

Integrated Biogeochemical Modeling of Microbial Consortia Mediating Anaerobic Oxidation of Methane in Dynamic Methane Hydrate-Bearing Sediments

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Abstract: Methane hydrate-bearing marine continental margin sediments are estimated to contain up to 2000 Pg carbon as methane, a potent greenhouse gas. This methane is released upon hydrate dissociation, dissolving into sediment pore water and migrating towards the sediment-seafloor interface; at which point it may enter the water column and potentially contribute to increasing atmospheric greenhouse gas concentrations. However, anaerobic oxidation of methane (AOM) mediated by consortia of anaerobic methanotrophic archaea and sulfate-reducing bacteria (ANME-SRB consortia) accounts for the oxidation of more than 90% of dissolved methane fluxing through methane hydrate-bearing marine continental margin sediments. Despite the biogeochemical significance of AOM, little is known about the cellular-level function of ANME-SRB consortia or the response of these consortia to changes in methane flux. Obtaining a deeper understanding is particularly important at the moment since warming caused by global climate change is expected to gradually induce methane hydrate instability, thereby increasing the flux of dissolved methane through hydrate-bearing continental margin sediments.

We propose to develop a coupled metabolic model of an ANME-SRB consortium in order to elucidate intercellular interactions between microbial partners within the consortium and predictively analyze how these consortia respond to changes in sediment methane flux. We will accomplish this by performing whole-genome shotgun sequencing on environmental isolates (using EMSL and JGI resources) and developing a novel metabolic model calibration technique based on metatranscriptomic (JGI), metabolomic (EMSL), and geochemical datasets obtained from sediments experiencing a range of methane flux regimes. The resulting dataset and model will be used to investigate metabolite transfer within ANME-SRB consortia, the biochemical mechanism of AOM, and the relationship between methane flux and the rate of AOM.

In addition, we propose to couple the ANME-SRB consortia metabolic model to a geochemical reactive-transport model of methane hydrate-bearing sediments through the AOM reaction terms in each model. This integrated biogeochemical model, informed by predictions of methane hydrate dissociation under anticipated future climate conditions, will be used to improve long-term predictions of methane efflux from methane hydrate-bearing sediments.

We anticipate that our model will demonstrate a novel application of 'omics datasets and open the way for metabolic modeling of a range of environmental microorganisms, including those involved in carbon, nutrient, and contaminant cycling. The results of this study will also provide a framework for development and testing of new hypotheses about the cellular-level function and biogeochemical roles of ANME-SRB consortia. Finally, we anticipate that our integrated biogeochemical model may be integrated into future global- and regional-scale models of carbon cycling and greenhouse gas emissions.