

USE OF MESSENGER RNA TO PREDICT MICROBIAL DEGRADATION KINETICS – DEVELOPMENT OF A NEW CONCEPTUAL MODEL FOR VINYL CHLORIDE DECHLORINATION BY DEHALOCOCCOIDES

Julie Chambon, Technical University of Denmark, +4545251413, jccc@env.dtu.dk

1. Jacob Baelum, Geological Survey of Denmark and Greenland
2. Julie Chambon, Technical University of Denmark
3. Philip J. Binning, Technical University of Denmark
4. Poul L. Bjerg, Technical University of Denmark
5. Troels Laier, Geological Survey of Denmark and Greenland

Reductive dechlorination, where trichloroethylene is sequentially degraded to ethene (through cis-dichloroethylene (cis-DCE) and vinyl chloride (VC)) by the specific degrader Dehalococcoides, occurs in the bioremediation of contaminated sites containing chlorinated solvents. The microbial degradation kinetics for this process are commonly simulated by an empirical Monod kinetics model, which often fails to accurately describe substrate degradation and microbial growth under different experimental conditions. The recent development of new molecular tools opens the possibility for improving the conceptual model of microbial degradation kinetics, taking into account the processes occurring at the cell scale. In particular some functional genes responsible for reductive dechlorination have been identified (*vcrA*, *bvcA*, *tceA*, etc...) and can be measured during sequential degradation. In Dehalococcoides cultures, the transcription of messenger RNA (mRNA) for the functional gene (*vcrA*, *bvcA* or *tceA*, etc...) controls the production of the enzyme responsible for dechlorination of VC to ethene. This means that the mRNA concentration for the functional gene can be used as a measure of the activity of a specific gene and as biomarker for reductive dechlorination.

In this study, a model was developed, which couples the dynamics of the system at a macroscopic level (VC degradation and bacteria growth) and at the molecular level (mRNA concentration). In the model, the presence of VC activates two regulatory loops, one responsible for halorespiration (degradation of VC to ethene) and one responsible for bacterial growth (carbon metabolism). The transcription of mRNA of the functional genes is up-regulated by VC. The produced mRNAs code then for the production of two distinct enzymes, responsible for VC degradation and specific bacterial growth, respectively. The activation, transcription and production processes are modeled using kinetics consistent with the recent literature. Such a model is a first attempt to combine transcript numbers with degradation and specific growth for reductive dechlorination.

The model is compared with experimental data, where cis-DCE or VC were introduced in batch containing sediments, groundwater and dechlorinating culture. Chlorinated solvents, Dehalococcoides, specific genes (*vcrA* and *bvcA*) and their gene expressions (mRNA) were measured regularly during sequential dechlorination. Laboratory results show that mRNA transcript levels of the functional genes were correlated with VC degradation. The modeling results were found to be consistent with observed data for chlorinated solvents, mRNA (*vcrA* and *bvcA*) and biomass concentration (Dehalococcoides).

Further experiments and modeling will be required to verify the conceptual assumptions developed in this study and improve the description of the control mechanisms occurring at the molecular scale.