論文の内容の要旨

Abstract of Dissertation

Characterization of Bacterial Community Responsible for Assimilable Organic Carbon Removal in Biological Activated Carbon Process for Advanced Drinking Water Treatment
(高度浄水処理生物活性炭プロセスにおける同化性有機炭素除去に関与する細菌群集の解析)

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Biological stability of drinking water has been gaining considerable attention in the fields of water treatment and water quality management. Bacterial regrowth in drinking water distribution system leads to deterioration of water quality, acceleration of pipe corrosion and the risk of microbial diseases. Assimilable organic carbon (AOC) is considered as the main substrate supporting the growth of microorganisms in distribution system. Ozonation combined with biological activated carbon (BAC) process widely used in advanced drinking water treatment plants achieve to remove AOC to maintain the biological stability of drinking water. However, the mechanisms of AOC removal involved in BAC process has not been elucidated yet, especially bacterial community responsible for AOC removal on BAC. This study aimed to characterize the bacterial community responsible for AOC removal on BAC to understand the biological mechanisms involved in BAC process for AOC removal and proposed the scientific information to develop strategy for biologically stable drinking water control.

In the first part of the study, the removal efficiencies of AOC by BAC process were evaluated and compared between three advanced drinking water treatment plants. In addition, the influences of microbial abundances and community structure associated with BAC were investigated. Ozonation process resulted in the increase of AOC concentrations, especially AOC-NOX fraction which mostly comprise of carboxylic acids. The AOC concentrations were highly reduced after BAC process. The highest AOC reduction was observed in plant A followed by plant C and plant B as in accordance with the cell-specific activities of AOC removal (1.18, 0.91, and 0.27 fgC/cell/hr, respectively). The bacterial community structures attached on BAC-A was different from those on BAC-B and BAC-C. The differences in service time and/or retention time of BAC might have some influences on bacterial community structures and related to the AOC removal performances of BAC.

Three carboxylic acids including formate, acetate, and oxalate were selected as representative of AOC since they were the major by-products after ozonation process for

profound studies on identification of AOC utilizing bacteria on BAC. The biological performances of BAC for carboxylic acids removal were conducted in batch mode. Acetate and formate were rapidly and preferably removed biodegradation only while oxalate was slower and removed through biodegradation as well as physical adsorption. The bacterial communities on BAC were then enriched with 1 mgC/l of carboxylic acids for 30 days and subsequently enriched with 10 mgC/l for additional 14 days using continuous column reactors. Total microbial cells attached on BAC were not increased in all substrates after fed with both 1 mgC/l and 10 mgC/l substrates. The increase of removal rate was observed in run A and run C which enriched with 10 mgC/l formate and oxalate, respectively. Minor changes in bacterial community structures on BAC were observed in formate and acetate enrichment. Total substrate loadings might not enough to enrich bacteria comparing to total biomass on BAC.

Stable isotope probing was applied to identify active bacteria responsible for AOC utilization on BAC. The optimum incubation time for SIP experiment was conducted in batch mode at 10 mgC/l acetate. The separation of $^{13}$C-DNA from $^{12}$C-DNA could be achieved when incubation time was extended to 48 hr and 120 hr. However, cross-feeding of bacteria occurred after incubation for 120 hr. Therefore, the optimum incubation was 48 hr. A small modification for incubation of $^{13}$C-labeled substrate was performed to reduce the substrate concentration closed to environment (0.5 mgC/l) using continuous-feed reactors. Moreover, the influence of different drinking water treatment plant on AOC utilizing bacteria on BAC was investigated by comparing between BAC-C and BAC-D. Bacteria corresponding to T-RF 330 bp were commonly found to be more abundant in $^{13}$C-treatment in all three carboxylic acids and both of water treatment plants comparing to $^{12}$C-treatment. These bacteria were closely related to *Hyphomicrobium sp.* in class of *Alphaproteobacteria.* This bacterium might be the key AOC utilizing bacteria on BAC in advanced drinking water treatment plants and can be used as an indicator to directly evaluate the biological performances of BAC for AOC removal.