

Bacterial community structure in different subsurface sediments of the southern Kanto Plain

OHKUBO, Satoshi^{1*} ; OHNISHI, Jun-ichi¹ ; A.K. AZAD, Muhammad¹ ; SUDA, Wataru² ; SAITO, Takeshi¹ ; SAITO, Hirota³ ; TAKEMURA, Takato⁴ ; HAMAMOTO, Shoichiro⁵ ; KOMATSU, Toshiko¹

¹Graduate School of Science and Engineering, Saitama University, ²Graduate School of Frontier Science, University of Tokyo, ³Department of Ecoregion Science, Tokyo University of Agriculture and Technology, ⁴College of Humanity and Science, Nihon University, ⁵Graduate School of Agriculture, University of Tokyo, ⁶CREST, JST

Ground source heat pump (GSHP) systems have become popular because of their efficiency in energy conservation and reduction of CO₂ emission. GSHP utilizes the groundwater or subsurface sediment, with an almost constant temperature during the year, as the heat source or sink. Although the temperature changes in subsurface would affect geological structure, groundwater quality, and subsurface microorganisms, very few studies have addressed temperature effects on subsurface biophysical processes. For evaluation of subsurface environmental effects and ensuring overall sustainability of GSHP use, it is essential to investigate how the temperature change may affect the subsurface microbial community structure. Before that, however, it is necessary to know the subsurface microbial community structure that has not yet been affected by temperature change. The purpose of this study was therefore to investigate initial (non-thermal-change-affected) bacterial community structure in deep boring core samples from three different sites in southern Kanto plain. The three sites were the university campuses of College of Humanity and Science, Nihon University (NU; Setagaya-ku, Tokyo), Saitama University (SU; Saitama-city) and Fuchu campus of Tokyo University of Agriculture and Technology (TAT; Fuchu-city, Tokyo). At all three sites, tests of GSHP systems and their environmental response are planned in the near future.

At each site, 10 to 12 sediment core samples were collected from different depths, and whole DNA was extracted from those core samples. PCR-amplified V2-V3 region of bacterial 16S rRNA gene was analyzed by pyrosequencing. The results showed that bacterial community structures of 0-30 m depth were distinctly different among the three boring sites. At the NU site, bacteria belonging to Actinobacteria and Firmicutes accounted for more than half of the whole bacteria population. On the other hand, Chloroflexi, γ -, and δ -proteobacteria were predominant at the SU site, and α -, β -, and γ -proteobacteria were mainly detected at the TAT site. Especially, OTUs assigned to the classes Dehalococcoidetes and Anaerolineae (both belonging to phylum Chloroflexi) were predominant in a wide range of depths at the SU site, and they were particularly detected in former marine sediment. Below 30-m depth, β -, and γ -proteobacteria were predominant at all sites. The relative amounts of some taxonomic groups of bacteria were correlated with depth, pH, electric conductivity of pore water, and particle size distribution. Thus, the variety of bacterial community structure could be attributed to the differences of the depositional ages and environments and/or present subsurface environment at each site. The fundamental data on subsurface bacterial community structures in the southern Kanto Plain from this study will be a useful platform for evaluating the future GSHP-induced temperature change effects on the subsurface environments.

Keywords: subsurface microorganisms, ground source heat pump, next generation DNA sequencing, bacterial community structures