

## Title

Omnitrophota: a diverse and ubiquitous candidate phylum of putative syntrophs, predators, and free-living nanobacteria

## Authors

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## Abstract

Candidate bacterial phylum *Omnitrophota* has never been isolated and is poorly understood. Here, we explored the systematics, distribution, cell size, and predicted physiology of *Omnitrophota* based on 316 genomes. Phylogenetic concordance using several marker sets identified seven classes accommodating 144 species. Calibration of the genome taxonomy to 16S rRNA gene phylogenies revealed *Omnitrophota* to be prevalent in the Earth Microbiome Dataset, particularly rhizosphere (96%), bulk soils (73%) and freshwater (92%) and saline (79%) sediments. Phylogenetic placement of single-amplified genomes with cell size measurements and differential size filtration experiments showed ultra-small (<400 nm) cells to be common across the phylum. Energy metabolism is conserved; classes share genes encoding either respiratory or fermentative pathways. Conserved fermentative pathways include the Wood-Ljungdahl pathway, suggesting

syntrophic acetogenesis. Parasitism-related genes are common: a conserved tight adherence (Tad) complex and ATP/ADP translocase are encoded by several classes. However, neither genome size nor biosynthetic pathways are reduced. These results suggest that candidate phylum *Omnitrophota* is diverse and ubiquitous, including putative syntrophs, predators, and free-living nanobacteria. Study of this lineage will provide insight into the evolution of parasitism and predation in bacteria, which likely evolved prior to eukaryotic multicellularity.