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Using metagenomics and metatranscriptomics to study specific bacterial species involved in biological phosphorus removal from wastewater

Mads Albertsen, Simon J. McIlroy, Mikkel Stokholm-Bjerregaard, Søren M. Karst & Per H. Nielsen
Center for Microbial Communities, Aalborg University, Aalborg, Denmark

Introduction
Enhanced Biological Phosphorous Removal (EBPR) from wastewater treatment plants is managed by Polyphosphate Accumulating Organisms (PAOs). The model PAO is “Candidatus Accumulibacter phosphatis” (Accumulibacter) and despite a large body of knowledge, their detailed physiology remains elusive.

In this study we combined metagenomics, metatranscriptomics and laboratory scale enrichment in order to examine the gene expression of the uncultured Accumulibacter and the co-enriched associated community.

Methods
Enrichment
Wastewater treatment plant
Seeding Batch Reactor

Genome recovery
Coverage
Tetranucleotide frequency
Taxonomic classification (PhyloPythiaS+)
Essential genes

Assembly
mmgenome

Binning
A toolbox for reproducible genome extraction from metagenomes

Transcriptomics

Example

Results

A GAO digested in a PNO. The putative GAO Propionibivrio (magenta) is hit by the probes used to quantify the PNO Accumulibacter (white). However, it does not accumulate large amounts of polyphosphate. Probes: PAO651 (FLUC, Accumulibacter); PAO492 (Cys, both); PAO486 (Cys, both); ORF665 (Cys, all bacteria).

Phylogenetic tree (16S-rRNA) of known PRB and GAOs. Until now the PRBs and GAOs have been separated into distinct phylogenetic lineages. The discovery of a GAO from the genus Propionibivrio makes interpretations more difficult. The named Accumulibacter genome was closely related to Accumulibacter clade IIK based on phylogenetic analysis of the ppk gene.

Accumulibacter transcriptomics. Relative expression of the core genes of the Accumulibacter bin under anaerobic feast (15 min) and aerobic famine (180 min) conditions.

ma@bio.aau.dk @MadsAlbertsen85