Report as of FY2007 for 2006HI159B: "Identification and control of membrane bioreactor biofouling organisms using genetic fingerprinting"

Publications

- Conference Proceedings:
  - Babcock, R.W., Jr.; T. Huang; Y. Chanthawornsawat, 2006, Characterizing biofouling in membrane bioreactors, in Proceedings of the 21st Annual WateReuse Symposium, Hollywood, California.

Report Follows

Problem and Research Objectives

Recycling of wastewater receiving primary treatment could be greatly expanded, saving conventional groundwater for potable uses, if costs of treatment could be reduced. Membrane bioreactors (MBRs) are a relatively new wastewater treatment technology that promises exceptional treatment efficiency and a reduced footprint compared to conventional treatment process trains. However, MBRs are susceptible to biofouling. Biofouling is not well understood but does increase operating pressure, reduce maximum flux (water passed through the membrane), increase recovery cleaning requirements, and possibly reduce total membrane life.

The overall goal of this research is to obtain a better understanding of biofouling in MBRs and methods to control said fouling in order to improve the economics of water recycling. Genetic fingerprinting methods will be developed to identify organisms responsible for biofouling.

Methodology

This study involves long-term operation of two different bench-scale MBRs. One MBR uses flat sheet membrane technology provided by Enviroquip Inc.; it utilizes Kubota membranes with a 0.4 μm pore size. A second MBR uses hollow fiber technology provided by Ionics Corp.; it utilizes Mitsubishi membranes with a 0.4 μm pore size. These bench-scale MBRs have been operated using raw sewage pretreated only by a 3-mm fine screen since the start of the project in March 2006. Operating parameters that have been and will be varied include flux rate (flow per unit area of membrane; 10 and 15 GFD), solids retention time (10 and 20 days so far, and 5 and 40 days to be completed), organic/nutrient loading (raw sewage with/without supplemental organics), and state of oxygenation (high, low, anoxic). Under each set of conditions, steady state is achieved before proceeding to the next set of conditions. Operating and water quality parameters monitored include TMP (continuous on-line measurement), biofilm/cake layer thickness, SMP/EPS carbohydrate and protein fractions (carbohydrates, proteins), viscosity, PSD, soluble COD, and colloidal TOC.

Microbial consortium samples from both mixed liquor and attached biofilms (cake layers) will be collected from the bench-scale MBRs under various conditions. Samples of microbial populations in full-scale conventional activated sludge systems and pilot-scale MBR systems will be collected for comparison. The dominant microbial species will be determined by DNA sequencing of genetic material taken from denaturing gradient gel electrophoresis (DGGE) bands. The sequenced DGGE bands will be compared with information in the GeneBANK database to identify the bacteria responsible for biofouling.

Principal Findings and Significance

We collected a great number of sludge and biofilm samples. A large percentage of these have been processed to extract community DNA, amplified by PCR, and then run through DGGE to determine the species diversity in each sample. We have data that show changes in bacterial speciation over time during different runs and under different fouling conditions. We also have data that show the species in the attached biofilm are different and less diverse than those in the bulk mixed sludge. We are in the process of having a number of the DGGE bands sequenced to determine bacterial types. We are also beginning to try to correlate certain dominant bacteria with operating and fouling conditions as well as water quality parameters. We will collect samples from conventional activated sludge systems for comparison. We will try to determine relationships between dominant microorganisms and water quality parameters as they relate to membrane biofouling.

In the second year of this project (currently under way), we plan to operate the bench reactors, mostly under high-fouling conditions, to get more data on speciation under these conditions. Also, we will monitor pilot- and full-scale MBRs to determine if diversity and speciation are similar or different and look for trends in terms of fouling rates. We will further determine relationships between dominant microorganisms and water quality parameters as they relate to membrane biofouling. We will begin to investigate the morphology and physiology of the identified dominant microorganisms to see if there are biological controls that could be effective to either select for desired organisms or inhibit undesirables. We will develop a chart correlating sets of conditions under which differing degrees of biofouling are expected

(and what microbes will dominate). Finally, we will develop life-cycle costs associated with different degrees of biofouling.

A presentation of project findings, entitled “Understanding and controlling fouling in MBRs,” by R.W. Babcock, Jr. and T. Huang, was made in February 2007, at the 29th Annual Hawaii Water Environment Association Conference, Honolulu, Hawaii.