, named in honor of Johannes H.P. Hackstein for his important contributions on the hydrogenosomes of anaerobic protists and methanogenesis in arthropod guts

Nomenclatural type

NCBI Assembly: GCA_032714515 ^{Ts}

Reference Strain

DSM 115570 = JCM 39383

Description

Irregular cocci cells 1–2 µm in diameter, non-motile. Use methanol and methylamines as methanogenesis substrates together with hydrogen. Requires acetate, Casamino acids, and coenzyme M. The optimum temperature is 37 °C. The G+C content of the type genome is 42.9%, and the estimated genome size is 2.04 Mbp.

Classification

Archaea » *Methanobacteriota* » “Methanomicrobia” » *Methanosarcinales* » *Methanosarcinaceae* » *Methanimicrococcus* » *Methanimicrococcus hacksteinii*

References

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

Registry URL

https://seqco.de/i:32595

Species *Methanimicrococcus stummii*

Etymology

[stumm'i.i] **N.L. gen. masc. n.** *stummii*, of Stumm, named in honor of Claudius K. Stumm for his important contributions on the symbiosis of methanogens with anaerobic protists

Nomenclatural type

NCBI Assembly: GCA_032594435 ^{Ts}

Reference Strain

Es2

Description

Irregular cocci cells 1–2 µm in diameter, non-motile. Use methanol and methylamines as methanogenesis substrates together with hydrogen. Requires acetate and Casamino acids; formate and yeast extract are stimulatory. The optimum temperature is 37 °C. The G+C content of the type genome is 43.1%, and the estimated genome size is 1.78 Mbp.

Classification

Archaea » *Methanobacteriota* » “Methanomicrobia” » *Methanosarcinales* » *Methanosarcinaceae* » *Methanimicrococcus* » *Methanimicrococcus stummii*

References

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

Registry URL

https://seqco.de/i:32599

Species *Methanimicrococcus hongohii*

Etymology

[hon.goh'i.i.] **N.L. gen. masc. n.** *hongohii*, of Hongoh, named after Yuichi Hongoh in recognition of his important contributions to arthropod gut microbiology

Nomenclatural type

NCBI Assembly: GCA_032594095 Ts

Reference Strain

Hf6 = DSM 114388 = JCM 39385

Description

Irregular cocci cells 1–2 µm in diameter, non-motile. Use methanol and methylamines as methanogenesis substrates together with hydrogen. Requires acetate and Casamino acids; formate is stimulatory. The optimum temperature is 37 °C. The G+C content of the type genome is 41.0%, and the genome size is 2.13 Mbp.

Classification

Archaea » *Methanobacteriota* » “Methanomicrobia” » *Methanosarcinales* » *Methanosarcinaceae* » *Methanimicrococcus* » *Methanimicrococcus hongohii*

References

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

Registry URL

https://seqco.de/i:32596

Species *Methanolapillus millepedarum*Ts

Etymology

[mil.le.pe.da'rum] **L. gen. pl. n.** *millepedarum*, of millipedes

Nomenclatural type

NCBI Assembly: GCA_032594115 Ts

Reference Strain

Ac7

Description

Irregular cocci cells 1–2 µm in diameter, non-motile. Use methanol and methylamines as methanogenesis substrates together with hydrogen.). Requires acetate, yeast extract, Casamino acids, and coenzyme M. The optimum temperature is 37 °C. The G+C content of the type genome is 42.9%, and the estimated genome size is 1.93 Mbp.

Classification

Archaea » *Methanobacteriota* » “Methanomicrobia” » *Methanosarcinales* » *Methanosarcinaceae* » *Methanolapillus* » *Methanolapillus millepedarum*Ts

References

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

Registry URL

https://seqco.de/i:32600

Species *Methanolapillus africanus*

Etymology

[a.fri.ca'nus] **L. masc. adj.** *africanus*, pertaining to Africa

Nomenclatural type

NCBI Assembly: GCA_032714475 Ts

Reference Strain

DSM 115569 = JCM 39381

Description

Irregular cocci cells, 1–2 µm in diameter, non-motile. Use methanol and methylamines as methanogenesis substrates together with hydrogen. Requires acetate, yeast extract, Casamino acids, and coenzyme M. The optimum temperature is 37 °C. The G+C content of the type genome is 44.4%, and the estimated genome size is 2.10 Mbp.

Classification

Archaea » *Methanobacteriota* » “Methanomicrobia” » *Methanosarcinales* » *Methanosarcinaceae* » *Methanolapillus* » *Methanolapillus africanus*

References

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

Registry URL

https://seqco.de/i:32602

Species *Methanolapillus ohkumae*

Etymology

[oh.ku'mae] **N.L. gen. masc. n.** *ohkumae*, of Ohkuma, named after Moriya Ohkuma in recognition of his important contributions to arthropod gut microbiology

Nomenclatural type

NCBI Assembly: GCA_032594355 Ts

Reference Strain

DSM 114424 = JCM 39382

Description

Irregular cocci cells 1–2 µm in diameter, non-motile. Use methanol and methylamines as methanogenesis substrates together with hydrogen. Requires acetate, formate, and coenzyme M; yeast extract is stimulatory. The optimum temperature is 37 °C. The G+C content of the type genome is 41.0%, and the estimated genome size is 1.84 Mbp.

Classification

Archaea » *Methanobacteriota* » “Methanomicrobia” » *Methanosarcinales* » *Methanosarcinaceae* » *Methanolapillus* » *Methanolapillus ohkumae*

References

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

Registry URL

https://seqco.de/i:32603

Species *Methanorbis furvi* Ts

Etymology

[fur'vi] **L. gen. masc. n.** *furvi*, of the black one, referring to the color of the host.

Nomenclatural type

NCBI Assembly: GCA_032714615 Ts

Reference Strain

Ag1 = DSM 115764

Description

Ovoid cocci cells 1−3 µm. Non-motile. H2 and CO2 are the substrates for methanogenesis; formate can substitute H2. Acetate and formate are required for growth. The optimum temperature is 33 °C. The G+C content of the type genome is 50.1 mol%, and the genome size is 1.84 Mbp.

Classification

Archaea » *Methanobacteriota* » “Methanomicrobia” » *Methanomicrobiales* » *Methanocorpusculaceae* » *Methanorbis* » *Methanorbis furvi* Ts

References

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

Registry URL

https://seqco.de/i:32572

References

1. Protasov et al. (2023). Diversity and taxonomic revision of methanogens and other archaea in the intestinal tract of terrestrial arthropods. *Frontiers in Microbiology*. DOI:10.3389/fmicb.2023.1281628

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:hfttq0ec** submitted by **Protasov, Evgenii** and including 61 new names has been successfully validated.

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