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Methanogenic community shifts during the transition from sewage mono-digestion to co-digestion of grass biomass

Justus Hardegen (1), Adriel Latorre- Pérez (2), Cristina Vilanova (2), Thomas Günther (3), Manuel Porcar (2,4), Olaf Luschning (5), Claudia Simeonov (1), Christian Abendroth (1,4,6)*

(1) Robert Boyle Institut e.V., Jena, Germany.

(2) Darwin Bioprospecting Excellence, S.L., Paterna, Valencia, Spain.

(3) Eurofins Umwelt Ost GmbH, Jena, Germany.

(4) Institute for Integrative Systems Biology (I2SysBio), Paterna, Valencia, Spain.

(5) Bio H2 Umwelt GmbH, Jena, Germany.

(6) Technische Universität Dresden, Chair of Waste Management, Pratzschwitzer Str. 15, Pirna, Germany.

*Corresponding author: Christian Abendroth (abendroth.ca@gmail.com)

Abstract

In this work, liquid and solid fractions of grass biomass were used as co-substrates for anaerobic co-digestion of sewage sludge. The input of grass biomass was increased gradually, and the underlying methanogenic microbiome was assessed by means of microscopy-based cell counting and full-length 16S rRNA gene high-throughput sequencing, proving for the first time the suitability of nanopore-based portable sequencers as a monitoring tool for anaerobic digestion systems. In both cases co-fermentation resulted in an increased number of bacteria and methanogenic archaea. Interestingly, the microbial communities were highly different between solid and liquid-fed batches. Liquid-fed batches developed a more stable microbiome, enriched in *Methanosarcina* spp, and resulted in higher methanogenic yield. In contrast, solid-fed batches were highly unstable at higher substrate concentrations, and kept *Methanosaeta* spp. -typically associated to sewage sludge- as the majoritary methanogenic archaea.

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