Carbon Isotope Fractionation Associated with Aerobic Microbial Oxidation of Natural Gas

Yane-Shih Wang（王彥士）[c,d], Kok-Yaoh Ng [c] (黃弒耀) , Suh-Huey Wu（吳素慧）[a], Chun-Yin Hwang（黃春鶯）[b], Jong-chang Wu (吳榮章) [a], Cheng-Lung Kuo（郭政隆）[a], Ded-Shih Huang (黃得時) [d] and Steve, S. –F. Yu（俞聖法）[c,d]

[a] Exploration and Development Research institute, Chinese Petroleum Corporation, Miaoli 360, Taiwan. [b] Refining and Manufacturing Research Institute, Chinese Petroleum Corporation, Chiayi 600 Taiwan. [c] Institutet of Chemistry, Academia Sinica, Taipei 115, Taiwan. [d] Department of Chemistry, National Cheng Kung University, Tainan 701, Taiwan

E-mail:ericwang@chem.sinica.edu.tw

Abstract

Carbon stable isotope fractionation associated with the aerobic microbial consumption of propane (C3), *n*-butane (*n*-C4) and *n*-pentane (*n*-C5) of natural gas were analyzed from the gas seepages of Chianan (Chiayi-Tainan) foothill zone and Hualine hot spring field of Taiwan. The aerobic biologic effect on natural gas is related to subsurface structure, the aerobic and anoxic environment of shallow depth and the ecology of microbial species (KINNAMAN et al., 2007). In the study, we focus on the secondary effect by aerobic microbial species during natural gas migration and emission process.

The natural gas samples were analyzed by the method, compound specific isotope analysis (CSIA) using continuous flow Gas Chromatography – Combustion – Isotope Ratio Mass Spectrometry (GC-C-IRMS) (BAYLIS et al., 1994). The results reveal the $\delta^{13}C$ distribution from methane (C1), ethane (C2), propane (C3), *n*-butane (*n*-C4), *i*-butane (*i*-C4), *n*-pentane (*n*-C5) to *i*-pentane (*i*-C5) in natural gas. Combining with the components analysis, we found these gases might be arisen from different types of natural gas such as thermogenic, biogenic and mixed gas. The secondary microbial consumption was estimated by components analysis as well as the carbon stable isotope ratio correlation plot, such as (δC_{iC4}-δC_{nC4}/ δC_{iC4}) (%) with (δC_{iC5}-δC_{nC5}/ δC_{iC5}) (%). The results reveal that four different patterns caused by microbial oxidation implicate with the temporary oxidative trap structure or longer migration pathway near surface. In addition, the commercial natural gas was treated with methanotroph, *Methylococcus capslatus* (Bath) in two different copper concentration which can express soluble methane monooxygenase (sMMO) and particule methane monooxygenase (pMMO) respectively (HANSON and HANSON,

1996) or normal alkane utilized strains, *Pseudomonas oleovorans* (JOHNSON and HYMAN, 2006; SMITH and HYMAN, 2004) and *Pseudomonas putida* C8101 (isolated from crude oil contaminated soil). The carbon oxidation fractionation investigation from pure cultured bacteria can help to build and classify the microbial species and ecology of the target field.

Reference

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