Register list for 16 new names including Kaelpiales ord. nov.

Submitted by Palmer, Marike

Class *Gorgyraeia*

Etymology

[Gor.gy.rae'i.a] **N.L. fem. n.** *Gorgyraea*, referring to the type genus Gorgyraea; *-ia*, ending to denote a class; **N.L. neut. pl. n.** *Gorgyraeia*, the Gorgyraea class

Nomenclatural type

Genus *Gorgyraea*

Description

This class belongs to the phylum *Omnitrophota*. Observed cell size vary greatly within the class, and cells of 0.2 µm to 2.5 µm have been observed. Sequence data of organisms belonging to the class is also frequently observed from larger cell fractions during serial-filtration experiments. Most members of the class lack several genes associated with parasitism and predation, like those encoding tight-adherence complexes and ATP/ADP translocases, suggesting that most may primarily be free-living. Predicted capacity for acetogenesis through the bacterial Wood-Ljungdahl pathway predominates in the class. Only group 4g hydrogenases are found within members of the class. Several members encode very large ORFs. Genome assemblies belonging to this class originate from a variety of environments, including river or lake water, groundwater, wastewater, saline water, geothermal springs, saline and aquatic sediments, and soil. The type for the class is the genus *Gorgyraea* Williams et al. 2021.

Classification

Bacteria » *Omnitrophota* » *Gorgyraeia*

References

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

Registry URL

https://seqco.de/i:23748

Class *Velaminicoccia*

Etymology

[Ve.la.mi.ni.coc'ci.a] **N.L. masc. n.** *Velaminicoccus*, referring to the type genus Velaminicoccus; *-ia*, ending to denote a class; **N.L. neut. pl. n.** *Velaminicoccia*, the Velaminicoccus class

Nomenclatural type

Genus *Velaminicoccus*

Description

This class belongs to the phylum *Omnitrophota*. All previously visualized cells belonging to this class were small, and of approximately 0.2 µm. In serial-filtration experiments, most organisms were retained by filters with pore sizes at or below 0.2 µm. Genes encoding the tight-adherence complex were largely conserved, and most taxa have predicted capacity for acetogenesis through the bacterial Wood-Ljungdahl pathway. Additionally, group 4g hydrogenases were primarily observed in this class. Very large ORFs are pervasive throughout this class. Genome assemblies belonging to this class originate from lake or river water, groundwater, geothermal springs, wastewater, saline and freshwater sediment, bulk soil, and other engineered environments. The nomenclatural type for the class is the genus *Velaminicoccus* Kizina et al. 2022.

Classification

Bacteria » *Omnitrophota* » *Velaminicoccia*

References

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

Registry URL

https://seqco.de/i:23749

Order *Gorgyraeales*

Etymology

[Gor.gy.rae.a'les] **N.L. fem. n.** *Gorgyraea*, referring to the type genus Gorgyraea; *-ales*, ending to denote an order; **N.L. fem. pl. n.** *Gorgyraeales*, the Gorgyraea order

Nomenclatural type

Genus *Gorgyraea*

Description

This order belongs to the class *Gorgyraia*, in the phylum *Omnitrophota*. As a monotypic order, the description for the order is currently the same as for the genus *Gorgyraea*, the nomenclatural type for the order.

Classification

Bacteria » *Omnitrophota* » *Gorgyraeia* » *Gorgyraeales*

References

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

Registry URL

https://seqco.de/i:44995

Order *Gygaellales*

Etymology
[Gy.ga.el.la'les] **N.L. fem. dim. n.** *Gygaella*, referring to the type genus Gygaella; *-ales*, ending to denote an order; **N.L. fem. pl. n.** *Gygaellales*, the Gygaella order

Nomenclatural type
Genus *Gygaella*

Description
This order belongs to the class *Velaminicoccia*, phylum *Omnitrophota*. Where data is available for putative cell sizes, the cells are below 0.3 µm. Very large ORFs are prevalent in the genomes belonging to this order. Most genomes code for tight-adherence complexes. Predicted energy metabolism in the order is acetogenesis through the Wood-Ljungdahl pathway. Members belonging to this order have been enriched for in a anaerobic bioreactor community grown on propionate at high dilution rate. Assemblies identified as belonging to this order originated from all environments reported for the class Velaminicoccia. Where available, samples from which assemblies were derived were collected at low oxygen concentrations or anaerobic conditions, at temperatures ranging from 10 °C to 40 °C, and at slightly acidic (pH 6) to slightly basic (pH 8.5) conditions. Most genomes belonging to this order possess a Group A [FeFe] and/or a Group 4g [NiFe] hydrogenase. The nomenclatural type of the order is the genus *Gygaella*.

