

## Untangling the Effect of Fatty Acid Addition at Species Level Revealed Different Transcriptional Responses of the Biogas Microbial Community Members - DTU Orbit (09/11/2017)

### Untangling the Effect of Fatty Acid Addition at Species Level Revealed Different Transcriptional Responses of the Biogas Microbial Community Members

In the present study, RNA-sequencing was used to elucidate the change of anaerobic digestion metatranscriptome after long chain fatty acids (oleate) exposure. To explore the general transcriptional behavior of the microbiome, the analysis was first performed on shotgun reads without considering a reference metagenome. As a second step, RNA reads were aligned on the genes encoded by the microbial community, revealing the expression of more than 51 000 different transcripts. The present study is the first research which was able to dissect the transcriptional behavior at a single species level by considering the 106 microbial genomes previously identified. The exploration of the metabolic pathways confirmed the importance of Syntrophomonas species in fatty acids degradation, and also highlighted the presence of protective mechanisms toward the long chain fatty acid effects in bacteria belonging to Clostridiales, Rykenellaceae, and in species of the genera Halothermothrix and Anaerobaculum. Additionally, an interesting transcriptional activation of the chemotaxis genes was evidenced in seven species belonging to Clostridia, Halothermothrix, and Tepidanaerobacter. Surprisingly, methanogens revealed a very versatile behavior different from each other, even among similar species of the Methanoculleus genus, while a strong increase of the expression level in Methanosarcina sp. was evidenced after oleate addition.

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