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Evaluation of performance, acetoclastic methanogenic activity and archaeal composition of full-scale UASB reactors treating alcohol distillery wastewaters

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Abstract

Two distinct full-scale upflow anaerobic sludge blanket (UASB) reactors, namely IUASB (143 m^3) and TUASB (476 m^3), treating alcohol (raki) distillery wastewaters were investigated in terms of performance, acetoclastic methanogenic activity and archaeal composition. The TUASB reactor was inoculated with the seed sludge taken from the IUASB reactor. An average of 90% COD removal efficiency at organic loading rates (OLRs) in a range of 6–11 kg COD/m^3 day was achieved in the IUASB reactor. However, 60–80% COD removal efficiency of the TUASB reactor was achieved at OLRs ranging 2.5–8.5 kg COD/m^3 day. Both UASB reactors showed almost the same acetoclastic methanogenic activity (350 and 376 ml CH_4/g VSS day). Distribution of archaeal populations within the two UASB reactors was investigated by denaturing gradient gel electrophoresis analysis of PCR amplified ribosomal RNA gene fragments. Both UASB reactors have shown quite similar archaeal composition (weighted similarity of 83.1%). Predominant archaeal sequences in both reactors belonged to *Methanobacterium formicicum* and *Methanosaeta soehngenii*.

Keywords: Acetoclastic methanogenic activity; Alcohol distillery wastewater; *Archaea*; DGGE; 16S rDNA analysis; UASB reactors

1. Introduction

Upflow anaerobic sludge blanket (UASB) reactors have been widely adopted for treatment of alcohol distillery wastewaters. The application of anaerobic processes in wastewater treatment requires careful operation and monitoring the conventional parameters such as pH, alkalinity, temperature, etc. Generally, little attention has been paid to the composition and activity of the microbial community compared to the conventional parameters during the operation of anaerobic reactors. However, an interdependent microbial community in anaerobic reactors reacts highly sensitively to sudden changes in environmental conditions and any imposed stress may lead to a change in species types, their relative population levels and their activity, which are ultimately reflected in the reactor performance [1]. Therefore, maintenance of active methanogenic populations in an anaerobic reactor is critical for stable performance [2]. Consequently, an understanding of both the microbial ecology and their activity are essential to operate the anaerobic reactors effectively. It is, therefore, necessary to determine the amount of active methanogenic populations in anaerobic reactors. In this respect the specific methanogenic activity (SMA) test gives information about activity of acetoclastic methanogens and also provides information on potential loading capacity and optimum operating conditions of anaerobic reactors [3].

Cultivation-dependent methods are known to be insufficient to characterize in situ the structure and dynamics of microbial assemblages. As a consequence of developments

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in molecular ecology, the application of both qualitative and quantitative molecular methods such as denaturing gradient gel electrophoresis (DGGE) [4] and fluorescence in situ hybridization (FISH) [5], have led to new insights into microbial processes in biological reactors. The DGGE technique provides valuable knowledge of dominant phylotypes within complex microbial communities such as those present in anaerobic reactors. Thus, the microbial population dynamics and species responsible for a specific degradation within the treatment system can be identified. In anaerobic bioreactors, where stability and performance are strongly dependent on complex microbial interactions, this information provides an opportunity to couple the microbial structure and the functional characteristics of the anaerobic reactors [6]. Determining the underlying principles of the structure and function of these complex microbial communities may help to design optimized biological treatment systems; thus process failure may be avoided. This may further make possible the ability to design more efficient anaerobic reactors in terms of loading capacity with higher methane yield.

In this study, therefore, performances of two full-scale upflow anaerobic sludge blanket (UASB) reactors, one was seeded from the other, treating alcohol distillery wastewaters were investigated along with their potential methane production capacities. Archaeal composition in both reactors was investigated using DGGE analysis of the PCR amplified 16S rDNA archaeal sequences followed by partial sequencing.

