学位論文内容の要旨

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学位論文題名

Investigation of bacteria that degrade bacterial cells

（微生物細胞を分解する微生物に関する研究）

Bacteria are one of the important decomposers that decay various organic compounds and release carbon dioxide (CO_2), hydrogen (H_2) and methane (CH_4) to the atmosphere for its recycling. Originally, organic compounds produced from CO_2 mainly by photosynthetic organisms (land plants, bacteria and algae) are eventually broken down to CO_2 by both aerobic and anaerobic microorganisms; finally, comprises the global carbon cycle. This breakdown or digestion process is also called biodegradation which is then categorized to aerobic (in the presence of oxygen) and anaerobic digestion (in the absence of oxygen). Although microorganisms are generally regarded as final consumers/degraders, the production and degradation of organic matter during their growth and after their death, individually, also significantly contribute to carbon cycles in natural environments. These contributed organic compounds resultant from bacterial cells also can be used as carbon and energy sources by bacteria. Many studies already have reported that bacteria contribute to an enormous amount of dissolved organic compounds in aquatic and terrestrial both environments but investigation on bacterial cell degrader bacteria was not studied well. Therefore, bacterial cell degradation by bacteria was investigated in both aerobic and anaerobic environments.

Investigation of peptidoglycan degrading aerobic bacteria

Some investigation in the aerobic environment stated that most of the organic compounds come from the bacterial cell wall (especially peptidoglycan) are considered as a recalcitrant part to be degraded by other bacteria. Peptidoglycan (PG) made from polysaccharide chains cross-linked by unusual peptides containing D-amino acids which is a complex structure and could vary depending on the bacterial species. In addition,

bacterial PG degradation also could be varied depending on the microbial community. Such as, gram-negative bacteria are abundant in the marine environments where gram-positive are abundant in the aquatic environments and it indicates that in that particular environments organic compounds will be derived from the dominant types of bacteria and therefore, a particular degrader assumed to be abundant there. Hence, in this study, I have focused on both terrestrial (soil aerobic community) and aquatic environments (pond water and river water aerobics community) to investigate the bacterial PG degradation and to identify the aerobic PG degrader. Results from the aerobic investigation showed some colony produced a clear zone on the given PG lawn. Phylogenetic analysis, based on 16S rRNA gene sequence analysis was performed to identify the clear zone producing colony. Results disclosed that most of the isolated colonies have very high identity to known bacteria and most of them were from the phylum Actinobacteria, Bacteroidetes, Firmicutes and Proteobacteria. These findings indicate that there are many known bacteria in aerobic environments which are capable to degrade bacterial PG.

Microbial community analysis of anaerobic enrichment cultures supplemented with bacterial whole-cell and peptidoglycan as the sole substrate

Bacterial cell degradation was rarely studied to date in the anaerobic environment although bacteria are abundant there. The degradation of microbial cells is also quite important in some engineering environments. Such as the degradation of waste activated sludge, of which bacterial cells are a major component, by anaerobic microorganisms (i.e., anaerobic digestion) is a well-established strategy to reduce solid waste derived from municipal wastewater treatment in an environmentally friendly manner. Hence, different methanogenic anaerobic the community was enriched using bacterial whole-cell and PG. CH_4 production was measured to speculate the successful degradation in the enriched culture and the result showed that most of the enriched communities produced a much higher amount of CH_4 than the control cultures (without inoculum and/or substrate bacteria), which suggests bacterial cells were degraded by microorganisms in the enrichments. Enriched community analysis revealed that a number of phylogenetically novel and uncultured bacteria, especially in the phyla Bacteroidetes, Chlorobi, Euryarchaeota, Firmicutes, Thermotogae, Verrumicrobia and WWE1 dominated the enrichment cultures, suggesting their possible involvement in anaerobic whole-cell and PG degradation. Further studies are needed to know detail about bacterial cell degradation and the molecular mechanisms for this degradation.