



Changes in bacterial community dynamics associated with submarine groundwater discharge in a coastal area

Eunhee Lee (1), Doyun Shin (2), Hee Sun Moon (1), Sung Pil Hyun (1), Dong-Chan Koh (1), and Kyoochul Ha (1)

(1) Geologic Environment Division, Korea Institute of Geoscience and Mineral Resources (KIGAM), Daejeon, Korea, Republic Of (eunheelee@kigam.re.kr), (2) Mineral Resources Research Division, Korea Institute of Geoscience and Mineral Resources (KIGAM), Daejeon, Korea, Republic Of

Submarine groundwater discharge (SGD) has been recognized as a potentially significant pathway of groundwater and dissolved chemical species in it to the coastal zone. Groundwater has different chemical and biological characteristics compared to seawater; therefore, mixing of the discharged groundwater with seawater can affect the microbial community in near-shore environments. Temporal variability of SGD rates in response to sea level fluctuations (tide, waves) can control the transport of terrestrial materials, periodically altering water quality and microbial communities. In this study, we investigated the impact of the submarine groundwater discharge on the microbial community structure in the coastal water body adjacent to the southern shore of Jeju Island, Korea. Near-shore water samples were collected as a function of tidal stage and subjected to DNA pyrosequencing and statistical community analyses. Phylogenetic classification showed that α -Proteobacteria was predominant in the seawater samples taken at a high tide or away from the coast while relative abundance of β -, and γ - Proteobacteria significantly increased in the samples mixed with groundwater at a flood and ebb tide. The genus level analysis showed that the dominant phlotypes in the seawater samples were *Roseovarius* (40.5%; mean abundance ratio of the samples), *DQ009083_g* (17.1%), and *Glaciecola* (3.7%). Distributions of the bacterial sequences in the mixed water samples showed a remarkable difference between the flood tide and ebb tide. The abundant phlotypes in the flood tide sample were *Candidatus Pelagibacter* (11.0%), *EU801223* (8.4%) and *ABVV* (6.2%) whereas *Shewanella* (34.8%) and *Candidatus Pelagibacter* (5.1%) were in the ebb tide sample. Several phlotypes were detected only in the mixed water samples, including *Sphingopyxis* (0.6%), *Rheinheimera* (1.0%), *Hydrogenophaga* (1.8%), *Colwelliaceae_uc* (0.9%), *Kinneretia* (0.5%), and *Collimonas* (1.2%). These were hypothesized to be originating from the fresh groundwater discharge. Heat map and hierarchical cluster analysis revealed that the mixed water samples were separated from seawater samples, which resulted from significant increase in *Shewanella* sp. (ebb tide sample) and marine bacteria such as SAR11 and SAR116 clade belonging to α -Proteobacteria (flood tide sample). Principal component analysis (PCA) showed that the first two principal components explained about 84% of the variance in the sequence data. The microbial community in the seawater samples formed a distinct cluster. The microbial diversity in the mixed water samples changed depending on the seawater stage, showing similar trends in the phylogenetic classification. Our study results demonstrate that the microbial environment in the coastal zone subject to SGD and sea level fluctuation may change dynamically over short time period (< 1day).

* This study was supported by the Basic Research Projects (14-3211-2) of the Korea Institute of Geoscience and Mineral Resources (KIGAM).