Monitoring microbial population dynamics in a labscale biogas reactor using flow cytometry

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Abstract

The use of biomass as a renewable energy resource is becoming increasingly important in the substitution of fossil fuels. Over 5000 biogas plants of different scales are already installed in Germany and cover already about 1.5 % of our total energy demand. An upward trend is found worldwide. Biogas reactors contain a highly divers microbial community comprising of Bacteria and Archaea. They are able to degrade complex substrates, ranging from energy crops to organic wastes and distillers grains, to biogas mainly composed of methane and carbon dioxide. Substrate choice, temperature, retention time, pH and the presence of trace metals or noxious compounds are just some factors influencing the community composition and the total reactor performance. So far, most studies only focused on the microbial composition at certain time points using fingerprinting techniques. Differences were found but distinct correlations to total reactor performance could hardly be made. At the moment only little is known about the behaviour of the biogas microorganisms in dependence on the bioreactor scheme. Flow cytometry offers a tool to follow the dynamics of these complex microbial communities as was already shown for wastewater systems. The combination with cell sorting of interesting subcommunities (either very stable or very fluctuating) and their molecular characterisation can help to identify the key organisms behind a stable or unstable process performance. The microbial community in a biogas reactor, run at the German Biomass Research Centre (DBfZ), was investigated over a period of 9 months and first results on the question "How stable is stable – community dynamics in a biogas reactor" will be presented with the aim of understanding the dynamics behind functional stability.

Keywords: biogas, methanogenesis, population dynamics, stability

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