

Initial analysis of microbial genes in core samples from Cascadian gas hydrate deposit (IODP#311)

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Submarine gas hydrate deposit has been considered as a future renewed biotic source of energy, despite its impact on global environment. In order to understand the microbial contribution to the cycle of methane in submarine gas hydrate, we aimed to analyze the microbial diversity based on culture-independent molecular techniques. Core samples, with different depths, were collected from gas hydrate deposit at Cascadian continental Margin, off the west coast of Canada, during IODP#311 cruise. The collected core samples were tested for external microbial contamination using both fluorescence microscopy and gas chromatography. Bulk microbial DNAs were extracted from core samples. The polymerase chain reaction (PCR) was applied on three genes. Beside the 16S rRNA gene, the genes *mcrA* and *mmo*, which contribute to biological methane production and methane consumption, respectively, were also amplified and analyzed. New archaeal phylotypes belonging to methane producers were recorded. *mcrA* was detected at several depth layers including surface sediment, MH, and much deeper zone characterized by high C1/C2 ratios. Our primary data indicated that methane-producing microbes were distributed in wide range of depths and not restricted to deeper zones. Molecular quantitative analyses of functional genes *mcrA* and *mmo* are going on in order to measure the microbial activity in the studied core samples. This study will be useful to understand the impact of depth on the diversity of methane-related microbes in submarine gas hydrate deposit.