

Changes in microbial community metagenome upon adaptation to protein substrate

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Facing energy crisis, the world is in need of green, efficient, carbon-neutral energy sources to replace fossil fuels. Biogas, formed by anaerobic digestion of organic materials, provides sustainable, renewable energy. There is a significant potential in biogas production from industrial waste, partly because waste treatment reduces the environmental impact of these materials and partly because biogas can replace fossil natural gas in all of its applications.

In this work biomethane production from protein-rich waste was studied in 5-litre continuously stirred tank reactor (CSTR) experiments at 37°C. The new generation SOLiD DNA metagenomic sequencing technique was employed to determine the taxonomic distribution and relative abundance of the members of the microbial community. During the anaerobic degradation (AD) fermentations, fed with protein-rich substrates and the sole source of biomass, the composition of microbial community was tested at three time points: at the start, halftime and at the end of the adaptation process. A shift in the population balance was clearly observed as part of the adaptation process to protein-rich substrates. Considering the entire period to adapt the microbial community to this unconventional substrate, the Bacteria domain, and within Bacteria the Firmicutes and Proteobacteria phyla showed the greatest alterations. The classes Clostridia and Bacilli and Gammaproteobacteria, belonging to these phyla, constitute the majority of the Bacteria in the biogas fermentor.

The biogas yield from the substrate (decomposition rate of the protein substrates) increased and both the activities of hydrolyzers and syntrophic acetate oxidizing bacteria (SAOB) were remarkably amplified. The results substantiated that the adaptation of the microbial community to the high protein content substrate is achievable and this modification leads to the intensification of biogas production. The findings extend the range of organic “waste” substrates, which are suitable for renewable energy production and predict routes for rational design of more effective microbial communities for industrial scale biogas production technologies.

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