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

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

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**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 enrichments in order to examine the gene expression of the uncultured Accumulibacter and the co-enriched associated community.

**Methods**

**Enrichment**
Wastewater treatment plant → Sequencing Batch Reactor

**Genome recovery**

<table>
<thead>
<tr>
<th>Samples</th>
<th>Metagenomes</th>
</tr>
</thead>
<tbody>
<tr>
<td>2013-06-06</td>
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</tr>
</tbody>
</table>

**Assembly**

- Taxonomic classification (PhyloPython)
- rRNA genes
- Ecotype specific genes
- Paired-end connections

**Binning**

A toolbox for reproducible genome extraction from metagenomes

**Transcriptomics**

- 400 million reads
- 9 timepoints
- 27 samples

**Results**

- Combining metagenomics, metatranscriptomics, and laboratory scale enrichments enables transcriptome studies of most individual species in the community.
- For the first time, we reveal the detailed transcriptome landscape of Accumulibacter during the anaerobic feast and aerobic famine conditions of the EBPR process.
- A new GAO (competitor to PAOs with a negative impact on EBPR) was discovered. Propionivibrio is closely related to Accumulibacter and hit by the current FISH probes used to define PAOs.

**Conclusions**

- 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 enrichments in order to examine the gene expression of the uncultured Accumulibacter and the co-enriched associated community.

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