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

References

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