

## Pyrosequencing Analysis for Characterization of the Microbial Communities in a Pilot-scale Membrane Bioreactor

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Membrane bioreactor (MBR) process is a pressure-driven separation process which has been extensively used in areas of wastewater treatment and reuse. However, the sharp reduction of the flux far below the theoretical capacity mainly due to membrane biofouling has become the detrimental problem in the efficiency and economics of the membrane separation process. Based on the literature review, little has been known about the microbial community in the biofoulants on the fouled membrane as well as the sludge in the MBRs. In this study, the pylogenetic structure of the microbial community residing in three samples (biomass, membrane biofoulants, scum) obtained from a pilot-scale MBR plant in Dukpyung was analyzed by an integrated approach using clone library sequences and metagenome sequence data obtained by 454-pyrosequencing. After trimming by SRA analysis and screening, total 34,031 reads were analyzed. This approach redefines the identification and tracking of the microbial community as well as provides new insight into the microbial composition and complexity of the biofoulants on the fouled membrane of the MBR. Acknowledgments: This research was supported by KEITI (Project No. 192-091-001)