Classification
Bacteria » *Omnitrophota* » *Velaminicoccia* » *Gygaellales*

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

Registry URL
https://seqco.de/i:23768

Order *Kaelpiales*

Etymology
[Ka.el.pi.a'les] **N.L. fem. n.** *Kaelpia*, referring to the type genus Kaelpia; *-ales*, ending to denote an order; **N.L. fem. pl. n.** *Kaelpiales*, the Kaelpia order

Nomenclatural type
Genus *Kaelpia*

Description
The taxonomic placement of this order is uncertain in the phylum *Omnitrophota*. This is a monotypic order and its description is currently the same as for its nomenclatural type, the genus *Kaelpia* Williams et al., 2021.

Classification
Incertae sedis (Bacteria) » *Kaelpiales*

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

Registry URL
https://seqco.de/i:45057

Order *Tantalellales*

Etymology

[Tan.ta.le.lla'les] **N.L. fem. dim. n.** *Tantalella*, referring to the type genus Tantalella; *-ales*, ending to denote an order; **N.L. fem. pl. n.** *Tantalellales*, the Tantalella order

Nomenclatural type

Genus *Tantalella*

Description

This order belongs to the class *Gorgyraia*, in the phylum *Omnitrophota*. Where available, cells of organisms belonging to the order are small (<0.3 µm). Very large ORFs is present in some members of the order, but are not pervasive within the order. Environmental samples from which assemblies are derived range in pH from acidic to circumneutral. The nomenclatural type of the order is the genus *Tantalella*.

Classification

Bacteria » *Omnitrophota* » *Gorgyraeia* » *Tantalellales*

References

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

Registry URL

https://seqco.de/i:23747

Order *Velaminicoccales*

Etymology

[Ve.la.mi.ni.coc.ca'les] **N.L. masc. n.** *Velaminicoccus*, referring to the type genus Velaminicoccus; *-ales*, ending to denote an order; **N.L. fem. pl. n.** *Velaminicoccales*, the Velaminicoccus order

Nomenclatural type

Genus *Velaminicoccus*

Description

This order belongs to the class *Velaminicoccia*, in the phylum *Omnitrophota*. Members of the order with available cell size data are < 0.3 µm. High-quality genomes of members of the order encode very large ORFs, components of tight-adherence complexes, and genes consistent with an acetogenic metabolism. Assemblies belonging to this order originate from lake and groundwater, as well as wastewater. The nomenclatural type for the order is the genus *Velaminicoccus*.

Classification

Bacteria » *Omnitrophota* » *Velaminicoccia* » *Velaminicoccales*

References

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

Registry URL

https://seqco.de/i:23751

Order *Zapsychrales*

Etymology

[Zap.sych.ra'les] **N.L. masc. n.** *Zapsychrus*, referring to the type genus Zapsychrus; *-ales*, ending to denote an order; **N.L. fem. pl. n.** *Zapsychrales*, the Zapsychrus order

Nomenclatural type

Genus *Zapsychrus*

Description

This order belongs to the class *Velaminicoccia* in the phylum *Omnitrophota*. Available cell size data indicate likely conservation of small cell sizes within the order. In contrast to other members of the class, the genomes belonging to this order encode diverse respiratory pathways and generally lack all genes associated with acetogenesis and the Wood-Ljungdahl pathway. Components for tight-adherence complexes and the very large ORFs are encoded by most genomes belonging to this order. Assemblies originated from water (including groundwater, wastewater and geothermal springs), soil, sediment and engineered environments. Environmental samples from which assemblies were derived were taken in the presence of oxygen at circumneutral to slightly basic pH. The type for this order is the genus *Zapsychrus*.

