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Comparative study of changes in reaction profile and microbial community structure in two anaerobic repeated-batch reactors started up with different seed sludges

Jaai Kim [a], Seungyong Lee [b], Changsoo Lee [a,*]

[a] School of Urban and Environmental Engineering, Ulsan National Institute of Science and Technology (UNIST), UNIST-gil 50, Eonyang-eup, Ulju-gun, Ulsan 689-798, Republic of Korea
[b] R&D Center, POSCO Engineering & Construction Co., Ltd., 36 Songdo-dong, Yeonsu-gu, Incheon 406-840, Republic of Korea

HIGHLIGHTS

- Two anaerobic repeated-batch reactors differing in seed source performed similarly.
- H_2-Utilizing pathway was likely the main route for methanogenesis in both reactors.
- The reactor methanogen communities were likely dominated by *Methanospirillum hungatei* strains.
- Bacterial community structure changed dynamically over cycles in both reactors.
- Bacterial community shifts caused little change in methanogen community structure.

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ABSTRACT

Microbial community structure and dynamics were examined in two anaerobic reactors run in repeated-batch mode to treat whey permeate. Despite being started up using different seeding sources, the reactors showed generally similar reaction patterns and performances. During the repeated-batch operation for three cycles, the overall reaction rate increased with the increase in the initial population size of both bacteria and methanogens over cycles. *Clostridium*- and *Methanospirillum*-related microorganisms were likely the main acidogenic and methanogenic populations, respectively, in both reactors. Bacterial community structure shifted dynamically over cycles, while little change was observed in methanogen community structure throughout the operation. This means that the changes in bacterial community structure changes had little influence on the formation and evolution of methanogen community structure in the reactors. The increased methanogenesis rate with cycles seemed therefore more likely due to the effect of the increase in methanogen abundance rather than the alteration of community structure.

1. Introduction

Anaerobic digestion (AD) has been widely applied to the treatment of organic pollutants due to its ability to produce combustible biogas (mainly methane) while reducing pollution load. Owing to the additional benefit of energy production, increasing attention is being paid to AD in these times of global energy and environmental crisis (Appels et al., 2011). AD is a multi-stage reaction conducted by diverse microbial populations which can be broadly grouped into acidogens and methanogens. Acidogens are a group of bacteria which hydrolyze and ferment complex organic molecules finally to hydrogen and acetate, the major substrates for methane formation, through various fermentation pathways. The acidogenic products are subsequently utilized for the growth of methanogens and converted to methane, whereby pollution load can be finally stabilized. Therefore, extremely diverse microorganisms of different physiological and biochemical types coexist in AD environments and their harmonized activity is necessary for complete decomposition of organic pollutants. The overall performance of an AD process is consequently dependent on the functioning and interactions of acidogens and methanogens involved.

With the development and application of culture-independent molecular techniques that typically target specific nucleic acid sequences, a large number of studies have recently been conducted to investigate microbial community structure and dynamics in anaerobic digesters. Microbial community analysis has been reported in various types of anaerobic digesters run in different operation modes, i.e., continuous and batch modes and their

* Corresponding author. Tel.: +82 52 217 2822; fax: +82 52 217 2819.
E-mail address: cslee@unist.ac.kr (C. Lee).

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