

Omnitrophota encompasses diverse and hyperactive nanobacteria within SURF and beyond: Putative metabolic traits and host-dependent lifestyles

Wednesday, May 11, 2022 2:00 PM (20 minutes)

Candidate bacterial phylum Omnitrophota has never been grown in axenic culture and is poorly understood. Here, we combined analysis of 421 Omnitrophota genomes representing six classes and 276 species and show that they are prevalent in water, sediments, and soils globally. Fluorescence-activated cell sorting and differential size filtration showed ultra-small (~0.2 µm) cells to be common across the phylum. Reduced genomes in all six classes maintained major biosynthetic and energy conservation pathways, particularly the acetogenic Wood-Ljungdahl pathway or diverse aerobic and anaerobic respirations. However, most genomes also encoded multiple systems typical of bacterial predators and intracellular parasites, suggesting possible predatory or parasitic lifestyles. In support of this, quantitative stable-isotope probing revealed three families with high isotope uptake rates comparable to obligate bacterial predators in diverse soils. Based on their ubiquity, small cell size, high metabolic activity, and genomic repertoire, many Omnitrophota are likely to be ecologically important in a wide range of ecosystems, possibly as predators or parasites.

Primary author: Dr HEDLUND, Brian (University of Nevada, Las Vegas)

Presenter: Dr HEDLUND, Brian (University of Nevada, Las Vegas)

Session Classification: Biology - Parallel

Track Classification: Biology