

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>

References

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