



Changes in microbial communities in a hybrid anaerobic reactor with organic loading rate and temperature



Kankana Kundu, Shilpi Sharma*, T.R. Sreerishnan

Department of Biochemical Engineering and Biotechnology, Indian Institute of Technology Delhi, Hauz Khas, New Delhi 110016, India

HIGHLIGHTS

- ▶ Study of the effect of hydraulic and organic shock load on performance of hybrid anaerobic reactor.
- ▶ Analysis of the transition of archaeal and bacterial community profile to shock loads using 16S rRNA based PCR-DGGE method.
- ▶ Diverse community at 37 °C leads to better tolerance of higher shock load.
- ▶ Different response of microbial community and reactor performance to shocks.
- ▶ Reactors with longer HRT were able to withstand higher organic loads.

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ABSTRACT

Poor understanding of the response of microbial communities to sudden changes in organic and hydraulic loads is one of the major reasons for the inability to prevent operational instabilities in anaerobic reactors. Effect of changes in hydraulic retention time (HRT) and organic loading rate (OLR) on reactor performance and its anaerobic microbial community were investigated in two anaerobic hybrid reactors operated at 37 and 55 °C. HRT was reduced stepwise, while OLR was increased along with influent chemical oxygen demand at fixed HRT until the performance of reactor deteriorated. The profile of archaeal 16S rRNA gene amplicons, resolved by denaturing gradient gel electrophoresis, reflected system status during disturbances. The more diverse archaeal community in the reactor operated at 37 °C showed better performance than the communities present at 55 °C at higher OLR and shorter HRT, suggesting that higher diversity is indicative of more stable operation of reactors despite organic and hydraulic shocks.

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1. Introduction

Anaerobic digestion is an effective method for treating high strength wastes. Its advantages over aerobic process are lower energy requirement, lower sludge generation, and production of methane that can be used as a fuel. A major limitation of anaerobic digestion process is the long duration and instability of their transition phases (starting, re-starting, organic load increase) because of the slow growth rates of anaerobic microorganisms and their sensitivity to perturbations such as organic overloads (Arnaiz et al., 2003; Cresson et al., 2009). The difficulty in retaining slow-growing anaerobic microorganisms in high-rate systems has always been a challenge. But, developments in high rate systems, which enable a significant difference between hydraulic retention time (HRT) and solid retention time (SRT), have brought back attention to anaerobic treatment. In these high-rate systems, the natural capability of anaerobic microorganisms to form aggregates,

with or without solid surface, has been used. This aggregation eventually improves the efficiency of anaerobic treatment systems by increasing biomass retention times (Cresson et al., 2009).

In anaerobic treatment processes, different members of microbial consortia interact in a dynamic manner. The performance of this process remains mostly stable for effluents with steady composition and flow rate; however, in practice domestic as well as industrial effluents are subjected to fluctuations in both quality and quantity of the wastewater, leading to variation in waste loads and flows entering the treatment units. Due to different responses of anaerobic microorganisms to these shock loads, the performance of the reactor deteriorates. Designs of anaerobic wastewater treatment plants are mostly based on engineering aspects, while only minimal knowledge of the structure of microbial communities is involved. As a consequence, the capability to control and predict system disturbances is restricted, leading to sudden failure of reactors in field applications.

Several molecular fingerprinting techniques, such as denaturing gradient gel electrophoresis (DGGE) (Muyzer et al., 1993), have been used to study bacterial and archaeal community in a biogas

* Corresponding author. Tel.: +91 11 26596192; fax: +91 11 26582282.

E-mail address: shilpi@dbeb.iitd.ac.in (S. Sharma).