

Microbial Interactions in The Anaerobic Oxidation of Methane: Model Simulations Constrained by Process Rates and Activity Patterns

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Project Goals: This research is focused on evaluating potential mechanisms governing anaerobic oxidation of methane (AOM) within the archaeal-bacterial consortia in marine sediments. We simulate the activity of AOM in microbial aggregates for methane oxidizing archaea, with electron transfer through diffusion of dissolved molecules to the bacteria which reduce sulfate (SRB-MIET), the disulfide mechanism in which ANME archaea coupling methane-oxidation to sulfate-reduction directly and DIET (direct interspecies electron transfer). We compare the resulting methane oxidation rates and activity distribution patterns to observational data from samples from seeps at Hydrate Ridge off the coast of Oregon, USA, and explore the effect of consortia size, the intra-consortium spatial distribution of archaeal and bacterial cells, and pH variations and the sensitivity towards poorly constrained model parameters. These model simulations are analyzed in the context of likely interactions between the archaea and bacteria in the light of this process-based quantitative analysis.

Abstract text. Anaerobic oxidation of methane (AOM) describes the conversion of methane to CO₂ in the absence of oxygen, and in marine sediments is commonly associated with the reduction of sulfate. AOM in marine sediments is estimated to consume about three-quarters of the global net methane emission to the atmosphere, thus acts as a significant sink for methane, a greenhouse gas with a warming potential ~25 times that of CO₂. However, the details of the physiological mechanism underlying AOM are still not completely understood. For microbial consortia consisting of archaea and bacteria, classical syntrophic electron transfer through the exchange of solutes (MIET) was proposed early on, where H₂, formate, acetate, have been considered as intermediates that diffuse from methane oxidizing archaea to sulfate reducing bacteria. Alternatively, Milucka et al. (2012) proposed the exchange of disulfide, produced by ANME archaea coupling methane-oxidation to sulfate-reduction directly and consumed by associated sulfur disproportionating bacteria. More recently, DIET has been proposed as a principal mechanism responsible for electron transfer in ANME-SRB consortia (McGlynn et al. 2015, Wegener et al. 2015). It has been shown that AOM by ANME-2 archaea in deep-sea sediments can be catabolically and anabolically decoupled from sulfate-reduction (Scheller et al. 2016).

We expand on preliminary modeling efforts (Orcutt and Meile 2008; McGlynn et al. 2015) by accounting for the effects of substrate availability on microbial activity, reaction energetics and chemical dynamics in a spatially explicit environmental context. A three-dimensional reaction transport model is implemented to evaluate these potential mechanisms governing AOM within the archaeal-bacterial consortia. In our model, each of these syntrophic mechanisms was implemented in a reactive transport model and the simulated activities were compared to empirical data for AOM rates and intra-consortia spatial patterns of cell-specific anabolic activity determined by FISH-nanoSIMS.

Simulated rates based on MIET were limited by the build-up of metabolites, making the reaction energetically unfavorable. The disulfide and DIET pathways yielded AOM rates that were consistent with measured values and produced intra-consortium anabolic activity distributions consistent with cell specific nanoSIMS data. Factors that significantly impacted DIET simulation results included the AOM rate constant, the concentration of redox molecules involved in cell-to-cell electron transport, and the relative contribution of conduction to the total exchange of electrons between microbial partners. Our simulations predict that electron transport and changes in pH caused by methane oxidation affected AOM only at rates exceeding those reported from methane seep environments. However, additional simulations with artificially accelerated proton diffusion allowed for higher rates, indicating the potential role of pH variations to limit AOM at higher rates and large aggregates. Consistent with these observations, our HS_2^- and DIET simulations suggest that AOM rates are largely unaffected by the spatial distribution of bacterial and archaeal cells. We conclude that the comparison of our modeling results with the intra-aggregate activity patterns are consistent with observational data presented by McGlynn et al. (2015) and Wegener et al. (2015) pointing towards DIET as a likely the pathway for electron transport within AOM consortia.

References

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