CHARACTERIZATION OF MOLECULAR BIOMARKERS OF MICROORGANISM RELATED TO METHANE IN GAS HYDRATE-BEARING SEDIMENT OF ULLEUNG BASIN, EAST SEA

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ABSTRACT
Gas hydrate has an importance as new alternative energy in the future and it is necessary to understand microorganism activity related to the production and consumption of the gas hydrate and methane biogeochemical cycle. In this study, we investigated origin and composition of sedimentary organic matter related to the production of gas hydrate in the gas hydrate-bearing core sediment (St.12-2) and non-bearing core sediment (St.21) using stable carbon isotopic ratio and C/N ratio. In addition, the methane related biomarker abundances and their δ¹³C isotopic signatures were determined in the sediment of both cores. Our study showed that the core sediment at St.12-2 has higher concentration of each anaerobic oxidation of methane (AOM) biomarker than St.21. Also, the biomarker peaks are coincided with bacteria community structure of delta-proteobacteria in 12-2 core, demonstrating that sulfate-methane transition zone (SMTZ) should be corresponded to the sediment core depth (130cm~160cm). In 12-2 core, the stable carbon isotope of methane indicates mostly biogenic origin.

Keywords: gas hydrate, biomarker, anaerobic oxidation of methane, delta-proteobacteria, sulfate methane transition zone

INTRODUCTION
The East Sea is a mid-latitude, semi enclosed deep marginal sea (average water depth of 1350m) surrounded by Korea, Japan, and Russia. Structurally, it comprises three basins (the Ulleung Basin, the Japan Basin, and the Yamato