

Study on mechanism of bacterial community changes during autothermal thermophilic aerobic digestion process of human excreta

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(自家発熱型高温好気消化プロセスによるし尿の液肥化における複合微生物の変遷メカニズムに関する研究)

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論 文 内 容 の 要 旨

Autothermal thermophilic aerobic digestion (ATAD) shows its special superiority as a bacterial self-heating process that aerobically transforms human and domestic animal excreta at high temperature into a hygienic and stable liquid fertilizer. Our previous study on the ATAD system of human excreta (HE) in Chikujō, Japan, have shown a unique microbial process, which was divided into 3 distinguishable phases according to its physicochemical properties and bacterial community structures. However, so far the mechanism of bacterial community changes has not been illustrated yet. In this study, to investigate this mechanism, enzymatic activity analysis and microcosm assay with vigorous shaking were performed.

First, microbial and biochemical characteristics of enzymatic powder (EP), a commercially supplied fermentation stimulator, were investigated. Few Gram-positive bacteria were isolated from EP at order of 10^6 CFU/g-EP, and low activities in relation to lysozyme, protease, β -1,4-glucanase, 1,3:1,4- β -glucanase and lipase were detected in EP. Next, lytic enzyme activities of the full-scale ATAD samples were measured, but no significant enzyme activities except for limited lipase activity was detected in any ATAD samples. As a result, lytic enzyme activities including lysozyme, glucanase, protease, and lipase were not sufficient to account for the bacterial community changes in the full-scale ATAD process. Thus to investigate the effect of vigorous shaking on the change of bacterial community structures in the ATAD process, microcosm assay was performed by incubation of original ATAD samples from each phase at the corresponding representative temperatures. During vigorous shaking of initial-phase samples at 30°C, major OTUs related to *Acinetobacter indicus* and *Arcobacter cibarius* dramatically increased along with decreases in several major OTUs. In middle-phase samples at 45°C, we observed a drastic increase of OTUs related to *Caldicellulosiruptor bescii* and *Aciditerrimonas ferrireducens*, together with distinct decreases in several other OTUs. Final-phase samples rather maintained a stable bacterial community at 54°C with major OTUs showing limited similarities to *Heliorestis baculata*, *C. bescii*, and *Ornatilinea*

apprima. These bacterial community changes partly resembled to those of the three phases of the original full-scale ATAD process: the bacterial community structures in samples at the initial and middle phases changed drastically, and ultimately maintained stable with unknown bacteria in the final-phase samples during vigorous shaking incubation at the corresponding temperatures.

In conclusion, a hypothesis was newly proposed that certain physical stresses on the bacterial cells such as high level of oxygen supply or mechanical shearing forces derived from vigorous shaking would be major factors affecting the dynamic changes of bacterial community structures in the unique ATAD process. This study would provide useful information to control the dynamic process of bacterial community structures in a mixed culture system.