Abstract

There is potential for the anaerobic baffled reactor (ABR) to be implemented on-site for pre-treatment of coloured wastewaters. The implementation of waste minimisation and cleaner production strategies in industry will result in the production of smaller volumes of concentrated wastewaters. With implementation of the ABR, the concentrated waste stream could be pre-treated, with an acclimated biomass, which should facilitate sufficient degradation such that the effluent could be discharged to sewer for further treatment.

The ABR is a high-rate compartmentalised anaerobic bioreactor, the design of which promotes the spatial separation of microorganisms. The use of molecular techniques to characterise the microbial populations and the dynamics of these populations with time and/or changing operating conditions will add to the current understanding of the process, which is based on the biochemical pathways and chemical analyses. This knowledge will allow for optimisation of the design of the ABR.

The hypothesis of the horizontal separation of acidogenesis and methanogenesis through the ABR was proven. Changes in the HRT affected the operation of the reactor, however, recovery from these upsets was almost immediate and operation of the reactor was stable.

Two synthetic dye waste streams, one food dye (tartrazine) and one textile dye (CI Reactive Red 141), and a real industrial dye wastewater, were treated in separate laboratory-scale ABRs. These investigations showed that successful treatment of a highly coloured wastewater is possible in the ABR. The design of the ABR facilitates efficient treatment of concentrated dye wastewaters by protecting the sensitive methanogens from the inhibitory dye molecules and promoting efficient colour and COD reduction.

The molecular-based method, fluorescent *in situ* hybridisation, allowed the direct identification and enumeration of microbial populations active in the ABR. In all of the reported investigations, there was a definite shift in the microbial populations through the ABR, with a predominance of eubacteria in the first compartments (acidogenesis) and archaea (methanogenesis) in the later compartments. The number of compartments involved in each depended on the strength of the substrate (organic loading rate - OLR). A combination of FISH probing, and the analysis of 98 archaeal 16S rDNA clone inserts provided useful descriptions of the methanogens actively involved within each compartment. These showed a predominance of the *Methanosaeta* spp., particularly in the last compartments of the reactor. Methanogens present in the first four compartments consisted of species of *Methanobacterium* and *Methanospirillum,* a relatively unstudied methanogen *Methanomethylovorans hollandica,* and an unidentified short filamentous species.