Abstract

The microbial commumity of a thermophilic anaerobic cellulose-degrading mixed culture was first analyzed by denaturing gradient gel electrophoresis (DGGE) in this study. Both eubacterial and archaeal communities were analyzed in this study. After comparing the eubacterial DNA fragments obtained from DGGE, most of the nucleotide sequences were similar to those of *Caldocellulosiruptor saccharolyticus*, *Thermoanaerobacter cellulolyticus* and *Anaerocellum thermophilum*, which are all thermophilic cellulose-degrading eubacteria. Two archaeal DNAs of genus *Methanothermobacter* were detected (Arc8 and Arc 9) in our samples. Genus *Methanothermobacter* is known as a thermophilic methanogen. Isolation of these thermophilic methanogens was conducted and their growth conditions were characterized in this study. Successful isolation of a thermophilic methanogen was obtained by using a medium containing yeast extract, formate and an atmosphere consisting of 80:20 of nitrogen-carbon dioxide. The isolate, strain THUT3 was gram-negative, nonmotile, 0.4×3-17 μm, and irregularly curved rods. $H_2/CO_2$ was the only catabolic substrate. The organism was found as an autotrophic methanogen who had an optimal growth pH of 7.0. The optimal temperature for growth was 65 to 70℃. Strain THUT3 grew well with 0-0.65 M of NaCl. The G+C content of strain T3 is 59.4 mol%. Phylogenetic analysis of the 16S rRNA genes of strain THUT3 showed high similarity (98%) to all known species of *Methanothermobacter* genus. A further analysis of DNA-DNA hybridization of strain THUT3 to *Methanothermobacter* species will be

needed to evaluate if strain THUT3 a new species of *Methanothermobacter*.

Key word: thermophilic anaerobic cellulose-degrading mixed culture, DGGE, *Methanothermobacter*, thermophilic methanogen.