論文 / 著書情報
Article / Book Information

題目(和文)	垂直カラムシミュレーターを用いた汚染河口における硫化水素生成機構の解析
Title(English)	Investigation of hydrogen sulfide production in a polluted estuary using a vertical column simulator
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種別(和文)	論文要旨
Type(English)	Summary

（博士課程）
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論 文 要 旨

THESIS SUMMARY

専攻： Department of	生物プロセス　専攻	申請学位（専攻分野）： Academic Degree Requested	博士（工学） Doctor of
学籍番号： Student ID Number		指導教員（主）： Academic Advisor(main)	丹治保典
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要旨（英文 800 語程度）
Thesis Summary (approx.800 English Words)

Sulfide is widely distributed in the aquatic (particularly marine) environment and high concentrations of sulfide compounds are usually present in wastewaters coming from many industrial treatments, such as leather tanning or papermaking. However, it affects inimically to the health and survival of aquatic organisms and causes an odor that humans find intolerable; furthermore, at high concentrations, it may cause damage to human organs. The emission of hydrogen sulfide near the estuary of a regional river (Tokyo, Japan), which is thought to be caused by biological reduction of sulfate in seawater mixing with overflow wastewater, poses a severe environmental problem. This study was done in order to investigate this phenomenon carefully and solve sulfide problem effectively.

In Chapter 2, we set up a vertical column simulator composed of artificial sewage–filled columns and packed-bed columns. In condition 1, H_2S was not detected in the top section, which was supplied with continuous aerated artificial wastewater, whereas H_2S was formed at high concentrations under anaerobic conditions. In condition 2, the supply position for aerated sewage was changed from the top to the middle of the simulator; subsequently, the sulfide concentrations in all sections, especially in sediment region dropped to negligible levels. Furthermore, under each condition, PCR-DGGE and pyrosequencing revealed that the microbial consortia differed significantly following the change of aerated sewage supply position. However, pyrosequencing analysis has advantages such as large number of reads and allowing the identification of minor bacterial components. Based on these results, purging oxygen at the border of water column and sediment could help to solve sulfide problem more effectively and enhance the growth of bacteria involved in sulfide oxidation process.

In Chapter 3, we compared the composition and diversity of communities in estuary rivers with communities in an inland river by applying pyrosequencing method. The results showed that the bacterial communities differ with respect to the biogeochemical properties of the sampling sites and sediment depth. The types of metabolic activities that can be inferred from sequence data suggest the occurrence of complex sulfur cycle in Nomi river. As a result, the diversity within these phyla and on microorganisms that can contribute to sulfur cycle were analyzed and compared with result of the previous research (chapter 2).

In Chapter 4, we presented the preliminary comparison of chemical and biological oxidation rates of sulfide in air-saturated condition with the initial sulfide concentration as 10 mg/L at room temperature. These data reveal that due to very low relative abundance of *Thiobacillus* in the estuary of Nomi river, chemical oxidation rate exceeds biological oxidation rate under examined conditions.

In summary, this research succeeded in partly simulating the condition of the polluted estuary in a regional river (Tokyo, Japan) and in elucidating the relationships between different types of microorganisms vertically in mixed communities, especially the bacteria involving in the sulfur cycle by applying PCR-DGGE and 454 pyrosequencing analysis. By investigating the impact of the oxygen supply position on the chemical properties and bacterial profile, we explored how the biological hydrogen sulfide production could be influenced by various parameters in order to develop the strategy to solve the hydrogen sulfide problem of the regional river. With the presence of hydrogen sulfide produced by SRB (mostly belonged to *Desulfobacterales* order), *Chlorobium phaeobacteroides* BS1, a species of the green sulfur bacteria, was identified as the predominant species under strictly anaerobic sediment part. The supply of oxygen to the transitional zone of the simulator completely inhibited the hydrogen sulfide production in the packed-bed region. However, under the laboratory scale of the simulator, some natural bacteria disappeared and specific bacterial communities have well adapted to these particular conditions. Therefore, the diversity of the bacterial community in the laboratory scale simulator in 2 conditions was significantly lower compared with the river samples. Meanwhile, the bacteria both in the simulator and the environmental samples only distributed some same phyla. Besides, in air-saturated condition, chemical sulfide oxidation is supposed to be significantly faster than the biological sulfide oxidation done by *Thiobacillus* species at the relative abundance as 0.2% of bacterial consortia in Nomi river. However, sulfate, the final oxidation product was obtained with higher concentration in the biological oxidation of sulfate. Besides, biological sulfide oxidation are also conducted by many other species belonged to green sulfur bacteria, purple sulfur bacteria and phototrophic communities such as *Cyanobacteria*, *Chloroflexi* and so on. Therefore, biological oxidation experiments should be also conducted with representative species from these groups in order to give the thorough understanding the nature of sulfide oxidation under effect of oxygen injection. In addition, further investigation of effect of tide condition to microbial distribution and the functional diversity of bacterial communities in these ecosystems is needed to address the impact of these factors on ecosystem function.