

Understanding Syntrophies within Methane Oxidizing Microbial Consortia: integrating Genome Scale Metabolic Models and Reactive Transport

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Project Goals:

The overarching goal is to expand the understanding of interactions and fundamental activities involved in cycling of carbon and nutrients by syntrophic methanotrophic archaeal-bacterial consortia and associated viruses in anoxic sedimentary environments. Specific objectives are to (1) quantify energy and nutrient exchange [e.g., nitrogen (N), phosphorus (P), iron (Fe) and vitamins] within AOM consortia and between ANME-bacterial partners; (2) identify virus-host interactions associated with AOM and assess C and N transfer through viruses in methane - impacted sediment ecosystems; (3) model energy and nutrient exchange in AOM consortia and viral-host interactions (i.e., viral activity), and their environmental distribution patterns.

Abstract:

Understanding the cycling of carbon and nutrients in the sediment environments requires an accounting of the feedback between microbial activities and environmental conditions. We approach this through the development of (1) flux balance community metabolic models consisting of methanotrophic archaea (ANME) and sulfate reducing bacteria (SRB) and (2) a reactive transport model that establishes a connection between processes at the pore scale and the macroscopic environment.

To build a community flux model, we started with the construction of flux balance models of ANME and SRB individually using ModelSEED in the DOE Systems Biology Knowledgebase (KBase) platform (www.kbase.us). ANME microbes are related to methanogenic bacteria but these organisms support “reverse methanogenesis” as the biochemical model for methane oxidation pathway and eventually for defining syntrophy. Towards this end, we curated pathways and model templates for archaeal microbes in our latest build of the ModelSEED genome-scale model reconstruction tool. The ModelSEED now has an archaea template with an archaea-specific biomass reaction and a more complete representation of archaeal metabolic pathways. On average, models of archaeal species constructed by the ModelSEED have 150 additional genes compared to before our curation efforts. To correctly mimic methane utilizing consortia behavior, flux constraints were also adjusted to ensure proper implementation of ANME behavior with respect to the flow of electrons along the methanogenesis pathway. In addition to archaeal template, significant progress was also made to improve the representation of the bacterial sulfur reduction pathway in the ModelSEED, curating the reactions and annotations based both on literature and

experimental data. This resulted in the addition of at least ten new reactions and unique annotations in a single sulfate reduction pathway. We will apply this improved ModelSEED tool to construct models for exemplar ANME and SRB strains assembled and binned from metagenomic data collected for this project. Presently, we are combining these models together in community flux simulations, while integrating transcriptomic data, to predict potential trophic interactions between various ANME and SRB strains under various conditions. Ultimately, these predictions will be tested in the reactive transport simulations described below, as well as new experimental studies.

To establish a connection between processes at the pore scale and the macroscopic environment, ongoing work aims at integrating microCT and multi-model imaging analysis into models that resolve the pore structure of carbonate rocks formed due to the alkalinity produced in the anaerobic oxidation of methane. CT scans of the rocks are collected through an x-ray microscope at an 8-micron isotropic resolution for the modeling component. Select, higher resolution scans are also collected at 0.8 microns for resolution of smaller pore network structures and the biomass of interest. This structural information is then being used to estimate the residence time distribution and local biogeochemical conditions that result from and shape niches for microbial metabolism.

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