Classification

Bacteria » *Omnitrophota* » *Velaminicoccia* » *Zapsychrales*

References

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

Registry URL

https://seqco.de/i:23755

Family *Aceulaceae*

Etymology

[A.ce.u.la'ce.ae] **N.L. fem. dim. n.** *Aceula*, referring to the type genus Aceula; *-aceae*, ending to denote a family; **N.L. fem. pl. n.** *Aceulaceae*, the Aceula family

Nomenclatural type

Genus *Aceula*

Description

This family belongs to the order *Zapsychrales*, class *Velaminicoccia*, phylum *Omnitrophota*. As only a single genus is known for this family, the description of the family is currently still the same as for its nomenclatural type, *Aceula*.

Classification

Bacteria » *Omnitrophota* » *Velaminicoccia* » *Zapsychrales* » *Aceulaceae*

References

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

Registry URL

https://seqco.de/i:45095

Family *Gorgyraeaceae*

Etymology
[Gor.gy.rae.a'ce.ae] **N.L. fem. n.** *Gorgyraea*, referring to the type genus Gorgyraea; *-aceae*, ending to denote a family; **N.L. fem. pl. n.** *Gorgyraeaceae*, the Gorgyraea family

Nomenclatural type
Genus *Gorgyraea*

Description
This family belongs to the order *Gorgyraeales*, class *Gorgyraia*, phylum *Omnitrophota*. As a monotypic family, the description of the family is currently the same as for the genus *Gorgyraea*, the nomenclatural type for the family.

Classification
Bacteria » *Omnitrophota* » *Gorgyraeia* » *Gorgyraeales* » *Gorgyraeaceae*

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

Registry URL
https://seqco.de/i:44994

Family *Gygaellaceae*

Etymology
[Gy.ga.el.la'ce.ae] **N.L. fem. dim. n.** *Gygaella*, referring to the type genus Gygaella; *-aceae*, ending to denote a family; **N.L. fem. pl. n.** *Gygaellaceae*, the Gygaella family

Nomenclatural type
Genus *Gygaella*

Description
This family belongs to the order *Gygaellales*, class *Velaminicoccia*, phylum *Omnitrophota*. The available genome assembly belonging to this family was recovered from Ace Lake, Antarctica. The nomenclatural type for the family is the genus *Gygaella*.

Classification
Bacteria » *Omnitrophota* » *Velaminicoccia* » *Gygaellales* » *Gygaellaceae*

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

Registry URL
https://seqco.de/i:45154

Family *Kaelpiaceae*

Etymology
[Ka.el.pi.a'ce.ae] **N.L. fem. n.** *Kaelpia*, referring to the type genus Kaelpia; *-aceae*, ending to denote a family; **N.L. fem. pl. n.** *Kaelpiaceae*, the Kaelpia family

Nomenclatural type
Genus *Kaelpia*

Description
This family belongs to the order *Kaelpiales*, but their taxonomic placement at the class-level within the *Omnitrophota* is uncertain. The nomenclatural type for the family is the genus *Kaelpia*.

Classification
Incertae sedis (Bacteria) » *Kaelpiales* » *Kaelpiaceae*

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

Registry URL
https://seqco.de/i:45056

Family *Tantalellaceae*

Etymology

[Tan.ta.le.lla'ce.ae] **N.L. fem. dim. n.** *Tantalella*, referring to the type genus Tantalella; *-aceae*, ending to denote a family; **N.L. fem. pl. n.** *Tantalellaceae*, the Tantalella family

Nomenclatural type

Genus *Tantalella*

Description

This family belongs to the order *Tantalellales*, class *Gorgyraia*, phylum *Omnitrophota*. The only observed cell size within the family is that of cells SKK-01, at 2.5 µm. Very large ORFs are intermittently encoded by genomes in this family. Parasitism and predation-related genes are largely absent from this family, and some genes linked to acetogenic metabolism is present in genomes belonging to the family. Members of this family has been recovered from saline water and sediment, and freshwater and lake sediment. The nomenclatural type for the family is the genus *Tantalella* Williams et al. 2021.