2. Materials and methods

2.1. Description of UASB reactors

Wastewaters produced from alcohol distillery effluents are treated in two-stage anaerobic–aerobic biological treatment systems located in Istanbul and Tekirdag, Turkey. Flow diagrams of wastewater treatment processes of Istanbul and Tekirdag alcohol distilleries are given in Fig. 1(a) and (b). Each wastewater is pumped through a screen having a pore size of 1 mm, where all anise seeds are retained. The wastewater then goes through a sedimentation tank after which pH, temperature, COD and nutrients, etc. of the wastewater are adjusted to desired levels for anaerobic treatment. 143 m^3 full-scale Istanbul UASB (IUASB) reactor and 476 m^3 full-scale Tekirdag UASB (TUASB) reactor are used as the anaerobic stages. The IUASB reactor

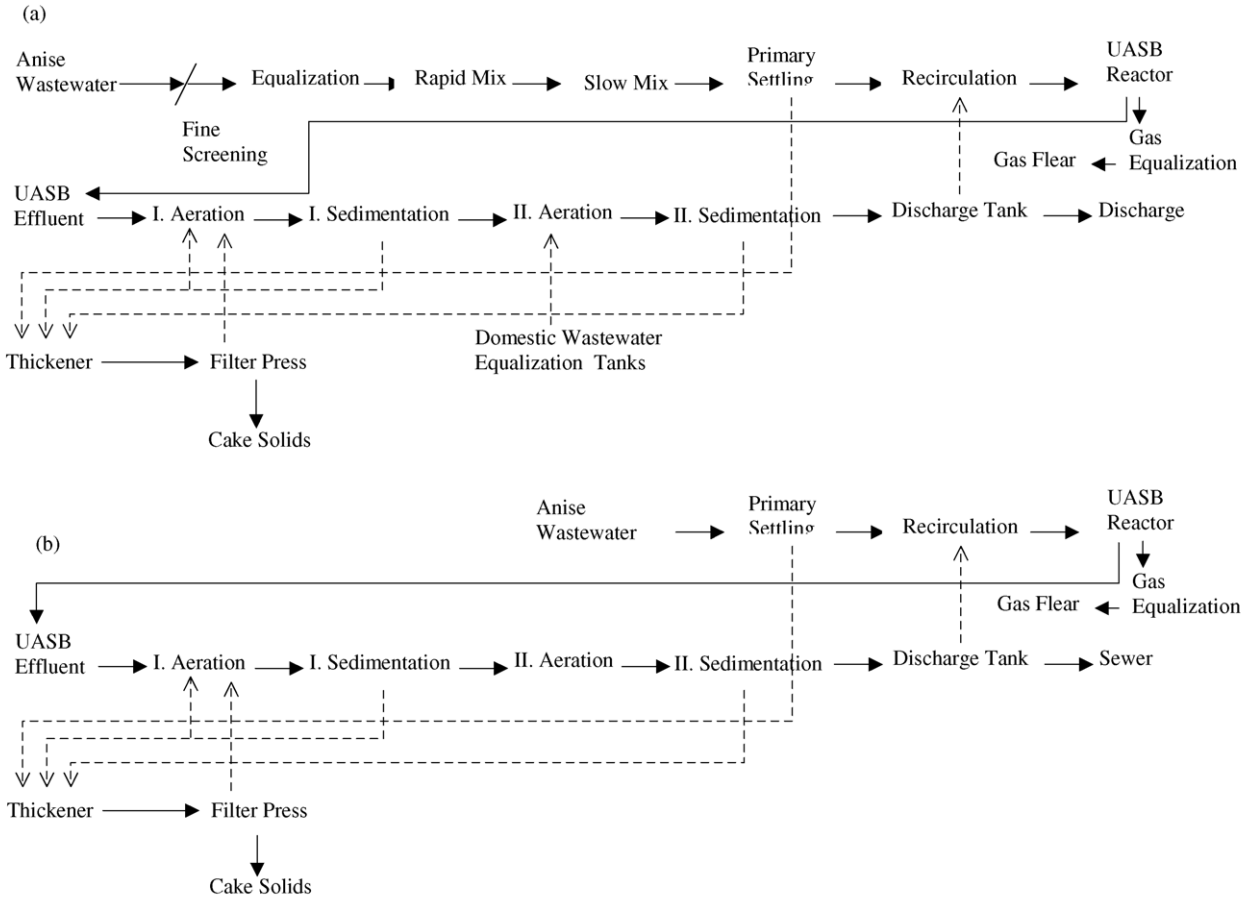

Fig. 1. Flow diagrams of alcohol distillery wastewater treatment plants at (a) Istanbul and (b) Tekirdag.