Microbial activity response to hydrogen injection in thermophilic anaerobic digesters revealed by genome-centric metatranscriptomics - DTU Orbit (09/11/2019)

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The expansion of renewable energy produced by windmills and photovoltaic panels has generated a considerable electricity surplus, which can be utilized in water electrolysis systems for hydrogen production. The resulting hydrogen can then be funneled to anaerobic digesters for biogas upgrading (biomethanation) purposes (power-to-methane) or to produce high value-added compounds such as short-chain fatty acids (power-to-chemicals). Genome-centric metagenomics and metatranscriptomic analyses were performed to better understand the metabolic dynamics associated with H2 injection in two different configurations of anaerobic digesters treating acidic wastes, specifically cheese manufacturing byproducts. These approaches revealed the key-genes involved in methanation and carbon fixation pathways at species level. The biogas upgrading process in the single-stage configuration increased the CH4 content by 7%. The dominant methanogenic species responsible for the upregulation of the hydrogenotrophic pathway in this reactor was Methanothermobacter wolfeii UC0008. In the two-stage configuration, H2 injection induced an upregulation of CO2 fixation pathways producing short-chain fatty acids, mainly acetate and butyrate. In this configuration, the abundant species Anaerobaculum hydrogeniformans UC0046 and Defluviitoga tunisiensis UC0050 primarily upregulated genes related to electron transport chains, suggesting putative syntrophisms with hydrogen scavenger microbes. Interestingly, Tepidanaerobacter acetatoxydans UC0018 did not act as an acetate-oxidizer in either reactor configurations, and instead regulated pathways involved in acetate production and uptake. A putative syntrophic association between Coprothermobacter proteolyticus UC0011 and M. wolfeii UC0008 was proposed in the two-stage reactor. In order to support the transcriptomic findings regarding the hydrogen utilization routes, an advanced bioconversion model was adapted for the simulation of the single- and two-stage reactor setups. This is the first study investigating biogas reactor metatranscriptome dynamics following hydrogen injection for biomethanation and carbon fixation to short-chain fatty acids purposes. The same microbes showed different patterns of metabolic regulation in the two reactor configurations. It was observed an effect of the specialized acidogenic reactor on the overall microbial consortium composition and activity in the two-stage digester. There were also suggested the main species responsible for methanation, short-chain fatty acids production, and electron transport chain mechanisms, in both reactor configurations.

General information
Publication status: Published
Organisations: Residual Resource Engineering, Department of Environmental Engineering, Catholic University of the Sacred Heart, University of Padova
Corresponding author: Treu, L.
Number of pages: 14
Publication date: 2018
Peer-reviewed: Yes

Publication Information
Journal: Microbiome
Volume: 6
Article number: 194
ISSN (Print): 2049-2618
Ratings:
BFI (2018): BFI-level 1
Scopus rating (2018): CiteScore 9.86 SJR 4.466 SNIP 2.545
Web of Science (2018): Indexed yes
Original language: English
Keywords: Anaerobic digestion, Biomethane, CO2 fixation, Cheese wastes, Metageneome assembled genomes, Metagenomics, Metatranscriptomics, Microbial community, Short-chain fatty acids, Syntrophism
Electronic versions:
s40168_018_0583_4.pdf
DOIs:
10.1186/s40168-018-0583-4
Source: FindIt
Source ID: 2440984216
Research output: Contribution to journal › Journal article – Annual report year: 2018 › Research › peer-review