Microbial Interactions at Micro-scale and Pore-scale Revealed by Process-based Reactive Transport Modeling

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Project Goals

The overarching scientific goal of this multidisciplinary research project 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.

The focus of this work is the metabolism of AOM consortia and microbial interactions with the environment. We present a three-dimensional model that simulates microbial activities in methane-oxidizing consortia and is validated using co-registered FISH-nanoSIMS observations [1]. Model results show that direct interspecies electron transfer (DIET) between archaeal and bacterial partners yields cell-specific activities that are consistent with observations, with little impact of the spatial distribution of bacterial and archaeal cells at commonly observed aggregate sizes (diameter 3 - 25 μm). Next, we explore the controls on interspecies electron transport of anaerobically methane-oxidizing consortia at a larger aggregate size [2]. Our simulations of metabolic interactions through DIET showed that ohmic resistance and activation loss are the two main factors causing the declining metabolic activity, where activation loss dominated at distance < ~6 μm. These simulations indicated that bacterial cells remain metabolically active at distance < ~30 μm from the archaea-bacteria interface, suggesting a maximum spatial distance between segregated syntrophic partners.

Moreover, we further expand our understanding of extracellular electron transfer in electroactive biofilms [3]. A one-dimensional reactive transport model representing cellular metabolism across a *Geobacter sulfurreducens* biofilm growing on an electrode is established to synthesize existing knowledge and provide a quantitative framework of the extracellular electron transfer that may guide further experimental studies. The model is able to reproduce high-resolution activity measurements under different anode potentials. At high anode potential (+0.24V), two metabolic activity peaks - one near the electrode and another one further away from the electrode – are simulated, consistent with observations using nanoSIMS. Our model attributes this to H^+ accumulation close to

the electrode, negatively impacting metabolic activity. The second peak approx. ~12 μm um away from the anode surface, is attributed to a shift between two redox-active systems allows *G. sulfurreducens* cells to respond to external electric potential.
Lastly, the role of heterogeneous distribution of microbial aggregates at the pore scale for upscaled microbial reaction rates is investigated. Our pore-scale reactive transport simulations reveal that the accuracy of macroscopic rate estimates depend strongly on the flow conditions and reaction kinetics, and to a lesser extent on the distribution of microbial aggregates [4]. Our modeling efforts further evaluate the physicochemical conditions suitable for microbial processes mediated by signaling molecules [5]. Modeling results show that advection dilutes signaling molecules so that faster flow conditions require higher microbial densities, faster signal production rates, or higher sensitivities for effective communication through signaling molecules. We present approximate analytical solutions of the advection-diffusion-reaction equation that allow to quantitatively estimate the effective communication distances amongst multiple microbial aggregates without further numerical simulations.

References

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