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Effect of operating temperatures on the microbial community profiles in a high cell density hybrid anaerobic bioreactor

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

Department of Biochemical Engineering and Biotechnology, Indian Institute of Technology Delhi, Hauz Khas, New Delhi 110 016, India

HIGHLIGHTS

- ► Correlation of performance of reactor with microbial structure.
- Temperature specific DGGE fingerprints.
- ► Higher richness and diversity at 37 °C leading to better reactor performance.
- ► Acetoclastic methanogens at 37 °C replaced by hydrogenotrophic methanogens at 55 °C.
- ► Self-immobilized fluidized granules developed and maintained at higher temperatures.

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ABSTRACT

Lack of knowledge about the microbial consortia involved in wastewater treatment at different operating temperatures, is a major reason for failure of anaerobic reactors in field applications. Present study was undertaken to correlate performance of hybrid anaerobic reactors operating at different temperatures (37, 45 and 55 °C) to structures of archaeal and bacterial communities involved. Self-immobilized granules were developed in the reactors continuously fed with synthetic wastewater (10,000 mg COD I⁻¹) and operated at an organic loading rate of 2.22 kg COD m⁻³ day⁻¹ and hydraulic retention time of 5 days. The reactor operated at 37 °C showed the best performance as well as the most diverse microbial community revealed by PCR-denaturing gradient gel electrophoresis analysis using 16S rRNA gene amplicons. Sequences derived from reactors operating at higher temperatures revealed presence of different methanogens, but lesser diversity caused a drop in COD degradation capability of the system indicating successful operation at low loading conditions.

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1. Introduction

Biological wastewater treatment has gained popularity because of its high potential for waste stabilization with minimal impact on environment and ecology. In the context of energy recovery, anaerobic wastewater treatment systems are mostly preferred because of their low energy consumption and low nutrient requirements. Energy recovery in the form of methane is an added attraction. Thus, high strength wastewater can be easily and profitably treated by anaerobic biological systems.

Anaerobic digestion is a biological decomposition process regulated by mutual metabolic interactions among at least four functional groups of microorganisms in the absence of oxygen – hydrolytic, acidogenic, acetogenic bacteria and methanogenic archaea. The first group of microorganisms hydrolyse complex polymeric substances mainly lipids, cellulose and proteins, by extracellular enzymes to fundamental structural building blocks such as glucose and amino acids. The subsequent microbial groups ferment these products to long chain fatty acids, acetate and hydrogen. The acetogenic bacteria convert higher fatty acids to acetate. This acetate and hydrogen along with carbon dioxide is used by methanogens to produce methane. While an efficient treatment process requires all groups of microorganisms to be present in proper balance, the composition of microbial community is determined by a number of selection pressures such as flow rate, wastewater characteristics, pH, temperature, sludge retention time (SRT), nutrient availability and presence of xenobiotics (Leitão et al., 2006).

Temperature plays a major role in anaerobic digestion. There are three temperature ranges generally used for anaerobic digestion, psychrophilic (<25 °C), mesophilic (25–40 °C) and thermophilic (>45 °C) (El-Mashad et al., 2004). Although better reduction of volatile solids and deactivation of pathogenic organisms are the advantages associated with thermophilic digestion, poor effluent quality and residual sludge dewatering capability are matters of concern. Moreover, thermophilic digestion is much more sensitive to

^{*} Corresponding author. Tel.: +91 11 26596192; fax: +91 11 26582282. *E-mail address:* shilpi@dbeb.iitd.ac.in (S. Sharma).

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