Classification

Bacteria » *Omnitrophota* » *Gorgyraeia* » *Tantalellales* » *Tantalellaceae*

References

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

Registry URL

https://seqco.de/i:23746

Family *Velaminicoccaceae*

Etymology

[Ve.la.mi.ni.coc.ca'ce.ae] **N.L. masc. n.** *Velaminicoccus*, referring to the type genus Velaminicoccus; *-aceae*, ending to denote a family; **N.L. fem. pl. n.** *Velaminicoccaceae*, the Velaminicoccus family

Nomenclatural type

Genus *Velaminicoccus*

Description

This family belongs to the order *Velaminicoccales*, class *Velaminicoccia*, phylum *Omnitrophota*. When known, cells are small (< 0.3 µm). Very large ORFS, or genomic scaffolds homologous to very large ORFs are found in all genomes in the family. Most genomes encode tight-adherence complexes and genes for acetogenesis through the bacterial Wood-Ljungdahl pathway. Assemblies assigned to the family have been recovered from ground- and wastewater. The nomenclatural type for the family is the genus *Velaminicoccus*.

Classification

Bacteria » *Omnitrophota* » *Velaminicoccia* » *Velaminicoccales* » *Velaminicoccaceae*

References

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

Registry URL

https://seqco.de/i:23750

Family *Zapsychraceae*

Etymology

[Zap.sych.ra'ce.ae] **N.L. masc. n.** *Zapsychrus*, referring to the type genus Zapsychrus; *-aceae*, ending to denote a family; **N.L. fem. pl. n.** *Zapsychraceae*, the Zapsychrus family

Nomenclatural type

Genus *Zapsychrus*

Description

This family belongs to the order *Zapsychrales*, in the class *Velaminicoccia*, phylum *Omnitrophota*. Most assemblies within this family encode very large ORFs. Genomes in this family are derived from samples of soil, ground- and wastewater, geothermal springs and engineered environments. When reported samples were typically taken at circumneutral pH, microaerobic conditions and temperatures between 10 °C and 30 °C. The nomenclatural type for the family is the genus *Zapsychrus*.

Classification

Bacteria » *Omnitrophota* » *Velaminicoccia* » *Zapsychrales* » *Zapsychraceae*

References

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

Registry URL

https://seqco.de/i:41975

Species *Zapsychrus unditaenarius*

Etymology

[un.di.tae.na.ri'us] **L. fem. n.** *unda*, water; **L. masc. adj.** *taenarius*, below ground; **N.L. masc. adj.** *unditaenarius*, water from below ground

Nomenclatural type

NCBI Assembly: GCA_001805965.1 ^{Ts}

Description

This species conservatively belongs to the genus *Zapsychrus*. Low AAI values, typically associated with family-level relationships are observed between this taxon and the nomenclatural type for the genus, however, relative evolutionary divergence based on a phylogenomic tree inferred from the condensed Bac120 marker set indicate likely genus-level relationships. In addition to characteristics provided for the genus, predicted genome sizes range between 2.2-2.7 Mb with %GC between 37.12 and 37.60%. Some genes associated with acetogenesis and an Rnf complex are encoded by the genome. A reversible acetyl-CoA synthetase coupled with a cytoplasmic Group A3 [FeFe] hydrogenase encoded by this species may facilitate acetogenesis. A respiratory F-type ATPase, and a conductive pilin are encoded by genomes of this species. All genes associated with the tight-adherence complex formation and Type-4a pilus production are present in the genomes. Additionally, a "symbiotic" F-type ATPase and very large ORF are present in the genomes. Assemblies for this species originated from soil and groundwater samples from Rifle, Colorado, USA, where a pH of 7.67 was reported for some samples. The nomenclatural type for the species is the genome GCA_001805965.1.

Classification

Bacteria » *Omnitrophota* » *Velaminicoccia* » *Zapsychrales* » *Zapsychraceae* » *Zapsychrus* » *Zapsychrus unditaenarius*

References

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

Registry URL

https://seqco.de/i:23775

References

1. Seymour et al. (2023). Hyperactive nanobacteria with host-dependent traits pervade Omnitrophota. *Nature Microbiology*. DOI:10.1038/s41564-022-01319-1

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:-x-tioq9** submitted by **Palmer, Marike** and including 16 new names has been successfully validated.

Date of Priority: 2025-01-24 11:23 UTC
DOI: 10.57973/seqcode.r:-x-tioq9