Microbial reduction of Fe(III) and SO_4^- and associated microbial communities in the alluvial aquifer groundwater and sediment

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Agricultural demands continuously increased use of groundwater, causing drawdown of water table and need of artificial recharge using adjacent stream waters. River water intrusion into groundwater can alter the geochemical and microbiological characteristics in the aquifer and subsurface. In an effort to investigate the subsurface biogeochemical activities before operation of artificial recharge at the test site, established at the bank of Nakdong river, Changwon, South Korea, groundwater and sediments were collected from the well cluster.

Laboratory incubations of the groundwater containing portions of sediments indicated microbial reduction of Fe(III) and sulfate, as evidenced by on site measurement of Fe(II) and sulfide. The incubated groundwaters were from 10 and 33 m below ground surface (bgs) from a well, MLW2, with distictively separated feature of electrical conductivities of ~200 and ~6000 μS/cm, respectively. The sulfate concentratoins were also different with ~0.6 and ~1.5 mM in 10 and 33 m groundwaters. There were one or two redox transition zones according to the well locations, and the subsurface was mostly in anoxic condition by depth of approximately 33 m bgs. Regardless of addtiion of organic carbons (lactate and acetate), the groundwater with residual sediments showed rapid reduction of Fe(III) and sulfide within 5 days in the anaerobic condition, wheareas autoclaved groundwaters remained the same with no obvious increase of Fe(II) or sulfide. Although X-ray diffraction, X-ray photoelectron spectroscopy, and transmission electron microscopy were not able to identify any sulfide mineral in the reduced sediments, it was obvious sulfide was generated by microbial sulfate reduction. Microbial community analysis performed on the incubations at three time points by MiSeq sequencing and Mothur processing showed increase of *Deltaproteobacteria* and phylum *Acidobacteria*, but decrease of *Betaproteobacteria*. Interestingly, *Clostridia* increased only in the presence of organic carbons addition.