Influences of Geological and Environmental Factors on Biostimulation at a PCE-Contaminated Site in Taiwan

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Background/Objectives. Chlorinated solvent contamination is a significant issue in Taiwan with over 165 affected sites and only 19 successful remediated cases. Recent advances in site characterization and molecular biology tools (MBTs) have shifted the paradigm for bioremediation, however the use of MBTs for soil and groundwater remediation is still new in Taiwan. Nonetheless, it also presents an opportunity for Taiwan EPA to establish the domestic guidelines for bioremediation. In this study, a PCE-contaminated site was selected to demonstrate the utilities of MBTs for bioremediation. From the historical groundwater monitoring data, it was hypothesized that dechlorinating bacteria was present in this area and substrates were selected based on geological information to stimulate microbial activity.

Approach/Activities. In addition to the old monitoring well, three injection wells were constructed downstream of the source area and new monitoring wells were constructed downstream of injection wells. Additional hydrogeological survey was also completed during well construction. During the ten months pilot study, sodium formate/EVO substrates were injected every 2 to 3 months (total three injections). In addition to groundwater analysis, PCR and qPCR assays targeted on *Dehalococcoides* genus bacteria (Dhc) 16S rRNA gene or vcrA/bvcA genes were conducted to demonstrate the method applicability for Taiwan EPA.

Results/Lessons Learned. Decreasing chlorinated compounds concentrations and detection of ethene were observed in injection wells but not in the upstream monitoring well, which suggested that biostimulation is effective for injection wells. On the other hand, chemical analysis of the new monitoring wells showed that the impacts of substrate supply on the changes in monitoring wells' environmental factors or chlorinated compounds concentrations were inconclusive. One reason could be the high permeability at this site therefore rapid groundwater replenishment which had diluted the impacts of substrates on monitoring wells. Using the empirical formula proposed by Lu et. al. (2006), results indicated that the probability to detect Dhc in injection wells were higher than monitoring wells. Identical trends were also observed for qPCR targeted on Dhc 16S rRNA genes, suggested that substrate injections indeed altered the subsurface environment and favored Dhc prosperity. Interestingly, we failed to amplify known bvcA or vcrA genes though Dhc was detected, which implied possible presence of novel VC reductase and worth further research.