



Microbial Degradation of Propylene Glycol – Modelling Approach of a Batch Experiment

Annette Dathe (1), Perrine Fernandez (2), Lars Bakken (2), Esther Bloem (1), Helen French (2,1)

(1) NIBIO, Norwegian Institute of Bioeconomy, Environment and Climate Division, Ås, Norway (annette.dathe@nibio.no),

(2) Norwegian University of Life Sciences, Department of Environmental Sciences, Ås, Norway

De-icing chemicals are applied in large amounts at airports during winter conditions to keep the runways and aircrafts ice-free. At Gardermoen airport, Norway, most of the applied chemicals can be captured, but about 10 to 20 % infiltrate into the soil along the runways and during take-off. While the commonly used propylene glycol (PG) is easily degradable by local microbial communities, its biological oxygen demand is high, anoxic zones can develop and soluble Fe⁺² and Mn⁺² ions eventually can reach the groundwater. The objectives of the presented study are to quantify the mechanisms, which control the order of reduction processes in an unsaturated sandy soil, and to test whether measured redox potentials can help to determine underlying biogeochemical reactions.

To investigate the mechanisms of microbial degradation, the water phase of soil samples from Gardermoen Airport was replaced by deionized water with 10 mMol PG or 10 mMol glutamate and the samples were incubated at 10°C for about two weeks. The gas phase was sampled and analyzed automatically every three hours. Microbial degradation of the substrate (PG or glutamate) was modelled following a Monod kinetics using the FME (Flexible Modelling Environment) package of R (Project for Statistical Computing). The model was calibrated against measurements of O₂ depletion and CO₂ production. The initial concentrations of O₂, CO₂ and PG or glutamate are known and microbial yields and stoichiometric constants can be calculated from the measurements. Parameter values for the initial microbial population size, maximum microbial growth rate, the half saturation constant, and microbial degradation and respiration rates were fitted using the FME package. The model accounts for carbon from the substrate (PG or glutamate) incorporated into the biomass. Results are promising, but because of the large number of parameters needed to fit a Monod kinetics it is challenging to accurately model a whole redox sequence. The ultimate goal of implementing PG degrading processes into a soil water transport model is still a challenge, and simpler approaches like a first- and second order kinetic are investigated and compared to the behavior of the Monod kinetic.