

The 18th International Symposium on Microbial Ecology (ISME)

Posters:

'Cold-adapted lipases and lipolytic bacteria found by metaproteogenomics in low-temperature anaerobic membrane bioreactors treating domestic wastewater'

& 'Monitoring the anaerobic digestion microbial community as a foaming risk prediction method'

Authors: Reihaneh Bashiri *et al.*

I am the first author of two accepted abstracts (both as poster presentation) in ISME 18th conference. One of the abstracts is from my PhD (*Cold-adapted lipases and lipolytic bacteria found by metaproteogenomics in low-temperature anaerobic membrane bioreactors treating domestic wastewater*) and the other is from the EBNet Proof of Concept (PoC) funding (*Monitoring the anaerobic digestion microbial community as a foaming risk prediction method*).

Both these abstracts have value for the environmental or industrial biotechnology sector and use combined omics tools: metagenomics to identify microbial individuals and metaproteomics to determine what are they doing within the communities of different environmental samples. In my PhD research, I looked for the cold-adapted bacterial lipases and their producers in anaerobic treatment of domestic wastewater at low temperatures. Cold-adapted bacterial lipases have value for many industries like detergent manufacturers.

In the EBNet PoC, I looked for foam causing/stabilising bacteria and their biomarker molecules which correlates to foaming incidents in full-scale anaerobic digesters with a wide range of mixed solid and liquid wastes. This project can both offer a prediction tool for foaming incidents in anaerobic digestion systems and produce value for industries which are interested in biosurfactant production by identifying novel biosurfactant producers.

Monitoring the anaerobic digestion microbial community as a foaming risk prediction method
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Foaming in anaerobic digestion (AD)


- Causes serious process instability
- Most foam-forming/stabilising bacteria in full-scale AD plant with mixed solid and liquid wastes are unknown

Methods

Hartlepool, Non-foaming plant
 Imperial Park, Foaming plant

Metagenomics
 Metaproteomics

Who are the putative foam-causing bacteria?



Cold-adapted lipases and lipolytic bacteria found by metaproteogenomics
 in low-temperature anaerobic membrane bioreactors treating domestic wastewater
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Introduction

Cold-adapted bacteria can treat domestic wastewater at low temperatures. But poor lipid degradation is still a barrier.

Methods

We used metagenomics and metaproteomics [1].

Metagenomics: Who are the lipase producing bacteria?
 Metaproteomics: Are the lipases produced?
 Bioinformatics: KBpse

Feed: Domestic wastewater (primary influent) from a full-scale activated sludge plant
 Inoculum: Soils & sediments from Lake Geneva, Switzerland and Svalbard, Norway

Results

Who are the lipase producing bacteria?

40 lipolytic MAGs with 78 lipases
 Genome completeness > 90 %
 Contamination < 10 %
 At least one lipase (EC 3.1.1.3) gene
 Out of 1519 total MAGs and 903 lipases (metagenome-assembled genomes)

How abundant are the lipolytic genera in reactors?

Relative abundance (%)

Who are the lipolytic genera from the metaproteomics side?

Metaproteomics: found no lipase!
 Fatty (long-chain fatty acid transporters) was found as a lipolysis biomarker protein in 4 genera not recovered in lipolytic MAGs by metagenomics!

Conclusions

- Extracellular lipases and lipolytic bacteria were not easily identifiable by metagenomics and metaproteomics.
- Metaproteomics did not provide sufficient proteome coverage for lower abundant proteins such as lipases.
- Better protein extraction methods for metaproteomics of enzymes should be developed.

References

1. Phipps, E., et al. 2018. Environmental Science: Water Research & Technology, 4, 1002-1013.
 2. Bashiri, R., et al. 2019. Water Research, 153, 11818-18.